

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: December 19, 2001, 16:22:42 ; Search time 88.82 Seconds
(without alignments)
24.014 Million cell updates/sec

Title: US-09-202-104A-11
Perfect score: 146
Sequence: 1 EMGPRSTPSLTAKVAVLVKRFQNSPAD 28

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

hed: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: p1r1:
2: p1r2:
3: p1r3:
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	146	100.0	468	1 A41242	interleukin-6 rece
2	72	49.3	440	2 J01014	interleukin-6 rece
3	72	49.3	460	2 J10145	interleukin-6 rece
4	70	47.9	462	1 A57986	interleukin-6 rece
5	56	38.4	242	1 D82609	hypothetical prote
6	50	34.2	189	1 LNRBC1	pulmonary surfacta
7	50	34.2	204	2 C40839	hypothetical prote
8	50	34.2	413	2 T02693	S-receptor kinase
9	49	33.6	636	2 T06793	receptor kinase ho
10	49	33.6	912	2 S59861	band 3 anion trans
11	49	33.6	918	2 S24318	probable 5'-methyl
12	48	32.9	265	2 A71056	hypothetical prote
13	48	32.9	269	2 T24637	wax synthase [limp
14	48	32.9	352	2 T48903	hypothetical 73.3k
15	47	32.2	646	1 G06C85	hypothetical prote
16	47	32.2	646	1 G85989	hypothetical prote
17	47	32.2	938	2 A56731	chromatin assembly
18	46.5	31.8	374	2 B82488	hypothetical prote
19	46.5	31.8	384	2 C64752	YagA protein - E3c
20	46.5	31.8	455	1 A71251	DNA repair protein
21	46.5	31.8	832	1 J0V1VA	DNA-directed DNA P
22	46	31.5	231	2 T35121	hypothetical prote
23	46	31.5	257	1 S32931	sensor protein sph
24	46	31.5	375	2 T19038	hypothetical prote
25	46	31.5	1049	2 A27079	hypothetical prote
26	45.5	30.8	1047	2 T16203	hypothetical prote
27	45	30.8	140	2 E72505	hypothetical prote
28	45	30.8	179	2 F71469	probable peptidyl
29	45	30.8	258	2 T00311	hypothetical prote

30	45	30.8	265	2 D75085	methylnucleoside
31	45	30.8	272	2 S03412	hypothetical prote
32	45	30.8	272	2 T44484	conserved hypothet
33	45	30.8	272	2 C85602	unknown protein in
34	45	30.8	272	2 D85653	unknown in IS600 f
35	45	30.8	572	1 FOHYH	retrovirus-related
36	45	30.8	572	1 T15059	hypothetical prote
37	45	30.8	855	2 B75191	probable ATP-depen
38	45	30.8	1069	2 T00377	KRA0642 protein -
39	45	30.8	1489	2 S60416	DNA helicase YGL15
40	44.5	30.5	161	2 T14817	pathogenesis-relat
41	44.5	30.5	187	2 A45878	hypothetical prote
42	44.5	30.5	402	2 S11772	polygalacturonase
43	44.5	30.5	402	2 S11773	polygalacturonase
44	44.5	30.5	406	2 J01219	polygalacturonase
45	44.5	30.5	415	2 T13651	hypothetical prote

ALIGNMENTS

Sequence Comparison

RESULT 1
A41242
Interleukin-6 receptor precursor - human
N:Contains: Interleukin-6 receptor, soluble form
C:Species: Homo sapiens (man)
C:Date: 27-Mar-1992 #sequence revision 02-Dec-1994 #text-change 21-Jul-2000
C:Accession: A41242; J00080; S17468; A61459; S14621
R:Yamasaki, K.; Taga, T.; Hirata, Y.; Kawasishi, Y.; Seed, B.; Taniguchi, R.; Yamazaki, K.; Taga, T.; Hirata, Y.; Yawata, H.; Kawanishi, Y.; Seed, B.; Taniguchi, Science 241, 825-828, 1988
A:Title: Cloning and expression of the human interleukin-6 (BSF-2/TNFbeta 2) receptor
A:Reference number: A41242; M01D:8505347
A:Accession: A41242
A:Molecule type: mRNA
A:Residues: 1-468 <YAM>
A:Cross-references: GB:M20566; NID:933845; PIDN:CAA31312.1; PID:933846
R:Yamasaki, K.; Taga, T.; Hirata, Y.; Yawata, H.; Kawanishi, Y.; Seed, B.; Taniguchi, Proc. Jpn. Acad. 64, 209-211, 1988
A:Title: Molecular structure of Interleukin 6 receptor.
A:Reference number: J00080
A:Accession: J00080
A:Molecule type: mRNA
A:Residues: 1-468 <YAM>
A:Cross-references: EMBL:X58298; NID:932580; PIDN:CAA41231.1; PID:932581
A:Experimental source: hepatoma cell line HepG2
R:Novick, D.; Engelmann, H.; Wallach, D.; Rudinstein, M.
J. Exp. Med. 170, 1409-1414, 1989
A:Title: Soluble cytokine receptors are present in normal human urine.
A:Reference number: A61459; M01D:90010793
A:Accession: A61459
A:Molecule type: protein
A:Residues: 20-49 <NOV>
C:Comment: Through this receptor, interleukin-6 induces proliferation, activation, an
C:Comment: This growth factor receptor does not have a tyrosine kinase domain.
C:Genetics:
A:Gene: GDB: IL6R
A:Cross-references: GDB:127966; OMIM:147880
A:Map position: 1q21-q21
C:Superfamily: ciliary neurotrophic factor receptor; cytokine receptor homology; immu
C:Keywords: acute phase; cytokine receptor; glycoprotein; transmembrane protein
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-468/Product: interleukin-6 receptor #status predicted <EXT>
F:20-468/Product: interleukin-6 receptor #status predicted <EXT>
F:40-98/Domain: immunoglobulin homology <IMM>
F:121-309/Domain: cytokine receptor homology <CRS>
F:364-386/Domain: transmembrane #status predicted <TM>

F:387-468/Domain: intracellular #status predicted <INT>
F:387-468/Disulfide bonds: #status predicted
F:55,93,221,245,350/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 100.0%; Score 146; DB 1; Length 468;
Best Local Similarity 100.0%; Pred. No. 1,6e-14;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EWGPRSPSLTKAVLVKRFQNSPAED 28
DB 133 EWGPRSPSLTKAVLVKRFQNSPAED 160

RESULT 2

JL0144
Interleukin-6 receptor precursor (clone lambda p1) - mouse
C:Species: Mus musculus (house mouse)
C>Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 21-Jan-2000
C:Accession: J10144
R:Baumann, M.; Saito, M.; Yamasaki, K.; Taga, T.; Hirano, T.; Kishimoto, T.
J. Biol. Chem. 265, 19853-19862, 1990
A:Title: Functional murine interleukin 6 receptor with the intracisternal a particle gene
A:Reference number: J10144; MUID:90278354
A:Accession: J10144
A>Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-440 <SUG>
A:Cross-references: GB:X51976; NID:953548; PIDN:CAA36238.1; PID:953549
C:Superfamily: ciliary neurotrophic factor receptor; cytokine receptor homology; Immunog
C:Keywords: cytokine receptor; transmembrane protein
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-440/Product: interleukin-6 receptor #status predicted <MAT>
F:40-94/Domain: immunoglobulin homology <IMM>
F:117-306/Domain: cytokine receptor homology <CRS>
F:358-385/Domain: transmembrane #status predicted <TRA>

Query Match 49.3%; Score 72; DB 2; Length 440;
Best Local Similarity 58.3%; Pred. No. 0.0037;
Matches 14; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

OY 1 EWGPRSPSLTKAVLVKRFQNS 24
DB 129 EWGPRSPSLTKAVLVKRFQNS 152

RESULT 3

JL0145
Leukin-6 receptor precursor (clone lambda 301) - mouse
C:Species: Mus musculus (house mouse)
C>Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 21-Jan-2000
C:Accession: J10145; S14543
R:Taga, T.; Saito, M.; Yamasaki, K.; Taga, T.; Hirano, T.; Kishimoto, T.
J. Exp. Med. 171, 2001-2009, 1990
A:Title: Functional murine interleukin 6 receptor with the intracisternal a particle gen
A:Reference number: J10144; MUID:90278354
A:Accession: J10145
A>Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-460 <SUG>
A:Cross-references: GB:X51975; NID:949725; PIDN:CAA36237.1; PID:949726
A:Experimental source: clone lambda 301
R:Forlillo, M.T.; Ciliberto, G.; Dente, L.
submitted to the EMBL data library, July 1990
A:Description: Cloning and expression of murine IL-6 receptor.
A:Reference number: S14543
A:Accession: S14543
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-373, 'R', 375-460 <FIO>
A:Cross-references: EMBL:X53802; NID:952692; PIDN:CAA37810.1; PID:952693
A:Family: ciliary neurotrophic factor receptor; cytokine receptor homology; Immunog

C:Keywords: cytokine receptor; transmembrane protein
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-460/Product: interleukin-6 receptor #status predicted <MAT>
F:40-94/Domain: immunoglobulin homology <IMM>
F:117-306/Domain: cytokine receptor homology <CRS>
F:358-385/Domain: transmembrane #status predicted <TRA>

Query Match 49.3%; Score 72; DB 2; Length 460;
Best Local Similarity 58.3%; Pred. No. 0.0039;
Matches 14; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

OY 1 EWGPRSPSLTKAVLVKRFQNS 24
DB 129 EWGPRSPSLTKAVLVKRFQNS 152

RESULT 4

A37986
Interleukin-6 receptor precursor - rat
N:Alternate names: IL-6 receptor
C:Species: Rattus norvegicus (Norway rat)
C>Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 22-Jun-1999
C:Accession: A37986
R:Baumann, M.; Baumann, H.; Rey, G.H.
J. Biol. Chem. 265, 19853-19862, 1990
A:Title: Molecular cloning, characterization and functional expression of the rat ILV
A:Reference number: A37986; MUID:91060602
A:Accession: A37986
A:Molecule type: mRNA
A:Residues: 1-462 <BAU>
A:Cross-references: GB:M58587; GB:J05668; NID:9204921; PIDN:AAA4131.1; PID:9204922
A:Comment: After binding IL-6, this chain associates with a 130K glycoprotein that is
C:Superfamily: ciliary neurotrophic factor receptor; cytokine receptor homology; Immu
C:Keywords: acute phase; cytokine receptor; transmembrane protein
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-462/Product: interleukin-6 receptor #status predicted <MAT>
F:40-362/Domain: extracellular #status predicted <EXT>
F:40-94/Domain: immunoglobulin homology <IMM>
F:117-306/Domain: cytokine receptor homology <CRS>
F:363-385/Domain: transmembrane #status predicted <TMM>
F:386-462/Domain: intracellular #status predicted <INT>
F:47-92/Disulfide bonds: #status predicted

Query Match 47.9%; Score 70; DB 1; Length 462;
Best Local Similarity 54.2%; Pred. No. 0.008;
Matches 13; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

OY 1 EWGPRSPSLTKAVLVKRFQNS 24
DB 129 EWGPRSPSLTKAVLVKRFQNS 152

RESULT 5

D82609
Hypothetical protein XF2042 [imported] - Xylella fastidiosa (strain 9a5c)
C:Species: Xylella fastidiosa
C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C:Accession: D82609
R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Seq
Nature 406, 151-157, 2000
A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A:Reference number: A62515; MUID:20355717
A>Note: for a complete list of authors see reference number A59328 below
A:Accession: D82609
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-242 <SIM>
A:Cross-references: GB:AE004021; GB:AE003849; NID:99107139; PIDN:AAF84844.1; GSPDB:GN
A:Experimental source: strain 9a5c
R:Simpson, A.J.G.; Relnach, F.C.; Arundel, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.
Birones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrier

PT diseases
 PS Claim 7; Page 17; 28pp; English.
 CC This sequence represents a interleukin-6 (IL-6) antagonist peptide. This
 CC sequence is a peptide of the invention, which are of 5-30 amino acids
 CC and have antagonistic activity against: (a) IL-6; (b) the alpha chain
 CC and/or beta chain of the IL-6 receptor (IL-6R); or (c) IL-6 activity. The
 CC antagonists are used to treat or prevent IL-6 related diseases (typical
 CC of many exemplified are multiple myeloma, acquired immune deficiency
 CC syndrome-related lymphoma, rheumatoid arthritis, psoriasis, sepsis,
 CC osteoporosis, Alzheimer's disease etc.), also to remove IL-6 or IL-6R
 CC from extracorporeal blood. They may also be used diagnostically for such
 CC diseases and IL-6 agonists are administered to subjects previously
 CC specific for the antagonists may be counter their effects, also in
 CC treated with the antagonists to counter their effects, also in
 CC extracorporeal dialysis and diagnosis. The antagonists are too small to
 CC induce an immune response and have minimal side effects (they are not
 CC lytic for erythrocytes nor toxic for polymorphonuclear cells or
 CC hepatocytes); contrast no human anti-IL-6 antibodies. The mixtures, or
 CC multimers, have greater activity (acting on both IL-6 and its receptor)
 CC and the peptides can be engineered for cell cultures. Antibodies
 CC against the peptides can be engineered to increase half-life or to target
 CC organs by incorporating unpertural aa or altering the
 CC hydrophilic/lipophilic balance.
 SQ Sequence 28 AA;
 QY 1 EWGPRSTSLTKAVLVKRFQNSPAED 28
 Db 1 ewgprstsltkavllvrkfqnspsaed 28
 Query Match 100.0%; Score 146; DB 19; Length 28;
 Best Local Similarity 100.0%; Pred. No. 5.7e-16;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 RESULT 2
 AAM00403
 ID AAM00403 standard; peptide: 182 AA.
 AC AAM00403;
 XX 29-AUG-1996 (first entry)
 DT Interleukin-6 antagonist peptide.
 DE Interleukin-6 antagonist peptide.
 DE IL-6; antagonist; autoimmune disease.
 KM Synthetic.
 PN JP07324097-A.
 XX 12-DEC-1995.
 PD 30-MAY-1994; 94JP-0117259.
 PF 30-MAY-1994; 94JP-0117259.
 XX 30-MAY-1994; 94JP-0117259.
 PR (DAIL) DAICEL CHEM IND LTD.
 PA (FUJI) FUJISAWA PHARM CO LTD.
 DR WPI; 1996-065476/07.
 PT Interleukin 6 antagonist - useful for treating autoimmune diseases
 PS Claim 1; Page 2; 19pp; Japanese.
 CC New IL-6 antagonists are provided which are of formula X-N-Y, in
 CC which X is H or an amino-protecting group, Y is OH or a carboxy-
 CC protecting group, and W is a peptide containing all or part of the
 CC sequence as given in AAM00401, AAM00402, AAM00403 (the present sequence)
 CC sequence as given in AAM00404, where any free mercapto groups in the sequence are

Sequen a lompaisu
 A

CC optionally protected. Specifically preferred partial peptides from the
 CC present sequence (AAM00428 - AAM00435) are claimed as new chemical
 CC compounds. The IL-6 antagonists are useful for treating autoimmune
 CC diseases.
 SQ Sequence 182 AA;
 QY 1 EWGPRSTSLTKAVLVKRFQNSPAED 28
 Db 14 ewgprstsltkavllvrkfqnspsaed 41
 Query Match 100.0%; Score 146; DB 17; Length 182;
 Best Local Similarity 100.0%; Pred. No. 5.1e-15;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 RESULT 3
 ID AAM70805
 AD AAM70805 standard; protein: 315 AA.
 AC AAM70805;
 XX 03-FEB-1999 (first entry)
 DT Amino acid sequence of the interleukin (IL)-6R-alpha/313 domain.
 DE gp130; cytokine antagonist; interleukin; gamma-interferon;
 KW granulocyte macrophage colony-stimulating factor; D peptide;
 KW transforming growth factor-beta.
 OS Synthetic.
 XX Key Location/Qualifiers
 FH 1..313
 FT Protein /note="truncated interleukin (IL)-6R-alpha domain"
 XX US5844099-A.
 PN 01-DEC-1998.
 PD 27-NOV-1995; 95US-0563105.
 PF 27-NOV-1995; 95US-0563105.
 XX 27-NOV-1995; 95US-0563105.
 PR 20-OCT-1993; 93US-0140222.
 XX (REG-) REGENERON PHARM INC.
 PA Economides A, Stahl N, Yancopoulos GD;
 PI WPI; 1999-044669/04.
 DR Cytokine antagonists - comprising extracellular domains of
 PT specificity-determining and signal-transducing components of
 PT cytokine receptor
 PS Example 4; Fig 16; 46pp; English.
 CC The present sequence/represents the amino acid sequence of interleukin
 CC (IL)-6R-alpha-313 domain. The protein is used in the course of the
 CC invention. The specification describes cytokine antagonists comprising
 CC only the extracellular domain of the specificity-determining component of
 CC the cytokine receptor and the extracellular domain of a
 CC signal-transducing component of the cytokine receptor. The cytokine
 CC is an interleukin (IL-1, IL-2, IL-3, IL-4, IL-5 or IL-15),
 CC granulocyte macrophage colony-stimulating factor (GM-CSF),
 CC gamma-interferon or transforming growth factor-beta (TGF-beta). The
 CC gamma-interferon is capable of binding the cytokine to form a nonfunctional
 CC complex. The compounds have therapeutic activity as cytokine antagonists
 CC and can also be used in assays for identifying novel agonists and
 CC antagonists of cytokines.
 SQ Sequence 315 AA;

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OM protein - protein search, using sw model

Run on: December 19, 2001, 16:13:35 ; Search time 170.68 seconds
(without alignments)
5.208 Million cell updates/sec

Title: US-09-202-104A-1
Perfect score: 57
Sequence: 1 RYILDGIALRL 12

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues
Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

A.Geneseq_1101.*
1: /SID8/gcgdata/geneseq/geneseq/AA1980.DAT.*
2: /SID8/gcgdata/geneseq/geneseq/AA1981.DAT.*
3: /SID8/gcgdata/geneseq/geneseq/AA1982.DAT.*
4: /SID8/gcgdata/geneseq/geneseq/AA1983.DAT.*
5: /SID8/gcgdata/geneseq/geneseq/AA1984.DAT.*
6: /SID8/gcgdata/geneseq/geneseq/AA1985.DAT.*
7: /SID8/gcgdata/geneseq/geneseq/AA1986.DAT.*
8: /SID8/gcgdata/geneseq/geneseq/AA1987.DAT.*
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11: /SID8/gcgdata/geneseq/geneseq/AA1990.DAT.*
12: /SID8/gcgdata/geneseq/geneseq/AA1991.DAT.*
13: /SID8/gcgdata/geneseq/geneseq/AA1992.DAT.*
14: /SID8/gcgdata/geneseq/geneseq/AA1993.DAT.*
15: /SID8/gcgdata/geneseq/geneseq/AA1994.DAT.*
16: /SID8/gcgdata/geneseq/geneseq/AA1995.DAT.*
17: /SID8/gcgdata/geneseq/geneseq/AA1996.DAT.*
18: /SID8/gcgdata/geneseq/geneseq/AA1997.DAT.*
19: /SID8/gcgdata/geneseq/geneseq/AA1998.DAT.*
20: /SID8/gcgdata/geneseq/geneseq/AA1999.DAT.*
21: /SID8/gcgdata/geneseq/geneseq/AA2000.DAT.*
22: /SID8/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	53	93.0	12	19	AAW52201
2	53	93.0	16	16	AAW68954
3	53	93.0	51	17	AAW00401
4	53	93.0	151	16	AAW77393
5	53	93.0	158	16	AAW77392
6	53	93.0	162	16	AAW77391
7	53	93.0	162	17	AAW00131
8	53	93.0	163	17	AAW00132
9	53	93.0	166	16	AAW77390
10	53	93.0	167	17	AAW77649
11	53	93.0	169	16	AAW77387

12	53	93.0	173	16	AAW77389
13	53	93.0	174	16	AAW75342
14	53	93.0	176	16	AAW75341
15	53	93.0	177	16	AAW77388
16	53	93.0	177	16	AAW75334
17	53	93.0	181	14	AAW31996
18	53	93.0	181	15	AAW72211
19	53	93.0	181	17	AAW05586
20	53	93.0	182	16	AAW75346
21	53	93.0	183	15	AAW60125
22	53	93.0	184	9	AAW81158
23	53	93.0	184	10	AAW94753
24	53	93.0	184	11	AAW05895
25	53	93.0	184	11	AAW06532
26	53	93.0	184	11	AAW03914
27	53	93.0	184	13	AAW20783
28	53	93.0	184	15	AAW72219
29	53	93.0	184	15	AAW54990
30	53	93.0	184	15	AAW55256
31	53	93.0	184	16	AAW75344
32	53	93.0	184	16	AAW74659
33	53	93.0	184	16	AAW68623
34	53	93.0	184	17	AAW02609
35	53	93.0	184	17	AAW02610
36	53	93.0	184	17	AAW02611
37	53	93.0	184	17	AAW02612
38	53	93.0	185	9	AAW81159
39	53	93.0	185	10	AAW90536
40	53	93.0	185	10	AAW94754
41	53	93.0	185	10	AAW91015
42	53	93.0	185	11	AAW05275
43	53	93.0	185	11	AAW05274
44	53	93.0	185	11	AAW05311
45	53	93.0	185	22	AAW73403

ALIGNMENTS

RESULT	ID	AAW52201	standard; peptide; 12 AA.
AC	AAW52201:		
XX			
DT	09-JUN-1998	(first entry)	
XX			
DE	Interleukin-6 antagonist peptide.		
XX			
KW	Interleukin-6; IL-6; antagonist; IL-6 related disease; multiple myeloma; acquired immune deficiency syndrome-related lymphoma; immune response;		
KW	rheumatoid arthritis; psoriasis; sepsis; osteoporosis; therapy;		
KW	Alzheimer's disease.		
XX			
OS	Synthetic.		
OS	Homo sapiens.		
XX			
PN	WO9748728-A1.		
XX			
PD	24-DEC-1997.		
XX			
PF	19-JUN-1997;	97WO-NL00345.	
XX			
PR	20-JUN-1996;	96EP-0201720.	
XX			
PA	(KOST/) KOSTER H W.		
XX			
PI	Hoebe KHN, Van Leengoed LAMG;		
XX			
DR	WPI; 1998-063080/06.		
XX			
PT	New peptide(s) with interleukin-6 agonist or antagonist activity - useful for treatment, prevention and diagnosis of IL-6 associated		

PT diseases
 XX
 PS Claim 6; Page 17; 28pp; English.
 CC
 CC This sequence represents a interleukin-6 (IL-6) antagonist peptide. This
 CC sequence is a peptide of the invention, which are of 5-30 amino acids
 CC and have antagonistic activity against: (a) IL-6; (b) the alpha chain
 CC and/or beta chain of the IL-6 receptor (IL-6R); or (c) IL-6 activity. The
 CC antagonists are used to treat or prevent IL-6 related diseases (typical
 CC of many exemplified are multiple myeloma, acquired immune deficiency
 CC syndrome-related lymphoma, rheumatoid arthritis, psoriasis, sepsis,
 CC osteoporosis, Alzheimer's disease etc.), also to remove IL-6 or IL-6R
 CC from extracorporeal blood. They may also be used diagnostically for such
 CC diseases and IL-6 agonists are additives for cell cultures. Antibodies
 CC specific for the antagonists may be administered to subjects previously
 CC treated with the antagonists to counter their effects, also in
 CC extracorporeal dialysis and diagnosis. The antagonists are too small to
 CC induce an immune response and have minimal side effects (they are not
 CC lytic for erythrocytes nor toxic for polymorphonuclear cells or
 CC hepatocytes); contrast no-human anti-IL-6 antibodies. The mixtures, or
 CC multimers, have greater activity (acting on both IL-6 and its receptor)
 CC and the peptides can be engineered to increase half-life or to target
 CC organs by incorporating unnatural aa or altering the
 CC hydrophilic/lipophilic balance.
 CC
 XX
 SQ Sequence 12 AA;
 Query Match 93.0%; Score 53; DB 19; Length 12;
 Best Local Similarity 100.0%; Pred. No. 0.0012;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 RYIDGISAIR 11
 |||||
 Db 1 rylldgisair 11
 RESULT 2
 AAR68954
 ID AAR68954 standard; Peptide; 16 AA.
 XX
 AC AAR68954;
 XX
 DT 05-SEP-1995 (first entry)
 XX
 DE Wild type Interleukin-6 helix A.
 XX
 KM Human: Interleukin-6; IL-6; helix A; biological activity; superagonist;
 KM binding activity; receptor; gp80; antagonist; superantagonist; hormone;
 KM gp130; receptor complex; oncostatin; leukaemia inhibitory factor; LIF;
 KM ciliary neurotrophic factor; CNTF; agonist.
 XX
 OS Homo sapiens.
 XX
 PN WO9500852-A.
 XX
 PD 05-JAN-1995.
 XX
 PF 23-JUN-1994; 94MO-IT00095.
 XX
 PR 23-JUN-1993; 93IT-0RM0409.
 XX
 PA (RICE-) IST RICERCHE BIOL MOLECOLARE ANGELETTI.
 XX
 PI Ciliberto G, Lahm A, Savino R;
 DR WPI: 1995-052231/07.
 XX
 PT Selecting superagonists, antagonists and superantagonists or
 PT hormones - partic. interleukin-6, oncostatin M, leukaemia
 PT inhibitory factor, ciliary neurotrophic factor or interleukin-11
 XX
 PS Example 2; Page 12; 35pp; English.

XX
 CC The amino acid sequence of the helix A of the human interleukin-6
 CC (IL-6). The gene encoding the IL-6 was mutated by PCR to change certain
 CC of the amino acids in helix A (see AAR68955-60). The biological activity
 CC and binding activity to receptor gp80 for the wild type and mutants
 CC sequences could then be compared. The interaction of the IL-6 and its
 CC mutants forms part of a method to detect the superagonists, antagonists
 CC or superantagonists of a hormone. This is performed by comparing the
 CC amino acid sequence of the hormone with its (ant)agonist; comparing the
 CC a.a. sequences of the (ant)agonist receptor with the hormone-specific
 CC receptor and gp130, and identifying residues forming a part of the site
 CC of interaction with the hormone receptor and gp130 based on a
 CC 3-dimensional model of the receptor complex. The method can be used to
 CC select super(ant)agonists of hormones such as interleukin-6 (IL-6),
 CC oncostatin M (OSM) leukaemia inhibitory factor (LIF) or ciliary
 CC neurotrophic factor (CNTF).
 CC
 XX
 SQ Sequence 16 AA;
 Query Match 93.0%; Score 53; DB 16; Length 16;
 Best Local Similarity 100.0%; Pred. No. 0.0017;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 RYIDGISAIR 11
 |||||
 Db 4 rylldgisair 14
 RESULT 3
 AAW00401
 ID AAW00401 standard; peptide; 51 AA.
 XX
 AC AAW00401;
 XX
 DT 29-AUG-1996 (first entry)
 XX
 DE Interleukin-6 antagonist peptide.
 XX
 KM IL-6; antagonist; autoimmune disease.
 XX
 OS Synthetic.
 XX
 PN JP07324097-A.
 XX
 PD 12-DEC-1995.
 XX
 PF 30-MAY-1994; 94JP-0117259.
 XX
 PR 30-MAY-1994; 94JP-0117259.
 XX
 PA (DAI) DAICEL CHEM IND LTD.
 PA (FUJI) FUJISAWA PHARM CO LTD.
 XX
 DR WPI: 1996-065476/07.
 XX
 PT Interleukin 6 antagonist - useful for treating autoimmune diseases
 XX
 PS Claim 1; Page 2; 19pp; Japanese.
 CC
 CC New IL-6 antagonists are provided which are of formula X-W-Y, in
 CC which X is H or an amino-protecting group, Y is OH or a carboxy-
 CC protecting group, and W is a peptide containing all or part of the
 CC sequence as given in AAW00401 (the present sequence), AAW00402, AAW00403
 CC or AAW00404, where any free mercapto groups in the sequence are
 CC optionally protected. Specifically preferred partial peptides from the
 CC present sequence (AAW00403 - AAW00411) are claimed as new chemical
 CC compounds. The IL-6 antagonists are useful for treating autoimmune
 CC diseases.
 CC
 XX
 SQ Sequence 51 AA;

Query Match 93.0%; Score 53; DB 17; Length 51;
Best Local Similarity 100.0%; Pred. No. 0.0059;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RYLDGISAIR 11
DB 11 rylldgisair 21

RESULT 4
AAR77393
ID AAR77393 standard; Protein; 151 AA.
XX
XX AAR77393;
XX
XX 17-APR-1996 (first entry)
XX
DE Human mutant IL-6a/C3 (amino acids 5-19, 44-50 and 73-83 deleted).
XX
XX Human interleukin-6; IL-6a/C3 mutant; increased stability;
XX
KW recombinant; production; deletion mutant;
KW amino acids 5-19, 44-50 and 73-83.
XX
XX Homo sapiens.
XX
XX JP07224097-A.
XX
XX 22-AUG-1995.
XX
XX 08-FEB-1994; 94JP-0014461.
XX
XX 08-FEB-1994; 94JP-0014461.
XX
XX (ASAG) ASahi GLASS CO LTD.
XX
XX WPI; 1995-325556/42.
XX
XX N-PSDB; AAQ94346.
XX
XX Interleukin-6 mutant, related DNA and expression vectors - has
XX
XX higher stability than natural Interleukin-6
XX
XX Claim 1; Pages 15-16; 18pp; Japanese.
XX
XX AAQ94346 encodes AAR77393 the human IL-6 deletion mutant IL-6a/C3
XX
XX which lacks the amino acids Gly5-Leu19, Cys44-Cys50 and Cys73-Cys83
XX
XX of the wild type protein. The cDNA can be used for the recombinant
XX
XX prodn. of IL-6a/C3 which has increased stability compared to wild
XX
XX type IL-6.
XX
XX Sequence 151 AA;
XX
XX

Query Match 93.0%; Score 53; DB 16; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.019;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RYLDGISAIR 11
DB 15 rylldgisair 25

RESULT 5
AAR77392
ID AAR77392 standard; Protein; 158 AA.
XX
XX AAR77392;
XX
XX 17-APR-1996 (first entry)
XX
XX Human mutant IL-6a/C2 (amino acids 5-19 and 73-83 deleted).
XX
XX Human interleukin-6; IL-6a/C2 mutant; increased stability;
XX
XX recombinant; production; deletion mutant;
XX

KW amino acids 5-19 and 73-83.
XX
XX Homo sapiens.
XX
XX
XX Key Location/Qualifiers
XX mat_peptide 1..474
XX /*tag= a
XX
XX
XX JP07224097-A.
XX
XX 22-AUG-1995.
XX
XX 08-FEB-1994; 94JP-0014461.
XX
XX 08-FEB-1994; 94JP-0014461.
XX
XX (ASAG) ASahi GLASS CO LTD.
XX
XX WPI; 1995-325556/42.
XX
XX N-PSDB; AAQ94347.
XX
XX Interleukin-6 mutant, related DNA and expression vectors - has
XX
XX higher stability than natural Interleukin-6
XX
XX Claim 1; Pages 14-15; 18pp; Japanese.
XX
XX AAQ94347 encodes AAR77392 the human IL-6 deletion mutant IL-6a/C2
XX
XX which lacks the amino acids Gly5-Leu19 and Cys73-Cys83 of the
XX
XX wild type protein. The cDNA can be used for the recombinant prodn.
XX
XX of IL-6a/C2 which has increased stability compared to wild type
XX
XX IL-6.
XX
XX Sequence 158 AA;
XX
XX

Query Match 93.0%; Score 53; DB 16; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RYLDGISAIR 11
DB 15 rylldgisair 25

RESULT 6
AAR77391
ID AAR77391 standard; Protein; 162 AA.
XX
XX AAR77391;
XX
XX 17-APR-1996 (first entry)
XX
XX Human mutant IL-6a/C1 (amino acids 5-19 and 44-50 deleted).
XX
XX Human interleukin-6; IL-6a/C1 mutant; increased stability;
XX
XX recombinant; production; deletion mutant;
XX
XX amino acids 5-19 and 44-50.
XX
XX Homo sapiens.
XX
XX JP07224097-A.
XX
XX 22-AUG-1995.
XX
XX 08-FEB-1994; 94JP-0014461.
XX
XX 08-FEB-1994; 94JP-0014461.
XX
XX (ASAG) ASahi GLASS CO LTD.
XX
XX WPI; 1995-325556/42.
XX
XX N-PSDB; AAQ94346.
XX


```
XX DE Human IL-6 mutant IL-6C3 (amino acids 44-50 and 73-83 deleted).
XX XX
XX KW Human interleukin-6; IL-6C3 mutant; increased stability;
XX KW recombinant; production; deletion mutant;
XX KW amino acids 44-50 and 73-83.
XX OS
XX XX Homo sapiens.
XX FH Key
XX FT mat_peptide 1..498
XX FT /*tag= a
XX XX
XX PN JP07224097-A.
XX PD 22-AUG-1995.
XX PF 08-FEB-1994; 94JP-0014461.
XX PR 08-FEB-1994; 94JP-0014461.
XX PA (ASAG ) ASAH1 GLASS CO LTD.
XX DR WPI: 1995-325556/42.
XX DR N-PSDB; AAQ94345.
XX PT Interleukin-6 mutant, related DNA and expression vectors - has
XX PT higher stability than natural interleukin-6
XX PS
XX PS Claim 1; Page 13; 18pp; Japanese.
XX CC AAQ94345 encodes AAR77390 the human IL-6 deletion mutant IL-6C3,
XX CC which lacks the amino acids Cys44-Cys50 and Cys73-Cys83 of the
XX CC wild type protein. The cDNA can be used for the recombinant prodn.
XX CC of IL-6C3, which has increased stability compared to wild type
XX CC IL-6.
XX SQ Sequence 166 AA;

Query Match 93.0%; Score 53; DB 16; Length 166;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RYILDGISAALR 11
   |||||
   30 ryildgisalr 40

Db

RESULT 10
AAR77649
ID AAR77649 standard; Protein: 167 AA.
XX AC AAR77649;
XX XX
XX DT 27-JUN-1996 (first entry)
XX DE Human interleukin-6 splice variant.
XX KW Human; interleukin-6; splice variant; IL-6SV; treatment;
XX KW immunotherapeutic; anti-inflammatory; bone marrow transplant;
XX KW chemotherapy; side effect; corneal damage; keratitis; ulcer;
XX KW antagonist; Castleman's disease; multiple myeloma;
XX KW cardiac myxoma; cervical cancer; rheumatoid arthritis;
XX KW autoimmune diabetes; sepsis.
XX OS
XX XX Homo sapiens.
XX PN W09532282-A1.
XX PD 30-NOV-1995.
XX PF 17-MAY-1995; 95WO-US06094.
```

```
XX PR 19-MAY-1994; 94US-0246427.
XX PA (HUMA-) HUMAN GENOME SCI INC.
XX PI Adams MD, LI H, Ruben S;
XX DR WPI: 1996-020577/02.
XX DR N-PSDB; AAT08558.
XX PT Polynucleotide encoding interleukin 6-splice variant - used for
XX PT treating auto-immune diseases and inflammation.
XX PS
XX PS Claim 1; Page 40; 54pp; English.
XX CC The human interleukin-6 splice variant (IL-6SV) AAR77649 is encoded
XX CC by AAT08558 (which is derived from an activated macrophage cDNA
XX CC library), and may be used in immunotherapeutic and
XX CC anti-inflammatory compns., and for the treatment of patients
XX CC suffering from bone marrow transplant chemotherapy side effects,
XX CC corneal damage, keratitis and ulcers. Antagonists of IL-6SV may
XX CC be used to treat diseases caused by the up-regulated prodn. of
XX CC IL-6 (i.e. Castleman's disease, multiple myeloma, cardiac myxoma,
XX CC cervical cancer, rheumatoid arthritis and autoimmune diabetes),
XX CC and sepsis.
XX SQ Sequence 167 AA;

Query Match 93.0%; Score 53; DB 17; Length 167;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RYILDGISAALR 11
   |||||
   31 ryildgisalr 41

Db

RESULT 11
AAR77387
ID AAR77387 standard; Protein: 169 AA.
XX AC AAR77387;
XX DT 17-APR-1996 (first entry)
XX DE Human IL-6 mutant IL-6a (amino acids 5-19 deleted).
XX KW Human interleukin-6; IL-6a mutant; increased stability;
XX KW recombinant; production; deletion mutant; amino acids 5-19.
XX OS
XX XX Homo sapiens.
XX PN JP07224097-A.
XX PD 22-AUG-1995.
XX PF 08-FEB-1994; 94JP-0014461.
XX PR 08-FEB-1994; 94JP-0014461.
XX PA (ASAG ) ASAH1 GLASS CO LTD.
XX DR WPI: 1995-325556/42.
XX DR N-PSDB; AAQ94342.
XX PT Interleukin-6 mutant, related DNA and expression vectors - has
XX PT higher stability than natural interleukin-6
XX PS
XX PS Claim 1; Page 10; 18pp; Japanese.
XX CC AAQ94342 encodes AAR77387 the human IL-6 deletion mutant IL-6a, which
XX CC lacks the amino acids Glys-leu19 of the wild type protein. The
```

CC cDNA can be used for the recombinant prodn. of IL-6a, which has
 CC increased stability compared to wild type IL-6.
 XX
 SQ Sequence 169 AA;

Query Match 93.0%; Score 53; DB 16; Length 169;
 Best Local Similarity 100.0%; Pred. No. 0.022;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RYIDGISAIR 11
 |||||
 DB 15 rylldglsair 25

RESULT 12
 AAR7389
 ID AAR7389 standard; Protein; 173 AA.
 XX
 AC AAR7389;

DT 17-APR-1996 (first entry)

XX Human IL-6 mutant IL-6C2 (amino acids 73-83 deleted).

KW Human Interleukin-6; IL-6C2 mutant; increased stability;
 KW recombinant; production; deletion mutant; amino acids 73-83.

OS Homo sapiens.

PH Key Location/Qualifiers
 FT mat_peptide 1..519
 FT /*tag- a

PN JP07224097-A.

PD 22-AUG-1995.

PF 08-FEB-1994; 94JP-0014461.

PR 08-FEB-1994; 94JP-0014461.

PA (ASAG) ASahi GLASS CO LTD.

DR WPI; 1995-325556/42.

DR N-PSDB; AAO94344.

PT Interleukin-6 mutant, related DNA and expression vectors - has
 PT higher stability than natural Interleukin-6

PS Claim 1; Page 12; 18pp; Japanese.

XX AA094344 encodes AAR7389 the human IL-6 deletion mutant IL-6C2,
 CC which lacks the amino acids Cys73-Cys83 of the wild type protein.
 CC The cDNA can be used for the recombinant prodn. of IL-6C2, which
 CC has increased stability compared to wild type IL-6.

XX Sequence 173 AA;

Query Match 93.0%; Score 53; DB 16; Length 173;
 Best Local Similarity 100.0%; Pred. No. 0.022;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RYIDGISAIR 11
 |||||
 DB 30 rylldglsair 40

RESULT 13
 AAR75342
 ID AAR75342 standard; Protein; 174 AA.
 XX

AC AAR75342;

DT 13-DEC-1995 (first entry)

XX Hybrid human cytokine IIII.

KW Hybrid cytokine; tumour proliferation; cancer therapy.

OS Synthetic.

PH Key Location/Qualifiers
 FT Misc-difference 173
 FT /note- "site of stop codon"

PN WO9513393-A.

PD 18-MAY-1995.

PF 07-NOV-1994; 94WO-US12873.

PR 08-NOV-1993; 93US-0149101.

PA (HUTC-) HUTCHINSON CANCER RES CENTER FRED.

PI Leung DW, Rose TM, Todaro GJ;

DR WPI; 1995-194111/25.

DR N-PSDB; AAC87161.

PT New hybrid cytokines with alpha helical sequences from different
 PT sources - also DNA encoding them, vectors and transformed cells,
 PT useful e.g. for treating cancer, remodelling bone etc.

PS Claim 11; Page 31; 52pp; English.

XX The cytokine encoding genes for leukemia inhibitory factor (L),
 CC granulocyte-colony stimulating factor (G), interleukin-6 (I),
 CC interleukin-11 (E), ciliary neurotrophic factor (C) and
 CC oncostatin-M (O) have been cloned and reported in the literature.
 CC I, G, L, E, C and O each comprise four alpha-helical sequences. In
 CC each cytokine, the four alpha-helical sequences are linked by non-
 CC alpha-helical 'linking' sequences of about 5-100 AAs. The invention
 CC provides a group of therapeutic hybrid cytokines, having a size ranging
 CC from about 10 to about 30 kDa. Each hybrid cytokine comprises three or
 CC four alpha-helical sequences and linking sequences, ranging from about
 CC 5-40 AAs in length. In the nomenclature of the hybrid cytokines,
 CC upper case letters designate alpha-helical sequences, lower case
 CC letters (whether Arabic numerals, alphabetic or symbolic) indicate
 CC a specific linking sequence. The first three alpha-helical
 CC sequences of IIL and IIL-alpha were derived from IL-6 and the
 CC fourth alpha sequence was derived from LIF. IIL-alpha has two
 CC additional AAs inserted in a linking sequence between alpha-helices
 CC III and IV, as compared with IIL.

XX Sequence 174 AA;

Query Match 93.0%; Score 53; DB 16; Length 174;
 Best Local Similarity 100.0%; Pred. No. 0.022;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RYIDGISAIR 11
 |||||
 DB 31 rylldglsair 41

RESULT 14
 AAR75341
 ID AAR75341 standard; Protein; 176 AA.
 XX
 AC AAR75341;
 XX
 DT 13-DEC-1995 (first entry)

```

XX DE Hybrid human cytokine IL-6C1 mutant; increased stability;
XX KM Hybrid cytokine; tumour proliferation; cancer therapy.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT Misc-difference 175 /note= "site of stop codon"
XX PA (HUTC-) HUTCHINSON CANCER RES CENTER FRID.
XX PR 08-NOV-1993; 93US-0149101.
XX PF 07-NOV-1994; 94WO-US12873.
XX PD 18-MAY-1995.
XX PN WO9513393-A.
XX PR 08-FEB-1994; 94JP-0014461.
XX PF 08-FEB-1994; 94JP-0014461.
XX PR 08-FEB-1994; 94JP-0014461.
XX PA (ASAG ) ASahi GLASS CO LTD.
XX XX WPI; 1995-325556/42.
XX DR N-PSDB; AA094343.
XX PT Interleukin-6 mutant, related DNA and expression vectors - has
XX higher stability than natural interleukin-6
XX PS Claim 1; Page 11; 18pp; Japanese.
XX CC AA094343 encodes AAR7388 the human IL-6 deletion mutant IL-6C1,
XX which lacks the amino acids Cys44-Cys50 of the wild type protein.
XX CC The cDNA can be used for the recombinant prodn. of IL-6C1, which
XX CC has increased stability compared to wild type IL-6.
XX SQ Sequence 177 AA;

XX PS Claim 1; Page 30; 52pp; English.
XX PT New hybrid cytokines with alpha helical sequences from different
XX PT sources - also DNA encoding them, vectors and transformed cells,
XX PT useful e.g. for treating cancer, remodelling bone etc.
XX PS

XX CC The cytokine encoding genes for leukemia inhibitory factor (L),
XX CC granulocyte-colony stimulating factor (G), Interleukin-6 (I),
XX CC interleukin-11 (E), ciliary neurotrophic factor (C) and
XX CC oncostatin-M (O) have been cloned and reported in the literature.
XX CC I, G, L, E, C and O each comprise four alpha-helical sequences. In
XX CC each cytokine, the four alpha-helical sequences are linked by non-
XX CC alpha-helical 'linking' sequences of about 5-100 AAs. The invention
XX CC provides a group of therapeutic hybrid cytokines, having a size ranging
XX CC from about 10 to about 30 kDa. Each hybrid cytokine comprises three or
XX CC four alpha-helical sequences and linking sequences, ranging from about
XX CC 5-40 AAs in length. In the nomenclature of the hybrid cytokines,
XX CC upper case letters designate alpha-helical sequences, lower case
XX CC letters (whether Arabic numerals, alphabetic or symbolic) indicate
XX CC a specific linking sequence. The first three alpha-helical
XX CC sequences of IIII and IIII-alpha were derived from IL-6 and the
XX CC fourth alpha-sequence was derived from LIF. IIII-alpha has two
XX CC additional AAs inserted in a linking sequence between alpha-helices
XX CC III and IV, as compared with IIII.
XX SQ Sequence 176 AA;

XX Query Match 93.0%; Score 53; DB 16; Length 176;
XX Best Local Similarity 100.0%; Pred. No. 0.023;
XX Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RYILDGISALR 11
   |||||||
   31 rylldgisalr 41

Db 31 rylldgisalr 41

RESULT 15
AAR7388
ID AAR7388 standard; Protein; 177 AA.
XX AC AAR7388;
XX DT 17-APR-1996 (first entry)
XX DE Human IL-6 mutant IL-6C1 (amino acids 44-50 deleted).
XX

```

```

KM Human interleukin-6; IL-6C1 mutant; increased stability;
KW recombinant; production; deletion mutant; amino acids 44-50.
XX OS Homo sapiens.
XX PN JP07224097-A.
XX PD 22-AUG-1995.
XX PF 08-FEB-1994; 94JP-0014461.
XX PR 08-FEB-1994; 94JP-0014461.
XX PA (ASAG ) ASahi GLASS CO LTD.
XX XX WPI; 1995-325556/42.
XX DR N-PSDB; AA094343.
XX PT Interleukin-6 mutant, related DNA and expression vectors - has
XX higher stability than natural interleukin-6
XX PS Claim 1; Page 11; 18pp; Japanese.
XX CC AA094343 encodes AAR7388 the human IL-6 deletion mutant IL-6C1,
XX which lacks the amino acids Cys44-Cys50 of the wild type protein.
XX CC The cDNA can be used for the recombinant prodn. of IL-6C1, which
XX CC has increased stability compared to wild type IL-6.
XX SQ Sequence 177 AA;

XX Query Match 93.0%; Score 53; DB 16; Length 177;
XX Best Local Similarity 100.0%; Pred. No. 0.023;
XX Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RYILDGISALR 11
   |||||||
   30 rylldgisalr 40

Db 30 rylldgisalr 40

Search completed: December 19, 2001, 16:19:33
Job time: 358 sec

```

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: December 19, 2001, 16:15:00 ; Search time 88.82 seconds
(without alignments)
10.292 Million cell updates/sec

Title: US-09-202-104a-1

Perfect score: 57

Sequence: 1 RYIUDGISALURL 12

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	53.0	212	1	IYHUB2	Interleukin-6 prec
2	42	73.7	402	2	N-acetyltransferase
3	41	71.9	386	2	probable acyl-CoA
4	39	68.4	284	2	hypothetical prote
5	39	68.4	284	2	ylfa protein - Esc
6	39	68.4	338	2	3-phosphoshikimate
7	39	68.4	516	1	3-phosphoshikimate
8	39	68.4	518	2	3-phosphoshikimate
9	39	68.4	520	1	3-phosphoshikimate
10	39	68.4	787	2	DNA polymerase II
11	38	66.7	124	2	hypothetical prote
12	38	66.7	699	2	NADH dehydrogenase
13	37	64.9	136	2	hypothetical prote
14	37	64.9	334	2	conserved hypotet
15	37	64.9	633	2	paraportal crystal
16	36	63.2	199	2	type II secretion
17	36	63.2	284	2	hypothetical prote
18	36	63.2	289	2	hypothetical prote
19	36	63.2	402	2	DNA-directed DNA p
20	36	63.2	473	2	pyruvate dehydroge
21	36	63.2	483	2	probable integral
22	36	63.2	783	1	DNA-directed DNA p
23	36	63.2	783	2	DNA polymerase II
24	36	63.2	1371	2	DNA primase XP2061
25	35	61.4	192	2	conserved hypotet
26	35	61.4	192	2	response regulator
27	35	61.4	366	2	DNA polymerase III
28	35	61.4	377	2	protein-glutamate
29	35	61.4	391	2	aspartate aminotra

30	35	61.4	391	2	S74720	DNA-directed DNA p
31	35	61.4	454	2	G70797	hypothetical prote
32	35	61.4	475	2	B29606	methylenomycin A r
33	35	61.4	638	2	F82990	probable ATP-bindi
34	35	61.4	790	2	E85726	hypothetical prote
35	35	61.4	790	2	B64903	ydbb protein precu
36	35	61.4	1436	2	B81704	conserved hypotet
37	34.5	60.5	1232	2	T47993	hypothetical prote
38	34	59.6	111	1	A32233	thioredoxin 2 [val
39	34	59.6	198	2	D83526	trp repressor bind
40	34	59.6	282	2	F82781	shikimate 5-dehydr
41	34	59.6	296	2	T13885	NADH dehydrogenase
42	34	59.6	448	2	S31129	hypothetical prote
43	34	59.6	454	2	A69017	dihydroorotase - M
44	34	59.6	464	2	G83331	anthranilate dioxy
45	34	59.6	467	2	C83195	hypothetical prote

ALIGNMENTS

RESULT 1
IYHUB2
Interleukin-6 precursor [validated] - human
N.Alternate names: B-cell differentiation factor; B-cell hybridoma growth factor; B-c
on factor
C.Species: Homo sapiens (man)
C.Date: 28-Dec-1987 #Sequence, revision 28-Dec-1987 #text-change 08-Dec-2000
C.Accession: A32648; A25692; A25696; A35515; A25801; A25921; I52133; I56003; A27601;
R.Yasukawa, K.; Hirano, T.; Watanabe, Y.; Muratani, K.; Matsuda, T.; Nakai, S.; Kishi
EMBO J. 6, 2939-2945, 1987
A.Title: Structure and expression of human B cell stimulatory factor-2 (BSF-2/IL-6) g
A.Reference number: A32648; MUID:88082654
A.Accession: A32648
A.Molecule type: DNA
A.Residues: 1-212 <YAS>
A.Cross-references: GB:X04430; NID:929494; PIDN:CAA68278.1; PID:929495
A.Note: The authors translated the codon CAG for residue 130 as Glu
R.Zilberstein, A.; Ruggieri, R.; Korn, J.H.; Revel, M.
EMBO J. 5, 2529-2537, 1986
A.Title: Structure and expression of cDNA and genes for human interferon-beta-2, a di
A.Reference number: A91051; MUID:87053818
A.Accession: A25692
A.Molecule type: mRNA
A.Residues: 1-212 <ZIL>
A.Cross-references: GB:X04430; NID:932673; PIDN:CAA28026.1; PID:932674
R.Hirano, T.; Yasukawa, K.; Harada, H.; Taga, T.; Watanabe, Y.; Matsuda, T.; Kashiwam
I, T.; Kishimoto, T.
Nature 324, 73-76, 1986
A.Title: Complementary DNA for a novel human interleukin (BSF-2) that induces B lymph
A.Reference number: A93387; MUID:87065033
A.Accession: A25696
A.Molecule type: mRNA
A.Residues: 1-212 <HIR>
A.Cross-references: GB:X04602; NID:933849; PIDN:CAA28268.1; PID:933850
R.Tonouchi, N.; Miwa, K.; Karasuyama, H.; Matsui, H.
Biochem. Biophys. Res. Commun. 163, 1056-1062, 1989
A.Title: Deletion of 3' untranslated region of human BSF-2 mRNA causes stabilization
A.Reference number: A33515; MUID:89391958
A.Accession: A33515
A.Molecule type: mRNA
A.Residues: 1-212 <TON>
A.Cross-references: GB:M29150; NID:9186349; PIDN:AAA59154.1; PID:9307063
R.Haegeman, G.; Content, J.; Voicckaert, G.; Derynck, R.; Tavernier, J.; Fiers, W.
Eur. J. Biochem. 159, 625-632, 1986
A.Title: Structural analysis of the sequence coding for an inducible 26-kDa protein i
A.Reference number: A25801; MUID:87004683
A.Accession: A25801
A.Molecule type: DNA; mRNA
A.Residues: 1-212 <HAE>
A.Cross-references: GB:X04403
A.Experimental source: fibroblast
R.May, L.T.; Helfgott, D.C.; Sehgal, P.B.

Proc. Natl. Acad. Sci. U.S.A. 83, 8957-8961, 1986
 A:Title: Anti-beta-Interferon antibodies inhibit the increased expression of HLA-B7 mRNA
 A:Reference number: A25921; MUID:87067433
 A:Accession: A25921
 A:Molecule type: mRNA
 A:Residues: 1-212 <MAX>
 A:Cross-references: GB:M14584; NID:q184628; PIDN:AAA52728.1; PID:q306310
 R:Wong, G.G.; Witek-Gianotti, J.; Hewick, R.M.; Clark, S.C.; Ogawa, M.
 Behring Inst. Milt. 83, 40-47, 1988
 A:Title: Interleukin 6: Identification as a hematopoietic colony-stimulating factor.
 A:Reference number: I52193; MUID:89193317
 A:Accession: I52193
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-212 <NON>
 A:Cross-references: GB:M54894; NID:q186351; PIDN:AAC41704.1; PID:q186352
 R:Brakenhoff, J.P.; de Groot, E.R.; Evers, R.F.; Pannekoek, H.; Aarden, L.A.
 J. Immunol. 139, 4116-4121, 1987
 A:Title: Molecular cloning and expression of hybridoma growth factor in *Escherichia coli*
 A:Reference number: I56003; MUID:88088768
 A:Accession: I56003
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-212 <BRA>
 A:Cross-references: GB:M18403; NID:q184631; PIDN:AAA52729.1; PID:q306911
 R:Van Damme, J.; Van Beeumen, J.; Decock, B.; Van Snick, J.; De Ley, M.; Billiau, A.
 J. Immunol. 140, 1534-1541, 1988
 A:Title: Separation and comparison of two monokines with lymphocyte-activating factor ad
 A:Reference number: A92816; MUID:88154445
 A:Accession: A27601
 A:Molecule type: protein
 A:Residues: 28-51, 'X', '53-57', 'X', '59', 'X', '61 <VANI>
 A:Accession: B27601
 A:Molecule type: protein
 A:Residues: 30-56, 'XX', '59-61', 'X', '63 <VAZ>
 R:Ramanoto, R.; Lin, L.S.; Lowe, R.; Warren, M.K.; White, T.J.
 J. Immunol. 144, 1808-1816, 1990
 A:Title: The human lung fibroblast cell line, MRC-5, produces multiple factors involved
 A:Reference number: A60400; MUID:9011574
 A:Accession: A60400
 A:Molecule type: protein
 A:Residues: 30-43 <YAM>
 R:Hirano, T.; Taga, T.; Yasukawa, K.; Nakajima, K.; Nakano, N.; Takatsuki, F.; Shimizu, Proc. Natl. Acad. Sci. U.S.A. 84, 228-231, 1987
 A:Title: Human beta-cell differentiation factor defined by an anti-peptide antibody and
 A:Reference number: A29085; MUID:87092370
 A:Accession: A29085
 A:Molecule type: protein
 A:Residues: 28-42 <HR2>
 R:Noda, M.; Takeda, K.; Sugimoto, H.; Hosoi, T.; Takechi, K.; Hara, T.; Ishikawa, H.; Anticancer Res. 11, 961-968, 1991
 A:Title: Purification and characterization of human fibroblast derived differentiation A
 A:Reference number: A61159; MUID:91290785
 A:Accession: A61159
 A:Molecule type: protein
 A:Residues: 30-42 <NOD>
 R:Kemp, J.E.; Cernetti, C.; Steinman, R.M.; Granelli-Piperno, A.
 J. Mol. Cell. Immunol. 4, 203-212, 1989
 A:Title: Interleukin 6 is the principal cytolytic T lymphocyte differentiation factor fo
 A:Reference number: A61462; MUID:90121567
 A:Accession: A61462
 A:Molecule type: protein
 A:Residues: 28-48 <MIN>
 A:Experimental source: leukocyte-conditioned medium
 R:May, L.T.; Shaw, J.E.; Khanna, A.K.; Zabriske, J.B.; Sehgal, P.B.
 Cytokine 3, 204-211, 1991
 A:Title: Marked cell-type-specific differences in glycosylation of human interleukin-6.
 A:Reference number: A48419; MUID:9135644
 A:Accession: A48419
 A:Molecule type: protein
 A:Residues: 30-37, 'X', '39-40 <MAX2>
 A:Experimental source: FS-4 fibroblasts

A:Note: sequence extracted from NCBI backbone
 A:Note: This 28-30K form contained both N-linked and O-linked carbohydrate; a 25K for
 A:Accession: C48419
 A:Molecule type: protein
 A:Residues: 28-40 <MAX3>
 A:Experimental source: FS-4 fibroblasts
 A:Note: sequence extracted from NCBI backbone (NCBI:63787)
 A:Note: This 23-25K form contained O-linked but not N-linked carbohydrate
 R:Orlita, T.; Oheba, M.; Hasegawa, M.; Kubonawa, H.; Esaki, K.; Ochi, N.
 J. Biochem. 115, 345-350, 1994
 A:Title: Polypeptide and carbohydrate structure of recombinant human interleukin-6 pr
 A:Reference number: JX0305; MUID:94267675
 A:Contents: annotation; modified sites in recombinant protein from CHO cells
 R:Clogston, C.L.; Boone, T.C.; Crandall, C.; Mendiaz, E.A.; Lu, H.S.
 Arch. Biochem. Biophys. 272, 144-151, 1989
 A:Title: Disulfide structures of human interleukin-6 are similar to those of human gr
 A:Reference number: S04981; MUID:89266115
 A:Contents: annotation; disulfide bonds in recombinant protein
 R:Rock, F.L.; Li, X.; Chong, P.; Ida, N.; Klein, M.
 Biochemistry 33, 5146-5154, 1994
 A:Title: Roles of disulfide bonds in recombinant human interleukin 6 conformation.
 A:Reference number: A54253; MUID:94227044
 A:Contents: annotation; lability and functional significance of each disulfide bond
 C:Comment: Produced by both lymphoid and nonlymphoid tissue in response to growth fac
 C:Comment: This protein plays a regulatory role in various host defense mechanisms an
 C:Genetics:
 A:Gene: GDB:IL6
 A:Cross-references: GDB:120748; OMIM:147620
 A:Map position: 7p21-7p21
 A:Introns: 7/1; 70/3; 108/3; 157/3
 C:Superfamily: Interleukin-6
 C:Keywords: Castleman's disease; cytokine; extracellular protein; glycoprotein; growth
 F:1-27/Domain: Signal sequence #status predicted <SIG>
 F:28-212/Product: Interleukin-6, long form #status experimental <MATL>
 F:30-212/Product: Interleukin-6, short form #status experimental <MATS>
 F:72-78,101-111/Disulfide bonds: #status experimental
 F:72/Binding site: carbohydrate (Asn) (covalent) (partial) #status experimental
 F:166/Binding site: carbohydrate (Thr) (covalent) (partial) #status experimental
 F:172/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 93.0% Score 53; DB 1; Length 212;
 Best Local Similarity 100.0% Pred. No. 0.0084;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RYLDGISAALR 11
 |||||
 Db 58 RYLDGISAALR 68

RESULT 2
 T13614 N-acetyltransferase homolog 8D8.6 - fruit fly (*Drosophila melanogaster*)
 C:Species: *Drosophila melanogaster*
 C>Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 17-Nov-2000
 C:Accession: T13614
 R:Papadimitrakaki, G.; Spanos, L.; Cox, S.; Siden-Kiamos, I.; Louis, C.
 Submitted to the EMBL Data Library, April 1999
 A:Description: Sequencing the distal X chromosome of *Drosophila melanogaster*.
 A:Reference number: 217695
 A:Accession: T13614
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-402 <PAP>
 A:Cross-references: EMBL:AL022018; NID:e1273253; PID:e1254560; PIDN:CAA17683.1
 C:Genetics:
 A:Cross-references: Flybase:FBgn0024367
 A:Introns: 348/3
 A:Note: EG:8D8.6

Query Match 73.7% Score 42; DB 2; Length 402;

Best Local Similarity 66.7%; Pred. No. 2.4;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 RYLDGISALR 12
|||:|:|
Db 386 RYLDGVALRL 397

RESULT 3
E83536
Probable acyl-CoA dehydrogenase PA0879 [imported] - Pseudomonas aeruginosa (strain PA01)
C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: E83536
R:Stover, C.K.; Pham, X.Q.; Ertyn, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Br
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lardig, K.; Lim,
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A:Reference number: A82950; MUID:20437337
A:Accession: E83536
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-386 <STO>
A:Cross-references: GB:AE004522; GB:AE004091, NID:g9946768; PIDN:AG04268.1; GSPDB:GN001
A:Experimental source: strain PA01
C:Genetics:
A:Gene: PA0879
C:Superfamily: acyl-CoA dehydrogenase

Query Match 71.9%; Score 41; DB 2; Length 386;
Best Local Similarity 72.7%; Pred. No. 3.7;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RYLDGISALR 11
|||||:|
Db 235 RYLDGVALNR 245

RESULT 4
B86134
Hypothetical protein z5951 [imported] - Escherichia coli (strain O157:H7)
C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Mar-2001
C:Accession: B86134
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: B86134
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-284 <STO>
A:Cross-references: GB:AE005174; NID:g12519371; PIDN:AGG59534.1; GSPDB:GN00145; UMGF:Z59
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: Z5951

Query Match 68.4%; Score 39; DB 2; Length 284;
Best Local Similarity 70.0%; Pred. No. 6.4;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RYLDGISAL 10
|||:|:|
Db 86 RYLDGVAL 95

RESULT 5
S56578
y1a protein - Escherichia coli

N:Alternate names: hypothetical 32k protein (mr-tsr intergenic region)
C:Species: Escherichia coli
C:Date: 28-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 08-Oct-1999
C:Accession: S56578; B65250; S18778
R:Burland, V.; Plunkett III, G.; Sofia, H.J.; Daniels, D.L.; Blattner, F.R.
Nucleic Acids Res. 23, 2105-2119, 1995
A:Title: Analysis of the Escherichia coli genome VI: DNA sequence of the region from
A:Reference number: S56314; MUID:95334362
A:Accession: S56578
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-284 <BLAT>
A:Cross-references: EMBL:U14003; NID:g1263172; PIDN:AAA97249.1; PID:g537194
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1994
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;
.; Rose, D.U.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of Escherichia coli K-12.
A:Reference number: A64720; MUID:97426617
A:Accession: B65250
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-284 <BLAT>
A:Cross-references: GB:AE00506; GB:U00096; NID:g2367377; PIDN:AAC77308.1; PID:g17908
A:Experimental source: strain K-12, substrain MG1655
R:Waite-Rees, P.A.; Keating, C.J.; Moran, L.S.; Slatko, B.E.; Hornstra, L.J.; Benner,
J. Bacteriol. 173, 5207-5219, 1991
A:Title: Characterization and expression of the Escherichia coli Mrr restriction syst
A:Reference number: A40368; MUID:91317743
A:Accession: S18778
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 5-284 <MAT>
A:Cross-references: EMBL:X54198; NID:g42018; PIDN:CAA38118.1; PID:g42021
C:Genetics:
A:Gene: y1a
A:Start codon: GTG

Query Match 68.4%; Score 39; DB 2; Length 284;
Best Local Similarity 70.0%; Pred. No. 6.4;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RYLDGISAL 10
|||:|:|
Db 86 RYLDGVAL 95

RESULT 6
S18354
3-phosphoshikimate 1-carboxyvinyltransferase (EC 2.5.1.19) - common tobacco
N:Alternate names: 5-enolpyruvylshikimate-3-phosphate synthase
C:Species: Nicotiana tabacum (common tobacco)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 18-Jun-1999
C:Accession: S18354
R:Wang, Y.; Jones, J.D.; Weller, S.C.; Goldsborough, P.B.
Plant Mol. Biol. 17, 1127-1138, 1991
A:Title: Expression and stability of amplified genes encoding 5-enolpyruvylshikimate-
A:Reference number: S18353; MUID:92032779
A:Accession: S18354
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-338 <MAN>
A:Cross-references: EMBL:M61905; NID:g170230; PIDN:AAA34072.1; PID:g170231
C:Superfamily: 3-phosphoshikimate 1-carboxyvinyltransferase; 3-phosphoshikimate 1-car
C:Keywords: chloroplast; transferase
F:1-330/Domain: 3-phosphoshikimate 1-carboxyvinyltransferase homology (fragment) <PSK

Query Match 68.4%; Score 39; DB 2; Length 338;
Best Local Similarity 54.5%; Pred. No. 7.8;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 RYLDGISA LR 11
11:111: :1
DB 13 RYVLDGVP RMR 23

RESULT 7

XU70VS
3-phosphoshikimate 1-carboxyvinyltransferase (EC 2.5.1.19) precursor - garden petunia
N:Alternate names: 5-enolpyruvylshikimate-3-phosphate synthase; EPSP synthase
C:Species: Petunia x hybrida (garden petunia)
C>Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 28-May-1999
C:Accession: A28198
R:Gasser, C.S.; Winter, J.A.; Hironaka, C.M.; Shah, D.M.
J. Biol. Chem. 263, 4280-4287, 1988
A:Title: Structure, expression, and evolution of the 5-enolpyruvylshikimate-3-phosphate
A:Reference number: A92711; MUID:88153749
A:Accession: A28198
A:Molecule type: mRNA
A:Residues: 1-516 <GAS>
A:Cross-references: GB:M21084; GB:J03227; NID:g169190; PIDN:AAA33699.1; PID:g169191
C:Comment: This enzyme catalyzes the synthesis of O(5)-(1-carboxyvinyl)-3-phosphoshikimate
hich leads to chorismate and thus to aromatic amino acids and related aromatic compounds
C:Superfamily: 3-phosphoshikimate 1-carboxyvinyltransferase; 3-phosphoshikimate 1-carboxy
C:Keywords: aromatic amino acid biosynthesis; chloroplast; transferase
F:1-72/Domain: transit peptide (chloroplast) #status predicted <TNP>
F:73-516/Product: 3-phosphoshikimate 1-carboxyvinyltransferase #status predicted <MAT>
F:87-508/Domain: 3-phosphoshikimate 1-carboxyvinyltransferase homology <PSK>

Query Match 68.4%; Score 39; DB 1; Length 516;
Best Local Similarity 54.5%; Pred. No. 12;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 RYLDGISA LR 11
11:111: :1
DB 191 RYVLDGVP RMR 201

RESULT 8

S18353
3-phosphoshikimate 1-carboxyvinyltransferase (EC 2.5.1.19) precursor - common tobacco
N:Alternate names: 5-enolpyruvylshikimate-3-phosphate synthase
C:Species: Nicotiana tabacum (common tobacco)
C>Date: 22-Nov-1993 #sequence_revision 03-Aug-1995 #text_change 18-Jun-1999
C:Accession: S18353
R:Wang, Y.; Jones, J.D.; Weller, S.C.; Goldsbrough, P.B.
Plant Mol. Biol. 17, 1127-1138, 1991
A:Title: Expression and stability of amplified genes encoding 5-enolpyruvylshikimate-3-P
A:Reference number: S18353; MUID:92032779
A:Accession: S18353
A:Molecule type: mRNA
A:Residues: 1-518 <MAN>
A:Cross-references: EMBL:M61904; NID:g170228; PIDN:AAA34071.1; PID:g170229
C:Genetics:
A:Gene: EPSPS-1
C:Function:
A:Description: catalyzes the synthesis of O(5)-(1-carboxyvinyl)-3-phosphoshikimate from
A:Pathway: shikimate pathway; aromatic amino acid biosynthesis
A>Note: leads to chorismate and thus to aromatic amino acids and related aromatic compounds
C:Superfamily: 3-phosphoshikimate 1-carboxyvinyltransferase; 3-phosphoshikimate 1-carboxy
C:Keywords: aromatic amino acid biosynthesis; chloroplast; transferase
F:1-74/Domain: transit peptide (chloroplast) #status predicted <TNP>
F:75-518/Product: 3-phosphoshikimate 1-carboxyvinyltransferase #status predicted <MAT>
F:89-510/Domain: 3-phosphoshikimate 1-carboxyvinyltransferase homology <PSK>

Query Match 68.4%; Score 39; DB 2; Length 518;
Best Local Similarity 54.5%; Pred. No. 13;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 RYLDGISA LR 11
11:111: :1
DB 193 RYVLDGVP RMR 203

RESULT 9

XU70VS
3-phosphoshikimate 1-carboxyvinyltransferase (EC 2.5.1.19) precursor - tomato
N:Alternate names: 5-enolpyruvylshikimate-3-phosphate synthase; EPSP synthase
C:Species: Lycopersicon esculentum (tomato)
C>Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 12-Apr-1996
C:Accession: B28198
R:Gasser, C.S.; Winter, J.A.; Hironaka, C.M.; Shah, D.M.
J. Biol. Chem. 263, 4280-4287, 1988
A:Title: Structure, expression, and evolution of the 5-enolpyruvylshikimate-3-phosphate
A:Reference number: A92711; MUID:88153749
A:Accession: B28198
A:Molecule type: mRNA
A:Residues: 1-520 <GAS>
A:CComment: This enzyme catalyzes the synthesis of O(5)-(1-carboxyvinyl)-3-phosphoshik
hich leads to chorismate and thus to aromatic amino acids and related aromatic compou
C:Superfamily: 3-phosphoshikimate 1-carboxyvinyltransferase; 3-phosphoshikimate 1-car
C:Keywords: aromatic amino acid biosynthesis; chloroplast; transferase
F:1-76/Domain: transit peptide (chloroplast) #status predicted <TNP>
F:77-520/Product: 3-phosphoshikimate 1-carboxyvinyltransferase #status predicted <MAT
F:91-512/Domain: 3-phosphoshikimate 1-carboxyvinyltransferase homology <PSK>

Query Match 68.4%; Score 39; DB 1; Length 520;
Best Local Similarity 54.5%; Pred. No. 13;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 RYLDGISA LR 11
11:111: :1
DB 195 RYVLDGVP RMR 205

RESULT 10

G83410
DNA polymerase II PA1866 [Imported] - Pseudomonas aeruginosa (strain PA01)
C:Species: Pseudomonas aeruginosa
C>Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: G83410
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.;
Adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa
A:Reference number: AB2950; MUID:20437337
A:Accession: G83410
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-787 <SNO>
A:Cross-references: GB:AE004614; GB:AE004091; NID:g9947868; PIDN:AA05275.1; GSPDB:GN
A:Experimental source: strain PA01
C:Genetics:
A:Gene: polB; PA1866
C:Superfamily: Escherichia coli DNA-directed DNA polymerase II

Query Match 68.4%; Score 39; DB 2; Length 787;
Best Local Similarity 72.7%; Pred. No. 20;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RYLDGISA LR 11
11:111: :1
DB 274 RLIDGISA LR 284

RESULT 11

D72506
hypothetical protein APE2026 - Aeropyrum pernix (strain K1)
C:Species: Aeropyrum pernix
C>Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
C:Accession: D72506
R:Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Halkawa, Y.; Jin-no, K.; Ta

awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K
DNA Res. 6, 83-101, 1999
A>Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr
A:Reference number: A72450; MUID:99310339
A:Accession: D72506
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-124 <KAM>
A:Cross-references: DDBJ:AP000063; NID:g5105654; PIDN:BAAB1036.1; PID:d1044822; PID:g510
A:Experimental source: strain K1
C:Genetics:
A:Gene: APE2026

Query Match 66.7%; Score 38; DB 2; Length 124;
Best Local Similarity 80.0%; Pred. No. 4.1;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 3 IIDGISALRL 12
||| ||||
DB 73 IIDGISALRL 82

RESULT 12
T13772
NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 5 - Verbena bracteata chloroplast (fr

C:Species: chloroplast Verbena bracteata
C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 11-Jan-2000
C:Accession: T13772
R:Olstead, R.G.; Reeves, P.A.
Ann. Mo. Bot. Gard. 82, 176-193, 1995
A>Title: Evidence for the polyphyly of the Scrophulariaceae based on chloroplast rbcL an
A:Reference number: Z17559
A:Accession: T13772
A>Status: translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-699 <OLM>
A:Cross-references: EMBL:L36418; NID:g703451; PID:g703452; PIDN:AAA84708.1
C:Genetics:
A:Genome: chloroplast
A>Note: ndhp
C:Superfamily: NADH dehydrogenase (ubiquinone) chain 5
C:Keywords: chloroplast; membrane-associated complex; NAD; oxidoreductase

Query Match 66.7%; Score 38; DB 2; Length 699;
Best Local Similarity 87.5%; Pred. No. 27;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RYLDGSL 8
||| ||||
DB 682 RYLDGSL 689

RESULT 13
E70736

hypothetical protein RV3408 - Mycobacterium tuberculosis (strain H37Rv)

C:Species: Mycobacterium tuberculosis
C>Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
C:Accession: E70736
R:Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A>Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A:Reference number: A70500; MUID:98295987
A:Accession: E70736
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-136 <COL>
A:Cross-references: GB:Z77165; GB:AL123456; NID:g3261609; PIDN:CAB01015.1; PID:g1449379
A:Experimental source: strain H37Rv

C:Genetics:
A:Gene: RV3408

Query Match 64.9%; Score 37; DB 2; Length 136;
Best Local Similarity 58.3%; Pred. No. 7.1;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 RYLDGSLRL 12
||| ||||
DB 63 RYLDGSLRL 74

RESULT 14
F83070

conserved hypothetical protein PA4604 [imported] - Pseudomonas aeruginosa (strain PAO
C:Species: Pseudomonas aeruginosa
C>Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: F83070
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warriner, P.; Hickey, M.J.;
Adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Latibig, K.; L
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A>Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pa
A:Reference number: AB2950; MUID:20437337
A:Accession: F83070
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-334 <STO>
A:Cross-references: GB:AE004874; GB:AE004091; NID:g9950849; PIDN:AA07992.1; GSPDB:GN
A:Experimental source: strain PAO1
C:Genetics:
A:Gene: PA4604

Query Match 64.9%; Score 37; DB 2; Length 334;
Best Local Similarity 70.0%; Pred. No. 19;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 RYLDGSLAL 10
||| ||||
DB 128 RYLDGSLAL 137

RESULT 15
C32053

parasporal crystal protein B1 - Bacillus thuringiensis subsp. kurstaki
M:Alternate names: parasporal crystal protein P2
C:Species: Bacillus thuringiensis subsp. kurstaki
C>Date: 13-Jul-1989 #sequence_revision 13-Jul-1989 #text_change 15-Oct-1999
C:Accession: C32053; A29913
R:Midner, W.R.; Whiteley, H.R.
J. Bacteriol. 171, 965-974, 1989
A>Title: Two highly related insecticidal crystal proteins of Bacillus thuringiensis s
A:Reference number: A32053; MUID:89123178
A:Accession: C32053
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-633 <MID>
R:Donovan, W.P.; Dankocsik, C.C.; Gilbert, M.P.; Gawron-Burke, M.C.; Groat, R.C.; Car
J. Biol. Chem. 263, 561-567, 1988
A>Title: Amino acid sequence and entomocidal activity of the P2 crystal protein. An i
A:Reference number: A29913; MUID:88087146
A:Accession: A29913
A:Molecule type: DNA
A:Residues: 1-587, 'FRY' <DON>
C:Genetics:
A:Gene: cryBI

Query Match 64.9%; Score 37; DB 2; Length 633;
Best Local Similarity 72.7%; Pred. No. 39;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 2 YILDIGISALRI 12
||| ||| ||
Db 306 YILSGISGTRL 316

Search completed: December 19, 2001, 16:22:34
Job time: 454 sec

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OM protein - protein search, using sw model

Run on: December 19, 2001, 16:16:45 ; Search time 48.45 Seconds
(without alignments)
9.081 Million cell updates/sec

Title: US-09-202-104A-1
57
Perfect score: 1 RYILDGTSALRL 12

Sequence: 1 RYILDGTSALRL 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SWISSPROT_39:*

Prod. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	53	93.0	212	1 IL6_CERTO	P46650 cercocebus
2	53	93.0	212	1 IL6_HUMAN	P05231 homo sapien
3	53	93.0	212	1 IL6_MACFA	P19341 macaca fasc
4	53	93.0	212	1 IL6_MACMU	P51494 macaca mul
5	39	68.4	318	1 YJTA_ECOLI	P24203 escherichia
6	39	68.4	338	1 ARO2_TOBAC	P23281 nicotiana t
7	39	68.4	516	1 ARO2_PETTY	P11043 nicotiana t
8	39	68.4	518	1 ARO1_TOBAC	P23281 nicotiana t
9	39	68.4	520	1 AROA_LYCES	P10748 lycopersico
10	37	64.9	133	1 YV08_MYCTU	O50717 mycobacteri
11	37	64.9	633	1 C2AA_BACTK	P21253 bacillus th
12	36	63.2	402	1 DP3B_MYCTU	O50790 mycobacteri
13	36	63.2	782	1 DP02_ECOLI	P21189 escherichia
14	35	61.4	207	1 IL6_CANFA	P41323 canis fami
15	35	61.4	209	1 IL6_PHOVI	O28819 phoca vitul
16	35	61.4	391	1 DP3B_SYNY3	P72856 synchocyst
17	35	61.4	454	1 Y1DA_MYCTU	O69701 mycobacteri
18	35	61.4	475	1 MMR_STRCO	P11445 streptomyce
19	35	61.4	790	1 YDDB_ECOLI	P31827 escherichia
20	34	59.6	110	1 TH12_ANASP	P20857 anaena sp
21	34	59.6	448	1 YMJ9_CAEEL	P34484 caenorhabdi
22	34	59.6	454	1 PYRC_METH	O27199 methanobact
23	34	59.6	516	1 AROA_BRANA	P17688 brassica na
24	34	59.6	520	1 AROA_ARATH	P05466 arabidopsis
25	34	59.6	681	1 TBRL_HUMAN	O16650 mus musculu
26	34	59.6	682	1 TBRL_HUMAN	O16650 mus musculu
27	34	59.6	823	1 UBPC_HUMAN	O9515 homo sapien
28	34	59.6	1707	1 194K_TRVSY	P05080 tobacco rat
29	34	59.6	1830	1 BP28_ARATH	O95824 arabidopsis
30	33	57.9	188	1 SPR_ECOLI	P7685 escherichia
31	33	57.9	205	1 IL6_ORCOR	O28747 orcinus orc
32	33	57.9	212	1 IL6_PIG	P26993 sus scrofa
33	33	57.9	282	1 AROE_METUA	O58484 methanococc

34	33	57.9	376	1 DP3B_STRCO	P27903 streptomyc
35	33	57.9	394	1 CHER_RHOCE	P72253 rhodospirill
36	33	57.9	428	1 AROA_EDMTC	O9442 edwardsiell
37	33	57.9	494	1 RNHL_CRIFA	O07762 crithidia f
38	33	57.9	633	1 C2AB_BACTK	P21254 bacillus th
39	33	57.9	681	1 NUSC_SYNY3	O55429 synchocyst
40	33	57.9	700	1 PURL_HALNL	O9hr49 halobacteri
41	33	57.9	1043	1 SYL_CHLPN	O92972 chlamydia p
42	33	57.9	3063	1 CALC_HUMAN	O99715 homo sapien
43	33	57.9	4273	1 PKSM_BACSU	P40872 bacillus su
44	32.5	57.0	56	1 VG36_BPMO2	O22001 mycobacteri
45	32	56.1	48	1 YVPX_LDV	P24124 lactate deh

ALIGNMENTS

RESULT ID	1 IL6_CERTO	STANDARD:	PRT:	212 AA.
AC	P46650;			
DT	01-NOV-1995 (Rel. 32, Created)			
DT	01-NOV-1995 (Rel. 32, Last sequence update)			
DT	15-JUL-1998 (Rel. 36, Last annotation update)			
DE	INTERLEUKIN-6 PRECURSOR (IL-6).			
GN	IL6.			
OS	Cercocebus torquatus atys (Red-crowned mangabey) (Sooty mangabey).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;			
OC	Cercopithecoidea; Cercocebus.			
OX	NCBI_TaxID=9531;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=F0J;			
RC	MEDLINE=96003435; PubMed=7561102;			
RA	Villinger F.J., Brar S.S., Mayne A.E., Chikhalia N., Ansari A.A.;			
RT	*Comparative sequence analysis of cytokine genes from human and			
RT	nonhuman primates.;			
RU	J. Immunol. 155:3946-3954(1995).			
CC	-I- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL			
CC	FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION			
CC	OF B-CELLS INTO IG-SECRETING CELLS, IT INDUCES MYELOMA AND			
CC	PLASMACYTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN			
CC	HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS (BY SIMILARITY).			
CC	-I- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.			
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
DR	EMBL: L26032; AAA99972.1; -			
DR	HSSP: P05231; IAITU			
DR	InterPro: IPR003573; IL6_MGF_GCSF.			
DR	InterPro: IPR003574; Interleukin_6.			
DR	Pfam: PF00489; IL6; 1.			
DR	PRINTS: PR00433; IL6GSEFMGF.			
DR	PRINTS: PR00434; INTERLEUKIN6.			
DR	PRODOM: PD004356; Interleukin_6; 1.			
DR	SMART: SM00126; IL6; 1.			
DR	PROSITE: PS00254; INTERLEUKIN_6; 1.			
KW	CYTOKINE; Glycoprotein; Growth factor; Signal.			
FT	SIGNAL 1 29			
FT	CHAIN 30 212			
FT	DISULFID 72 78			
FT	DISULFID 101 111			
FT	CARBOHYD 73 73			
FT	CARBOHYD 172 172			
FT	SEQUENCE 212 AA; 23668 MW; C73C035226B44B9F CRC64;			

Query Match 93.0%; Score 53; DB 1; Length 212;
 Best Local Similarity 100.0%; Pred. No. 0.0032;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RYLDGSLR 11
 |||||
 DB 58 RYLDGSLR 68

RESULT 2
 ID IL6_HUMAN STANDARD: PRT: 212 AA.
 AC P05231;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, last sequence update)
 DT 20-AUG-2001 (Rel. 40, last annotation update)
 DE INTERLEUKIN-6 PRECURSOR (IL-6) (B-CELL STIMULATORY FACTOR 2) (BSF-2)
 DE (INTERFERON BETA-2) (HYBRIDOMA GROWTH FACTOR).
 GN IL6 OR IFNB2.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_TaxID=9606;
 RX MEDLINE-87065033; PubMed-3491322;
 RA Hirano T., Yasukawa K., Harada H., Taga T., Watanabe Y., Matsuda T.,
 RA Kashihara S., Nakai S., Nakata J., Koyama K., Yamatsu A., Tsunashima S.,
 RA Sakihama F., Matsui H., Takahara Y., Taniguchi T., Kishimoto T.,
 RT Complementary DNA for a novel human interleukin (BSF-2) that induces
 RT B lymphocytes to produce immunoglobulin.";
 RL Nature 324:73-76(1986).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-87065033; PubMed-3500852;
 RA Yasukawa K., Hirano T., Watanabe Y., Muratani K., Matsuda T.,
 RA Nakai S., Kishimoto T.,
 RT "Structure and expression of human B cell stimulatory factor-2
 RT (BSF-2/IL-6) gene.";
 RL EMBO J. 6:2939-2945(1987).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-87067433; PubMed-3538015;
 RA May L.T., Helfgott D.C., Sehgal P.B.,
 RT "Anti-beta-interferon antibodies inhibit the increased expression of
 RT HLA-B7 mRNA in tumor necrosis factor-treated human fibroblasts:
 RT structural studies of the beta 2 interferon involved.";
 RL Proc. Natl. Acad. Sci. U.S.A. 83:8957-8961(1986).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-87053818; PubMed-3023045;
 RA Zilberstein A., Ruggieri R., Korn J.H., Revel M.,
 RT "Structure and expression of cDNA and genes for human
 RT interferon-beta-2, a distinct species inducible by growth-stimulatory
 RT cytokines.";
 RL EMBO J. 5:2529-2537(1986).
 RN [5]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-88087668; PubMed-3320204;
 RA Brakehoff J.P.J., de Groot E.R., Evers R.F., Pannekoek H.,
 RA Aarden L.A.,
 RT "Molecular cloning and expression of hybridoma growth factor in
 RT Escherichia coli.";
 RL J. Immunol. 139:4116-4121(1987).
 RN [6]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-89391958; PubMed-2789513;
 RA Torouchi N., Miwa K., Karasuyama H., Matsui H.,
 RT "Deletion of 3' untranslated region of human BSF-2 mRNA causes
 RT stabilization of the mRNA and high-level expression in mouse NIH3T3
 RT cells.";
 RL Biochem. Biophys. Res. Commun. 163:1056-1062(1989).

RN [7]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Fibroblast;
 RX MEDLINE-87004683; PubMed-3758081;
 RA Haegeman G., Content J., Volckaert G., Derynck R., Tavernier J.,
 RA Fiers W.,
 RT "Structural analysis of the sequence coding for an inducible 26-kDa
 RT protein in human fibroblasts.";
 RL Eur. J. Biochem. 159:625-632(1986).
 RN [8]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-89193317; PubMed-3266463;
 RA Wong G., Witek-Gianotti J., Hewick R., Clark S., Ogawa M.,
 RT "Interleukin 6: identification as a hematopoietic colony-stimulating
 RT factor.";
 RL Behring Inst. Mitt. 83:40-47(1988).
 RN [9]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-93178270; PubMed-1291290;
 RA Chen Q.Y.,
 RT "Stable and efficient expression of human interleukin-6 cDNA in
 RT mammalian cells after gene transfer.";
 RL Chung-Hua Chung Liu Tsa Chih 14:340-344(1992).
 RN [10]
 RP SEQUENCE OF 30-63.
 RX MEDLINE-88154445; PubMed-3279116;
 RA van Damme J., van Beeumen J., Decock B., van Snick J., de Ley M.,
 RA Billiau A.,
 RT "Separation and comparison of two monokines with
 RT lymphocyte-activating factor activity: IL-1 beta and hybridoma growth
 RT factor (HGF). Identification of leukocyte-derived HGF as IL-6.";
 RL J. Immunol. 140:1534-1541(1988).
 RN [11]
 RP SEQUENCE OF 50-212 OF RECOMBINANT FORM LACKING 1ST DISULFIDE BOND.
 RX MEDLINE-95154344; PubMed-7851440;
 RA Breton J., la Flura A., Bertolero F., Orsini G., Valsasina B.,
 RA Zilio R., de Filippi V., Polverino de Lauro P., Fontana A.,
 RT "Structure, stability and biological properties of a N-terminally
 RT truncated form of recombinant human interleukin-6 containing a single
 RT disulfide bond.";
 RL Eur. J. Biochem. 227:573-581(1995).
 RN [12]
 RP DISULFIDE BONDS.
 RX MEDLINE-89286115; PubMed-2472117;
 RA Clogston C.L., Boone T.C., Crandall B.C., Mendiaz E.A., Lu H.S.,
 RT "Disulfide structures of human interleukin-6 are similar to those of
 RT human granulocyte colony stimulating factor.";
 RL Arch. Biochem. Biophys. 272:144-151(1989).
 RN [13]
 RP MUTAGENESIS.
 RX MEDLINE-91243808; PubMed-2037043;
 RA Luetticken C., Krueitgen A., Moeller C., Heinrich P.C., Rose-John S.,
 RT "Evidence for the importance of a positive charge and an
 RT alpha-helical structure of the C-terminus for biological activity of
 RT human IL-6.";
 RL FEBS Lett. 282:265-267(1991).
 RN [14]
 RP STRUCTURE BY NMR.
 RX MEDLINE-96134845; PubMed-8555185;
 RA Nishimura C., Watanabe A., Gouda H., Shimada I., Arita Y.,
 RT "Folding topologies of human interleukin-6 and its mutants as studied
 RT by NMR spectroscopy.";
 RL Biochemistry 35:273-281(1996).
 RN [15]
 RP STRUCTURE BY NMR.
 RX MEDLINE-97303053; PubMed-9159484;
 RA Xu G.-Y., Yu H.-A., Hong J., Stahl M., McDonagh T., Kay L.E.,
 RA Cunnning D.A.,
 RT "Solution structure of recombinant human interleukin-6.";
 RL J. Mol. Biol. 268:468-481(1997).
 RN [16]
 RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
 RX MEDLINE-97224126; PubMed-9118960;

RA Somers W., Stahl M., Seehra J.S.;
RT "1.9-A crystal structure of interleukin 6: implications for a novel
RL mode of receptor dimerization and signaling.";
EMBO J. 16:989-997(1997).
CC -1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
CC FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
CC OF B-CELLS INTO IG-SECRETING CELLS, IT INDUCES MYELOMA AND
CC PLASMACYTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN
CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS.
CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.

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CC EMBL; X04430; CAA28026.1; -
CC DR EMBL; M14584; AAA52728.1; -
CC DR EMBL; X04602; CAA28268.1; -
CC DR EMBL; Y00081; CAA68278.1; -
CC DR EMBL; M18403; AAA52729.1; -
CC DR EMBL; M29150; AAA59154.1; -
CC DR EMBL; X04402; CAA27990.1; -
CC DR EMBL; X04403; CAA27991.1; -
CC DR EMBL; M54894; AAC41704.1; -
CC DR EMBL; S56892; AAD13886.1; -
CC DR EMBL; A09363; CAA00839.1; -
CC DR PIR; A32648; IVH0B2.
CC DR PIR; A25921; A25921.
CC DR PDB; 1IL6; 04-FEB-98.
CC DR PDB; 2IL6; 04-FEB-98.
CC DR PDB; 1ALU; 03-JUN-98.
CC DR MIM; 147620; -
CC DR InterPro: IPR003573; IL6_MGF_GCSF.
CC DR InterPro: IPR003574; Interleukin_6.
CC DR Pfam: PF00489; IL6; 1.
CC DR PRINTS; PR00433; IL6GCSFMGF.
CC DR PRINTS; PR00434; INTERLEUKIN6.
CC DR ProDom; PD004356; Interleukin_6; 1.
CC DR SMART; SM00126; IL6; 1.
CC DR PROSITE; PS00254; INTERLEUKIN_6; 1.
CC KM Cytokine; Glycoprotein; Growth factor; Signal; 3D-structure.
CC FT SIGNAL 1 29
CC FT CHAIN 30 212 INTERLEUKIN-6.
CC FT DISULFID 72 78
CC FT DISULFID 101 111
CC FT CARBOHYD 73 73
CC FT MUTAGEN 173 173 N-LINKED (GLCNAC...).
CC FT MUTAGEN 185 185 A->V: ALMOST NO LOSS OF ACTIVITY.
CC FT MUTAGEN 204 204 W->R: NO LOSS OF ACTIVITY.
CC FT MUTAGEN 210 204 S->P: 13% ACTIVITY.
CC FT MUTAGEN 212 210 R->K,E,Q,T,A,P: LOSS OF ACTIVITY.
CC FT MUTAGEN 212 212 M->T,N,S,R: LOSS OF ACTIVITY.
CC SO SEQUENCE 212 AA; 23718 MW; 1F1ED1FE1B734079 CRC64;

Query Match 93.0%; Score 53; DB 1; Length 212;
Best Local Similarity 100.0%; Pred. No. 0.0032;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE INTERLEUKIN-6 PRECURSOR (IL-6).
GN IL6.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OC NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RA Tatsumi M.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
CC FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
CC OF B-CELLS INTO IG-SECRETING CELLS, IT INDUCES MYELOMA AND
CC PLASMACYTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN
CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.

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CC EMBL; AB000554; BAA19148.1; -
CC DR HSSP; P05231; 2IL6.
CC DR InterPro: IPR003573; IL6_MGF_GCSF.
CC DR InterPro: IPR003574; Interleukin_6.
CC DR Pfam: PF00489; IL6; 1.
CC DR PRINTS; PR00433; IL6GCSFMGF.
CC DR PRINTS; PR00434; INTERLEUKIN6.
CC DR ProDom; PD004356; Interleukin_6; 1.
CC DR SMART; SM00126; IL6; 1.
CC DR PROSITE; PS00254; INTERLEUKIN_6; 1.
CC KM Cytokine; Glycoprotein; Growth factor; Signal.
CC FT SIGNAL 1 29
CC FT CHAIN 30 212
CC FT DISULFID 72 78 INTERLEUKIN-6.
CC FT DISULFID 101 111
CC FT CARBOHYD 73 73
CC FT CARBOHYD 172 172
CC FT SEQUENCE 212 AA; 23654 MW; CF8173FCBF0B0389 CRC64;

Query Match 93.0%; Score 53; DB 1; Length 212;
Best Local Similarity 100.0%; Pred. No. 0.0032;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DT 15-JUL-1998 (Rel. 36, Last sequence update)
DE INTERLEUKIN-6 PRECURSOR (IL-6).
GN IL6.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OC NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=RAC 2;

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RX MEDLINE-96003435; PubMed-7561102;
RA Villinger F.J., Bar S.S., Mayne A.E., Chikkala N., Ansari A.A.;
RT "Comparative sequence analysis of cytokine genes from human and
RT nonhuman primates.";
RT J. Immunol. 155:3946-3954(1995).
CC -1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
CC FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
CC OF B-CELLS INTO IG-SECRETING CELLS, IT INDUCES MYELOMA AND
CC PLASMACYTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN
CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
CC -----
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CC -----
CC EMBL; L26028; AAA99978.1; -.
CC DR HSSP; P05231; 1ALU.
CC DR InterPro: IPR003573; IL6_MGF_GCSF.
CC DR InterPro: IPR003574; Interleukin_6.
CC DR Pfam: PF00489; IL6; 1.
CC DR PRINTS; PR00433; IL6GCSFNGF.
CC DR PRINTS; PR00434; INTERLEUKIN6.
CC DR ProDom: PD004356; Interleukin_6; 1.
CC DR SMART: SM00126; IL6; 1.
CC DR PROSITE; PS00254; INTERLEUKIN_6; 1.
CC KW Cytokine; Glycoprotein; Growth factor; Signal.
CC FT SIGNAL 1 29 BY SIMILARITY.
CC FT CHAIN 30 212 INTERLEUKIN-6.
CC FT DISULFID 72 78 POTENTIAL.
CC FT DISULFID 101 111 POTENTIAL.
CC FT CARBOHYD 73 73 N-LINKED (GLCNAC...) (POTENTIAL).
CC FT CARBOHYD 172 172 N-LINKED (GLCNAC...) (POTENTIAL).
CC SO SEQUENCE 212 AA; 23728 MW; 4130DFECF0BCCAD CRC64;

Query Match 93.0%; Score 53; DB 1; Length 212;
Best Local Similarity 100.0%; Pred. No. 0.0033;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RYLDIGISALR 11
DB 58 RYLDIGISALR 68

RESULT 5
YJIA_ECOLI
ID YJIA_ECOLI STANDARD; PRT; 318 AA.
AC P24203;
DT 01-MAR-1992 (Rel. 21, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE HYPOTHETICAL 35.7 KDA PROTEIN IN MRR-TSR INTERGENIC REGION.
DE YJIA OR B4352.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-K12 / MG1655.
RX MEDLINE-95334362; PubMed-7610040.
RA Burland V.D., Plunkett G. III, Sofia H.J., Daniels D.L.,
RA Blattner F.R.;
RT "Analysis of the Escherichia coli genome VI: DNA sequence of the
RT region from 92.8 through 100 minutes.";
RL Nucleic Acids Res. 23:2105-2119(1995).
RN [2]
RP SEQUENCE OF 39-318 FROM N.A.

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RC STRAIN-K12;
RX MEDLINE-91317743; PubMed-1650347;
RA Walte-Rees P.A., Keating C.J., Moran L.S., Slatko B.E., Hornstra L.J.,
RA Benner J.S.;
RT "Characterization and expression of the Escherichia coli Mrr
RT restriction system.";
RT J. Bacteriol. 173:5207-5219(1991).
CC -----
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CC -----
CC EMBL; U14003; AAA97249.1; ALT_FRAME.
CC DR EMBL; AE000506; AAC77308.1; ALT_INIT.
CC DR EMBL; X54198; CAA38118.1; -.
CC DR PIR; S18778; S18778
CC DR EcoGene; EG10021; YJIA.
CC DR InterPro: IPR003495; CoBW.
CC DR Pfam: PF02492; CoBW; 1.
CC KW Hypothetical protein; Complete proteome.
CC SO SEQUENCE 318 AA; 35659 MW; 6D68463182031C41 CRC64;

Query Match 68.4%; Score 39; DB 1; Length 318;
Best Local Similarity 70.0%; Pred. No. 3.1;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RYLDIGISAL 10
DB 120 RYLDIGISAL 129

RESULT 6
AR02_TOBAC
ID AR02_TOBAC STANDARD; PRT; 338 AA.
AC P23281;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE 3-PHOSPHOSHIKIMATE 1-CARBOXYINYLTRANSFERASE 2 (PC 2.5.1.19) (5'-
DE ENOLPYRUVYLSHIKIMATE-3-PHOSPHATE SYNTHASE 2) (EPSP SYNTHASE 2)
DE (FRAGMENT).
OS Nicotiana tabacum (Common tobacco).
OS EPSPS-2.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asceridae; easterids I; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-92032779; PubMed-1932690;
RA Wang Y., Jones J., Weller S., Goldsborough P.B.;
RT "Expression and stability of amplified genes encoding 5-
RT enolpyruvylshikimate-3-phosphate synthase in glycosate-tolerant
RT tobacco cells.";
RT Plant Mol. Biol. 17:1127-1138(1991).
CC -1- CATALYTIC ACTIVITY: PHOSPHOENOLPYRUVATE + 3-PHOSPHOSHIKIMATE -
CC ORTHOPHOSPHATE + O(5)-(1-CARBOXYVINYL)-3-PHOSPHOSHIKIMATE.
CC -1- PATHWAY: SIXTH STEP IN THE BIOSYNTHESIS OF CHORISMATE WITHIN
CC THE BIOSYNTHESIS OF AROMATIC AMINO ACIDS (THE SHIKIMATE PATHWAY).
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST.
CC -1- MISCELLANEOUS: THIS ENZYME IS THE TARGET OF THE POTENT,
CC BROAD-SPECTRUM HERBICIDE, GLYPHOSATE (N-(PHOSPHONOMETHYL)GLYCINE).
CC OVERPRODUCTION OF EPSP LEADS TO GLYPHOSATE TOLERANCE.
CC -1- SIMILARITY: BELONGS TO THE EPSP SYNTHASE FAMILY.
CC -----
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CC -----
DR EMBL, M61905; AAA34072.1; -
DR PIR, S18354; S18354.
DR InterPro; IPR001986; EPSP_synthase.
DR Pfam; PF00275; EPSP_synthase; 1.
DR Prodom; PD001867; EPSP_synthase; 1.
DR PROSITE; PS00104; EPSP_SYNTHASE_1; PARTIAL.
DR PROSITE; PS00885; EPSP_SYNTHASE_2; 1.
DR Aromatic amino acid biosynthesis; Transferase; Chloroplast.
FT NON_TER 1
FT SEQUENCE 338 AA; 36319 MW; 569E9021BAD68B89 CRC64;
SQ

Query Match 68.4%; Score 39; DB 1; Length 338;
Best Local Similarity 54.5%; Pred. No. 3.3;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RYLDGISAALR 11
Db 13 RYLDGVPFMR 23
11:111: :1
13 RYLDGVPFMR 23

RESULT 7
AROA_PETHY STANDARD; PRT; 516 AA.
ID AROA_PETHY
AC P11043;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE 3-ENOLPYRUVYLTRANSFERASE PRECURSOR (EC 2.5.1.19)
DE (5-ENOLPYRUVYLSHIKIMATE-3-PHOSPHATE SYNTHASE) (EPSP SYNTHASE).
OS Petunia hybrida (Petunia).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Petunia.
OX NCBI_TaxID=4102;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=CV. MITCHELL;
RC MEDLINE=88153749; PubMed=3346248;
RA Gasser C.S., Winter J.A., Hironaka C.M., Shah D.M.;
RT "Structure, expression, and evolution of the
RT 5-enolpyruvylshikimate-3-phosphate synthase genes of petunia and
RT tomato.";
RL J. Biol. Chem. 263:4280-4289(1988).
[2]
RN MUTAGENESIS OF GLY-173.
RP MEDLINE=92042175; PubMed=1939260;
RA Padgett S.R., Re D.B., Gasser C.S., Elcholtz D.A., Frazier R.B.,
RA Hironaka C.M., Levine E.B., Shah D.M., Fraley R.T., Kishore G.M.;
RT "Site-directed mutagenesis of a conserved region of the 5-
RT enolpyruvylshikimate-3-phosphate synthase active site.";
RL J. Biol. Chem. 266:22364-22369(1991).
[3]
RN CATALYTIC ACTIVITY: PHOSPHOENOLPYRUVATE + 3-PHOSPHOSHIKIMATE -
RN ORTHOPHOSPHATE + O(5)-(1-CARBOXYVINYL)-3-PHOSPHOSHIKIMATE.
CC -1- PATHWAY: SIXTH STEP IN THE BIOSYNTHESIS OF CHORISMATE WITHIN
CC THE BIOSYNTHESIS OF AROMATIC AMINO ACIDS (THE SHIKIMATE PATHWAY).
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST.
CC -1- MISCELLANEOUS: THIS ENZYME IS THE TARGET OF THE POTENT,
CC BROAD-SPECTRUM HERBICIDE, GLYPHOSATE [N-(PHOSPHONOMETHYL)GLYCINE].
CC OVERPRODUCTION OF EPSP LEADS TO GLYPHOSATE TOLERANCE.
CC -1- SIMILARITY: BELONGS TO THE EPSP SYNTHASE FAMILY.
CC -----
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CC -----
DR EMBL, M21084; AAA33699.1; -
DR PIR, A28198; XUPYVS.
DR InterPro; IPR001986; EPSP_synthase.
DR Pfam; PF00275; EPSP_synthase; 1.
DR Prodom; PD001867; EPSP_synthase; 1.
DR PROSITE; PS00104; EPSP_SYNTHASE_1; 1.
DR PROSITE; PS00885; EPSP_SYNTHASE_2; 1.
DR Aromatic amino acid biosynthesis; Transferase; Transit peptide;
KW Chloroplast; Herbicide resistance.
FT CHAIN 1 72
FT TRANSIT 1 72
FT CHAIN 73 516
FT TRANSIT 73 516
FT CHAIN 173 173
FT TRANSIT 173 173
FT MUTAGEN 516 AA; 55537 MW; 1A753E717BE7BAF8 CRC64;
SQ

Query Match 68.4%; Score 39; DB 1; Length 516;
Best Local Similarity 54.5%; Pred. No. 5.3;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RYLDGISAALR 11
Db 191 RYLDGVPFMR 201
11:111: :1
191 RYLDGVPFMR 201

RESULT 8
AROL_TOBAC STANDARD; PRT; 518 AA.
ID AROL_TOBAC
AC P23981;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE 3-PHOSPHOSHIKIMATE 1-CARBOXYVINYLTRANSFERASE 1 PRECURSOR (EC 2.5.1.19)
DE (5-ENOLPYRUVYLSHIKIMATE-3-PHOSPHATE SYNTHASE 1) (EPSP SYNTHASE 1).
GN EPSPS-1.
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
[1]
RN SEQUENCE FROM N.A.
RP MEDLINE=92032779; PubMed=1932690;
RA Wang Y., Jones J., Weller S., Goldsbrough P.B.;
RT "Expression and stability of amplified genes encoding 5-
RT enolpyruvylshikimate-3-phosphate synthase in glyphosate-tolerant
RT tobacco cells.";
RL Plant Mol. Biol. 17:1127-1138(1991).
[2]
RN CATALYTIC ACTIVITY: PHOSPHOENOLPYRUVATE + 3-PHOSPHOSHIKIMATE -
RN ORTHOPHOSPHATE + O(5)-(1-CARBOXYVINYL)-3-PHOSPHOSHIKIMATE.
CC -1- PATHWAY: SIXTH STEP IN THE BIOSYNTHESIS OF CHORISMATE WITHIN
CC THE BIOSYNTHESIS OF AROMATIC AMINO ACIDS (THE SHIKIMATE PATHWAY).
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST.
CC -1- MISCELLANEOUS: THIS ENZYME IS THE TARGET OF THE POTENT,
CC BROAD-SPECTRUM HERBICIDE, GLYPHOSATE [N-(PHOSPHONOMETHYL)GLYCINE].
CC OVERPRODUCTION OF EPSP LEADS TO GLYPHOSATE TOLERANCE.
CC -1- SIMILARITY: BELONGS TO THE EPSP SYNTHASE FAMILY.
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CC -----
DR EMBL, M61904; AAA34071.1; -
DR PIR, S18353; S18353.
DR InterPro; IPR001986; EPSP_synthase.
DR Pfam; PF00275; EPSP_synthase; 1.
DR Prodom; PD001867; EPSP_synthase; 1.

DR PROSITE; PS00104; EPSP-SYNTASE_1; 1.
 DR PROSITE; PS00885; EPSP-SYNTASE_2; 1.
 KW Aromatic amino acid biosynthesis; transferase; transit peptide;
 KW Chloroplast.
 FT TRANSIT 1 74 CHLOROPLAST
 FT CHAIN 75 518 CARBOXYINYLTRANSFERASE 1
 SQ SEQUENCE 518 AA; 55711 MW; 4F03C514EAE1681 CRC64;

Query Match 68.4%; Score 39; DB 1; Length 518;
 Best Local Similarity 54.5%; Pred. No. 5.3;
 Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 RYLDGISAIRL 11
 Db 193 RYLDGVPFMR 203

RESULT 9
 AROA_LYCES STANDARD; PRT; 520 AA.
 ID AC P10748;
 DT 01-JUL-1989 (Rel. 11, Created)
 DT 01-JUL-1989 (Rel. 11, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE 3-PHOSPHOSHAKIMATE 1-CARBOXYINYLTRANSFERASE PRECURSOR (EC 2.5.1.19)
 OS (5-ENOLPYRUVYLSHIKIMATE-3-PHOSPHATE SYNTHASE) (EPSP SYNTHASE).
 OC Eucaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
 NC NCBI_TaxID=4081;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88153749; PubMed=3346248;
 RA Gasser C.S., Winter J.A., Hironaka C.M., Shah D.M.;
 RT "Structure, expression, and evolution of the
 5-enolpyruvylshikimate-3-phosphate synthase genes of petunia and
 tomato";
 RL J. Biol. Chem. 263:4280-4289(1988).
 CC -1- CATALYTIC ACTIVITY: PHOSPHOENOLPYRUVATE + 3-PHOSPHOSHAKIMATE -
 CC -1- PATHWAY: SIXTH STEP IN THE BIOSYNTHESIS OF CHORISMATE WITHIN
 CC -1- THE BIOSYNTHESIS OF AROMATIC AMINO ACIDS (THE SHIKIMATE PATHWAY).
 CC -1- SUBCELLULAR LOCATION: CHLOROPLAST.
 CC -1- MISCELLANEOUS: THIS ENZYME IS THE TARGET OF THE POTENT,
 CC BROAD-SPECTRUM HERBICIDE, GLYPHOSATE [N-(PHOSPHONOMETHYL)GLYCINE].
 CC OVERPRODUCTION OF EPSP LEADS TO GLYPHOSATE TOLERANCE.
 CC -1- SIMILARITY: BELONGS TO THE EPSP SYNTHASE FAMILY.
 CC -----
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 CC -----
 CC EMBL; M21071; AAA34136.1; -;
 DR EMBL; B28198; XUTQVS;
 DR InterPro; IPR001986; EPSP_synthase.
 DR Pfam; PF00275; EPSP_synthase; 1.
 DR ProDom; PD001867; EPSP_synthase; 1.
 DR PROSITE; PS00104; EPSP-SYNTASE_1; 1.
 DR PROSITE; PS00885; EPSP-SYNTASE_2; 1.
 KW Aromatic amino acid biosynthesis; transferase; transit peptide;
 KW Chloroplast.
 FT TRANSIT 1 76 CHLOROPLAST (POTENTIAL).
 FT CHAIN 77 520 CARBOXYINYLTRANSFERASE.
 FT SEQUENCE 520 AA; 55715 MW; 82B206182E8C8F4C CRC64;

Query Match 68.4%; Score 39; DB 1; Length 520;
 Best Local Similarity 54.5%; Pred. No. 5.3;
 Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 RYLDGISAIRL 11
 Db 195 RYLDGVPFMR 205

RESULT 10
 TY08_MYCTU STANDARD; PRT; 133 AA.
 ID TY08_MYCTU
 AC Q50717;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 20-AUG-2001 (Rel. 40, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE HYPOTHETICAL 14.3 KDA PROTEIN RV3408.
 GN RV3408 OR MT3516 OR MYC78.20C.
 OS Mycobacterium tuberculosis.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 NC NCBI_TaxID=1773;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=H37RV;
 RX MEDLINE=98295987; PubMed=9634230;
 RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
 RA Gordon S.V., Eigmeier K., Gas S., Barry C.E. III, Tekala F.,
 RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
 RA Davies R., Devlin K., Feltham T., Gentles S., Hamlin N., Holtroyd S.,
 RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
 RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
 RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
 RA Stulson J.E., Taylor K., Whitehead S., Barrett B.G.;
 RA "Deciphering the biology of Mycobacterium tuberculosis from the
 RT complete genome sequence.";
 RL Nature 393:537-544(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX STRAIN=CDC 1551 / Oshkosh;
 RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
 RA Peterson J., Deboy R., Dodson R., Gwinn M.L., Hatt D., Hickey E.,
 RA Kolony J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
 RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
 RA Bishop W.;
 RT "Whole genome comparison of Mycobacterium tuberculosis clinical and
 RT laboratory strains.";
 RL Submitted (Apr-2001) to the EMBL/GenBank/DBJ databases.

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 CC -----
 CC EMBL; Z77165; CAB01015.1; ALT_INIT.
 DR EMBL; AE007157; AAK47854.1; -;
 DR TIGR; MT3516; -;
 DR TubercuList; RV3408; -;
 KW Hypothetical protein; Complete proteome.
 FT CONFLICT 43 43 S -> L (IN REF. 2).
 FT SEQUENCE 133 AA; 14294 MW; 4F3F25F3C816C8FB CRC64;

Query Match 64.9%; Score 37; DB 1; Length 133;
 Best Local Similarity 58.3%; Pred. No. 2.9;
 Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RYLDGISAIRL 12
 I I I I I I I I

DB 60 RYLDGDLPL 71

RESULT 11

C2AA_BACTK STANDARD: PRT: 633 AA.

ID C2AA_BACTK P21253; 052764;

AC 01-MAY-1991 (Rel. 18, Created)

DT 01-MAY-1991 (Rel. 18, Last sequence update)

DT 20-AUG-2001 (Rel. 40, Last annotation update)

DE PESTICIDIAL CRYSTAL PROTEIN CR2AA (INSECTICIDAL DELTA-ENDOTOXIN (P2 CRYSTAL PROTEIN) (CRYSTALLINE ENTOMOCIDAL PROTOXIN) (71 KDA CRYSTAL PROTEIN) (P2 CRYSTAL PROTEIN) (MOSQUITO FACTOR).

GN CR2AA OR CR2IIA(A) OR CR2BI OR CR2II.

OS Bacillus thuringiensis (subsp. kurstaki), and Bacillus thuringiensis (subsp. kenyae).

OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillus/Staphylococcus group; Bacillus.

OX NCBI_TaxId=29339, 33930;

RN [1]

RP SEQUENCE FROM N.A.

RC SPECIES-B.t.kurstaki; STRAIN-HD-1;

RX MEDLINE=89123178; PubMed=2914879;

RA Widner W.R., Whiteley H.R.;

RT "Two highly related insecticidal crystal proteins of Bacillus thuringiensis subsp. kurstaki possess different host range specificities.";

RT J. Bacteriol. 171:965-974(1989).

RN [2]

RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-26.

RC SPECIES-B.t.kurstaki; STRAIN-HD-263, AND HD-1;

RX MEDLINE=88087146; PubMed=3121615;

RA Donovan W.P., Dankosik C.C., Gilbert M.P., Gawron-Burke M.C., Groat R.G., Carlton B.C.;

RT Amino acid sequence and entomocidal activity of the P2 crystal protein. An insect toxin from Bacillus thuringiensis var. kurstaki.;

RT J. Biol. Chem. 263:561-567(1988).

RN [3]

RP REVISIONS.

RA Donovan W.P., Dankosik C.C., Gilbert M.P., Gawron-Burke M.C., Groat R.G., Carlton B.C.;

RT J. Biol. Chem. 264:4740-4740(1989).

RN [4]

RP SEQUENCE FROM N.A.

RC SPECIES-B.t.kenyae; STRAIN-4A4C / HD-549;

RA Mista H.S., Kallinar N.P., Mathur M., Donnelly R.J., Mahajan S.K.;

RT Submitted (Feb-1998) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT EPITHELIAL CELLS OF BOTH DIPTERAN (Aedes Aegypti) AND LEPIDOPTERAN (Manduca sexta) LARVAE.

CC -1- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING SPOROULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART OF THE SPORE COAT.

CC -1- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE N-TERMINUS.

CC -1- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.

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CC EMBL, M23723; AAA83516.1; -

DR EMBL, M31738; AAA22335.1; -

DR EMBL, AF047038; AAC04867.1; -

DR PIR, A29913; A29913.

DR PIR, C32053; C32053.

DR InterPro, IPR001178; Endotoxin.

DR Pfam, PF00555; endotoxin; 1.

KW Toxin; Sporulation.

FT VARIANT 1 1 MISSING (IN 50% OF THE MOLECULES).

FT VARIANT 3 3 N -> S (IN STRAIN 4A4C / HD-549).

FT VARIANT 409 409 F -> S (IN STRAIN 4A4C / HD-549).

FT VARIANT 541 541 N -> S (IN STRAIN 4A4C / HD-549).

FT VARIANT 588 588 S -> P (IN STRAIN 4A4C / HD-549).

SO SEQUENCE 633 AA; 70852 MW; 15182FAC78E58A4 CRC64;

Query Match 64.9%; Score 37; DB 1; Length 633;

Best Local Similarity 72.7%; Pred. No. 17;

Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 YINDGISALRL 12

DB 306 YILGIGSIRL 316

RESULT 12

DP3B_MVCTU STANDARD: PRT: 402 AA.

ID DP3B_MVCTU

AC 050730; 053602;

DT 15-DEC-1998 (Rel. 37, Created)

DT 15-DEC-1998 (Rel. 37, Last sequence update)

DT 20-AUG-2001 (Rel. 40, Last annotation update)

DE DNA POLYMERASE III, BETA CHAIN (EC 2.7.7.7).

GN DNAN OR RV0002 OR MFO002 OR MTW029.02 OR MTCY10H4.0.

OS Mycobacterium tuberculosis.

OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;

OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.

OX NCBI_TaxId=1773;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-H37RV;

RX MEDLINE=96310367; PubMed=8733228;

RA Salazar L., Fsihi H., de Rossi E., Riccardi G., Rios C., Cole S.T., Takiff H.E.;

RT "Organization of the origins of replication of the chromosomes of Mycobacterium smegmatis. Mycobacterium lepre and Mycobacterium tuberculosis and isolation of a functional origin from M. smegmatis.;"

RT Mol. Microbiol. 20:283-293(1996).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN-H37RV;

RX MEDLINE=98295967; PubMed=9634230;

RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D., Gordon S.V., Eigmeier K., Gas S., Barry C.E. III, Tekala F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feldwell T., Gentles S., Hamlin N., Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrett B.G.;

RT "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.;"

RT Nature 393:537-544(1998).

RN [3]

RP SEQUENCE FROM N.A.

RC STRAIN-CDC 1551 / Oshkosh;

RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E., Kolony J.F., Nelson W.C., Umayam L.A., Esmolaeva M.D., Salzberg S.L., Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A., Bishai W.;

RT "Whole genome comparison of Mycobacterium tuberculosis clinical and laboratory strains.;"

RT Submitted (Apr-2001) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: DNA POLYMERASE III IS A COMPLEX, MULTISUBUNIT ENZYME RESPONSIBLE FOR MOST OF THE REPLICATIVE SYNTHESIS IN BACTERIA. THIS DNA POLYMERASE ALSO EXHIBITS 3' TO 5' EXONUCLEASE ACTIVITY. THE BETA CHAIN IS REQUIRED FOR INITIATION OF REPLICATION ONCE IT IS CLAMPED ONTO DNA. IT SLIDES FREELY (BIDIRECTIONAL AND ATP-INDEPENDENT) ALONG DUPLEX DNA (BY SIMILARITY).

```

CC -1- CATALYTIC ACTIVITY: N DEOXYNUCLEOSIDE TRIPHOSPHATE -
CC N PYROPHOSPHATE + DNA(N).
CC -1- SUBUNIT: CONTAINS A CORE (COMPOSED OF ALPHA, EPSILON, AND
CC THEA CHAINS) THAT CAN REPAIR SMALL GAPS CREATED BY NUCLEASE
CC IN DUPLEX DNA. FOR EFFICIENT REPLICATION OF THE LONG, SINGLE-
CC STRANDED TEMPLATES, POL III REQUIRES THE AUXILIARY CHAINS BETA,
CC GAMMA, AND DELTA (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
CC -----
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CC -----
DR EMBL: X92504: CAA63258.1; -
DR EMBL: AL021427: CAA16239.1; -
DR EMBL: AE006915: AAK44225.1; -
DR TIGR: MT0002; -
DR TubercuList: Rv0002; -
DR InterPro: IPR001001: DNA_polIII_beta.
DR Pfam: PF00712: DNA_pol3_beta.1.
DR SMART: SM00480: POL3Bc.1.
DR Transferrase: DNA-directed DNA polymerase; DNA replication;
DR Complete proteome.
FT FT CONFLICT 171 184 ILGTYVLAATDR -> SLVRGSCARDS (IN REF.
FT FT CONFLICT 192 192 K -> E (IN REF. 1).
SQ SEQUENCE 402 AA; 42113 MW; 1ABA86D18653B42D CRC64;

Query Match 63.2%; Score 36; DB 1; Length 402;
Best Local Similarity 60.0%; Pred. NO. 16;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 YLIDGISLR 11
   1: 111111
Db 339 YLIDGISLR 348

RESULT 13
DP02_ECOLI STANDARD; PRT; 782 AA.
AC P2189;
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE DNA POLYMERASE II (Ec 2.7.7.7) (POL II).
GN POLB OR DINA OR B0060.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OC NCBI_TaxID=562;
RN NM [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-8.
RC STRAIN-K12 / W3110;
RX MEDLINE=91238699; PubMed=2034216;
RA Iwasaki H., Ishino Y., Toh H., Nakata A., Shinagawa H.;
RT "Escherichia coli DNA polymerase II is homologous to alpha-like DNA
RT polymerases."
RL Mol. Gen. Genet. 226:24-33(1991).
RN NM [2]
RP SEQUENCE FROM N.A.
RC STRAIN-K12;
RX MEDLINE=91083835; PubMed=2261080;
RA Chen H., Sun Y., Stark T., Beattie W., Moses R.E.;
RT "Nucleotide sequence and deletion analysis of the polB gene of
RT Escherichia coli."
RL DNA Cell Biol. 9:631-635(1990).
RN NM [3]
RP SEQUENCE FROM N.A.

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RC STRAIN-K12;
RX MEDLINE=92334977; PubMed=1630901;
RA Yara T., Mori H., Nagai H., Nagata T., Ishihama A., Fujita N.,
RA Isono K., Mizobuchi K., Nakata A.;
RT "Systematic sequencing of the Escherichia coli genome: analysis of
RT the 0-2.4 min region."
RL Nucleic Acids Res. 20:3305-3308(1992).
RN NM [4]
RP SEQUENCE FROM N.A.
RC STRAIN-K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blatner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Colado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12."
RL Science 277:1453-1474(1997).
RN NM [5]
RP SEQUENCE OF 1-457 FROM N.A., AND SEQUENCE OF 1-27.
RC STRAIN-K12;
RX MEDLINE=91017565; PubMed=2217198;
RA Bonner C.A., Hays S., McEntee K., Goodman M.F.;
RT "DNA polymerase II is encoded by the DNA damage-inducible dna gene
RT of Escherichia coli."
RL Proc. Natl. Acad. Sci. U.S.A. 87:7663-7667(1990).
RN NM [6]
RP VARIANT MUTANT ALLELE POLB100.
RX MEDLINE=97236820; PubMed=9079692;
RA Olin Z., Goodman M.F.;
RT "The Escherichia coli polB locus is identical to dnaA, the structural
RT gene for DNA polymerase II. Characterization of Pol II purified from
RT a polB mutant."
RL J. Biol. Chem. 272:8611-8617(1997).
CC -1- FUNCTION: THOUGHT TO BE INVOLVED IN DNA REPAIR AND/OR MUTAGENESIS.
CC -1- CATALYTIC ACTIVITY: N DEOXYNUCLEOSIDE TRIPHOSPHATE -
CC N PYROPHOSPHATE + DNA(N).
CC -1- ENZYME REGULATION: DNA POLYMERASE II ACTIVITY IS REGULATED BY
CC THE LEXA GENE DURING THE SOS RESPONSE.
CC -1- SIMILARITY: BELONGS TO DNA POLYMERASE TYPE-B FAMILY.
CC -----
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CC -----
DR EMBL: X54847: CAA38616.1; -
DR EMBL: M37727: AAA23684.1; -
DR EMBL: M62646: AAA24406.1; -
DR EMBL: M35371: AAA24407.1; -
DR EMBL: M38283: AAA63764.1; -
DR EMBL: D10483: BAA01331.1; -
DR EMBL: AE000116: AAC73171.1; -
DR PIR: S15943: JDEC22.
DR PIR: B36236: B36236.
DR PIR: J00780: J00780.
DR PIR: S19263: S19263.
DR Ecogene: IG10747: POLB.
DR InterPro: IPR002064: DNA_POL_B.
DR Pfam: PF00136: DNA_POL_B.1.
DR PRINTS: PR00106: DNAPOLB.
DR SMART: SM00486: POLBc.1.
DR PROSITE: PS00116: DNA_POLYMERASE_B.1.
DR Transferrase: DNA-directed DNA polymerase; SOS response; DNA repair;
DR DNA-binding: Complete proteome.
FT FT INT_MEF 0 0
FT FT VARIANT 400 400 G -> D (IN POLB100 ALLELE).
FT FT CONFLICT 171 171 G -> A (IN REF. 2).
FT FT CONFLICT 256 257 EH -> DD (IN REF. 5).
FT FT CONFLICT 271 271 R -> G (IN REF. 5).
FT FT CONFLICT 734 734 N -> T (IN REF. 2).

```

FT CONFLICT 739 782 LDYORSPUDYEHYLTROLOPVAEGILPEIDNEFATL
FT FTMTGOLGLE -> PCILPFTTGLRPLSPDPATRGCG
FT NTPFY (IN REF. 2)
SQ SEQUENCE 782 AA; 89921 MM; 286B40412ACF45A1 CRC64;

Query Match 63.2%; Score 36; DB 1; Length 782;
Best Local Similarity 63.6%; Pred. No. 33;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 RYLDGISALR 11
1:111111
Db 271 RLIDIGLEALK 281

RESULT 14

IL6_CANFA STANDARD; PRT; 207 AA.
AC P41323;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE INTERLEUKIN-6 PRECURSOR (IL-6).
GN IL6.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MONGREL;
RX MEDLINE=94303924; PubMed=7913298;
RA Kujala G.L., Youker K.A., Hawkins H.K., Perrard J.L.,
Michael L.H., Ballantyne C.M., Smith C.W., Entman M.L.;
RT Regulation of ICAM-1 and IL-6 in myocardial ischemia: effect of
reperfusion.*;
RL Ann. N.Y. Acad. Sci. 723:258-270(1994).

CC -1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
CC FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
CC OF B-CELLS INTO IG-SECRETING CELLS, IT INDUCES MYELOMA AND
CC PLASMACYTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN
CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS.
CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
CC -----
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CC EMBL: U12234; AAA83030.1; -.
DR HSSP; P05231; 21L6.
DR InterPro: IPR003573; IL6_MGF_GCSF.
DR InterPro: IPR003574; Interleukin_6.
DR Pfam: PF00489; IL6; 1.
DR PRINTS: PR00433; IL6GCSFMGF.
DR PRINTS: PR00434; INTERLEUKIN6.
DR PRODOM: PD004356; Interleukin_6; 1.
DR SMART: SM00126; IL6; 1.
DR PROSITE: PS00254; INTERLEUKIN_6; 1.
KW Cytokine; Glycoprotein; Growth factor; Signal.
FT SIGNAL 1
FT CHAIN ? 207 POTENTIAL.
FT DISULFD 67 73 BY SIMILARITY.
FT DISULFD 96 106 BY SIMILARITY.
SQ SEQUENCE 207 AA; 22945 MM; 45540154EA9C0F50 CRC64;

Query Match 61.4%; Score 35; DB 1; Length 207;
Best Local Similarity 72.7%; Pred. No. 12;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 RYLDGISALR 11
:11111111
Db 53 KYILGRISALR 63

Query Match 61.4%; Score 35; DB 1; Length 209;
Best Local Similarity 72.7%; Pred. No. 12;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 RYLDGISALR 11
:11111111
Db 55 KYILGRISALR 65

IL6_PROVI STANDARD; PRT; 209 AA.
AC Q28819;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE INTERLEUKIN-6 PRECURSOR (IL-6) (FRAGMENT).
GN IL6.
OS Phoca vitulina (Harbor seal).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Pinnipedia; Phocidae; Phoca.
OX NCBI_TaxID=9720;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96163018; PubMed=8575817;
RA King D.P., Schrenzel M.D., McKnight M.L., Reidarson T.H., Hanni K.D.,
Stolt J.L., Ferrick D.A.;
RT Molecular cloning and sequencing of interleukin 6 cDNA fragments from
RT the harbor seal (Phoca vitulina), killer whale (Orcinus orca), and
RT Southern sea otter (Enhydra lutris nereis).*;
RL Immunogenetics 43:190-195(1996).

CC -1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
CC FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
CC OF B-CELLS INTO IG-SECRETING CELLS, IT INDUCES MYELOMA AND
CC PLASMACYTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN
CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: SECRETED.
CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
CC -----
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CC EMBL: I46802; AAB01430.1; -.
DR HSSP; P05231; 21L6.
DR InterPro: IPR003573; IL6_MGF_GCSF.
DR InterPro: IPR003574; Interleukin_6.
DR Pfam: PF00489; IL6; 1.
DR SMART: SM00126; IL6; 1.
DR PROSITE: PS00254; INTERLEUKIN_6; 1.
KW Cytokine; Glycoprotein; Growth factor; Signal.
FT NON_TER 1
FT SIGNAL 1
FT CHAIN ? 209 BY SIMILARITY.
FT DISULFD 69 75 BY SIMILARITY.
FT DISULFD 98 108 BY SIMILARITY.
SQ SEQUENCE 209 AA; 23483 MM; 75144922EA3B48E9 CRC64;

Search completed: December 19, 2001, 16:26:13
Job time: 568 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: December 19, 2001, 16:16:15 ; Search time 157.32 Seconds
(without alignments)
11.157 Million cell updates/sec

Title: US-09-202-104A-1
Perfect score: 57
Sequence: 1 RYLDGISAALRL 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : SPREMBL_17:*
1: sp.archaea:*
2: sp.bacteria:*
3: sp.fungi:*
4: sp.human:*
5: sp.invertebrate:*
6: sp.mammal:*
7: sp.mhc:*
8: sp.organelle:*
9: sp.phage:*
10: sp.plant:*
11: sp.podent:*
12: sp.virus:*
13: sp.vertebrate:*
14: sp.unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	53	93.0	209	6	097540
2	49	86.0	175	6	097540
3	49	86.0	209	6	097540
4	46	80.7	160	6	097535
5	42	73.7	383	5	09W5A3
6	42	73.7	387	2	09A984
7	42	73.7	402	5	046309
8	41	71.9	386	2	091566
9	39	68.4	261	2	046988
10	39	68.4	641	10	09F095
11	39	68.4	787	2	0912L1
12	38	66.7	124	1	09YAB3
13	38	66.7	673	12	067469
14	38	66.7	699	8	033257
15	38	66.7	737	12	09DW97
16	37	64.9	334	2	09HVI5
17	37	64.9	377	1	09HJ49
18	37	64.9	551	2	09RM89
19	37	64.9	633	2	09S6N5

20	37	64.9	633	2	09S6N4	09S6N4 bacillus th
21	36	63.2	199	2	032572	032572 escherichia
22	36	63.2	284	2	025696	025696 helicobacte
23	36	63.2	289	2	09ZM54	09ZM54 helicobacte
24	36	63.2	297	2	09RQD4	09RQD4 zymomonas m
25	36	63.2	402	2	09EVN6	09EVN6 mycobacteri
26	36	63.2	473	2	09KCG6	09KCG6 bacillus ha
27	36	63.2	483	2	09S242	09S242 streptomyc
28	36	63.2	774	2	09F175	09F175 pseudomonas
29	36	63.2	1371	2	09PBS8	09PBS8 xyloella fas
30	35	61.4	139	2	09RNB9	09RNB9 microcystis
31	35	61.4	183	2	09K5A3	09K5A3 erwinia chr
32	35	61.4	192	2	044531	044531 azotobacter
33	35	61.4	192	2	0912V7	0912V7 pseudomonas
34	35	61.4	194	1	09HJ04	09HJ04 thermoplas
35	35	61.4	207	6	09MYZ7	09MYZ7 canis famli
36	35	61.4	323	2	09RDP4	09RDP4 streptomyc
37	35	61.4	366	2	09PHE2	09PHE2 xyloella fas
38	35	61.4	376	10	09FKG7	09FKG7 arabidopsis
39	35	61.4	391	1	09HMR6	09HMR6 vibrio chol
40	35	61.4	638	2	09HTU2	09HTU2 halobacteri
41	35	61.4	813	2	09A909	09A909 pseudomonas
42	35	61.4	841	10	09FS92	09FS92 samanea sam
43	35	61.4	1135	2	09LI16	09LI16 streptomyc
44	35	61.4	1436	2	09PKP1	09PKP1 chlamydia m
45	35	61.4	1436	2	09PKP1	09PKP1 chlamydia m

ALIGNMENTS

RESULT 1

097540 ID 097540 PRELIMINARY; PRT. 209 AA.

AC 097540:

DT 01-MAY-1999 (TREMBLrel. 10, Created)

DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)

DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)

DE INTERLEUKIN-6 (FRAGMENT).

GN IL-6.

OS Aotus nancymae (Owl monkey).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.

OX NCBI_TaxID=37293;

RN [1]

RP SEQUENCE FROM N.A.

RA Echeverry S.J., Hernandez E., Moreno A., Patarroyo M.E., Murillo L.A.;

RT "Identification, cloning and sequencing of different interleukin genes

in 4 Aotus species";

RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.

DR HSSP; AF014510; AAD01536.1; ..

DR InterPro; IPR003573; IL6_MGF_GCSF.

DR Pfam; PF00489; IL6; 1.

DR PRINTS; PR00433; IL6GCSFMGF.

DR SMART; SM00126; IL6; 1.

DR PROSITE; PS00254; INTERLEUKIN_6; 1.

FT NON_TER 1

FT NON_TER 1

SQ SEQUENCE 209 AA; 23406 MW; E84F085DD84002DD CRC64;

Query Match 93.0%; Score 53; DB 6; Length 209;

Best Local Similarity 100.0%; Pred. No. 0.031;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RYLDGISAALRL 11
|||||

DB 58 RYLDGISAALRL 68

RESULT 2

ID 09TTH4 PRELIMINARY; PRT; 175 AA.
AC 09TTH4;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE INTERLEUKIN-6 (FRAGMENT).
GN IL-6.
OS Aotus nigriceps (black-headed night monkey).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.
OX NCBI_TaxID=57175;
RN [1]
RP SEQUENCE FROM N.A.
RA Murillo L.A., Hernandez E., Echeverry S.J., Mendez J.A.,
RA Patarroyo M.E.;
RT *Aotus nigriceps gene for IL-6.*;
RT Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF097322; AAF21297.1; -.
DR HSSP: P05231; 1ALU.
DR InterPro: IPR003573; IL6_MGF_GCSF.
DR Pfam: PF00489; IL6; 1.
DR PRINTS: PR00433; IL6GCSFMGF.
DR SMART: SM00126; IL6; 1.
DR PROSITE: PS00254; INTERLEUKIN_6; 1.
DR NON_TER 1 1
FT SEQUENCE 175 AA; 19205 MW; 2BCCE574CB99B189 CRC64;
SQ

Query Match 86.0%; Score 49; DB 6; Length 175;
Best Local Similarity 90.9%; Pred. No. 0.15;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RYILDGISALR 11
Db 58 RYILEGISALR 68

RESULT 3
O9TTH3 PRELIMINARY; PRT; 209 AA.
AC 09TTH3;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE INTERLEUKIN-6 (FRAGMENT).
GN IL-6.
OS Aotus lemurinus (Northern gray-necked night monkey).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.
OX NCBI_TaxID=43147;
RN [1]
RP SEQUENCE FROM N.A.
RA Murillo L.A., Hernandez E., Echeverry S.J., Mendez J.A.,
RA Patarroyo M.E.;
RT *Aotus lemurinus gene for IL-6.*;
RT Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF097323; AAF21298.1; -.
DR HSSP: P05231; 1ALU.
DR InterPro: IPR003573; IL6_MGF_GCSF.
DR Pfam: PF00489; IL6; 1.
DR PRINTS: PR00433; IL6GCSFMGF.
DR SMART: SM00126; IL6; 1.
DR PROSITE: PS00254; INTERLEUKIN_6; 1.
DR NON_TER 1 1
FT SEQUENCE 209 AA; 23115 MW; A0A3DFAA4BF560CC CRC64;
SQ

Query Match 86.0%; Score 49; DB 6; Length 209;
Best Local Similarity 90.9%; Pred. No. 0.18;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RYILDGISALR 11

Db 58 RYILEGISALR 68

RESULT 4
O9T535 PRELIMINARY; PRT; 160 AA.
AC 09T535;
DT 01-MAY-1999 (TReMBLrel. 10, Created)
DT 01-MAY-1999 (TReMBLrel. 10, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE INTERLEUKIN-6 (FRAGMENT).
GN IL-6.
OS Aotus vociferans (noisy night monkey).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.
OX NCBI_TaxID=57176;
RN [1]
RP SEQUENCE FROM N.A.
RA Echeverry S.J., Hernandez E., Moreno A., Patarroyo M.E., Murillo L.A.;
RA *Identification, cloning and sequencing of different interleukin genes
in 4 Aotus species.*;
RT Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF014505; AAD01531.1; -.
DR HSSP: P05231; 1IL6.
DR InterPro: IPR003573; IL6_MGF_GCSF.
DR Pfam: PF00489; IL6; 1.
DR PRINTS: PR00433; IL6GCSFMGF.
DR SMART: SM00126; IL6; 1.
DR PROSITE: PS00254; INTERLEUKIN_6; 1.
DR NON_TER 1 1
FT SEQUENCE 160 AA; 17855 MW; 07A021338650A46D CRC64;
SQ

Query Match 80.7%; Score 46; DB 6; Length 160;
Best Local Similarity 81.8%; Pred. No. 0.51;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 RYILDGISALR 11
Db 58 RYILEGISALR 68

RESULT 5
O9W5A3 PRELIMINARY; PRT; 383 AA.
AC 09W5A3;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE EG:BD8.6 PROTEIN.
GN EG:BD8.6 OR CG11412.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BREKLEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Cealiker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Mortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazey R.G., Chame M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballen R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durkin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
 RA Palazzolo M., Pitman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spletter E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svitskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT *The genome sequence of Drosophila melanogaster.*;
 RL Science 287:2185-2195(2000).
 DR EMBL: AE003420: AAP45606.1;
 DR FlyBase: FBgn0024362; EG:8D8.6;
 DR InterPro: IPR000182: Acetyltransferase; GCN5.
 DR Pfam: PF00583: Acetyltransferase; 1.
 DR SEQUENCE 383 AA; 43005 MW; E3B528F4BC8A0CFD CRC64;

Query Match 73.7%; Score 42; DB 5; Length 383;
 Best Local Similarity 66.7%; Pred. No. 8.2;
 Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 RYLDGISAALRL 12
 |||:|:|:|:|
 DB 367 RYLDGISAALRL 378

RESULT 6
 O9A984 PRELIMINARY; PRT: 387 AA.
 AC O9A984;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE ACYD-COA DEHYDROGENASE FAMILY PROTEIN.
 GN CC110.
 OS Caulobacter crescentus.
 OC Bacteria; Proteobacteria; alpha subdivision; Caulobacter group;
 OC Caulobacter.
 OX NCBI_TaxID=69394;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE:21173696; PubMed:11259647;
 RA Niemman W.C., Feldblum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
 RA Eisten J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
 RA Potocka I., Nelson W.C., Newton A., Stephens C., Placke N.D., Ely B.,
 RA Deboy R.T., Dodson R.J., Durkin A.S., Gwin M.L., Haft D.H.,
 RA Kolony J.F., Smit J., Craven M.B., Kouri H., Shetty J., Berry K.,
 RA Utterback T., Tran K., Wolf A., Yamachyan J., Ermolaeva M., White O.,
 RA Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;
 RT *Complete genome sequence of Caulobacter crescentus.*;
 RL Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
 DR EMBL: AE005789; AAK23094.1;
 DR TIGR: CC110;
 KW Complete proteome.
 SQ SEQUENCE 387 AA; 41983 MW; C68AAB83D2D6779F CRC64;

Query Match 73.7%; Score 42; DB 2; Length 387;
 Best Local Similarity 66.7%; Pred. No. 8.3;
 Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 RYLDGISAALRL 12
 |||:|:|:|:|
 DB 236 RYLDGISAALRL 247

RESULT 7
 O46309 PRELIMINARY; PRT: 402 AA.
 AC O46309;
 DT 01-JUN-1998 (TREMBLrel. 06, Created)
 DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE EG:8D8.6 OR CG11412.
 GN EG:8D8.6 OR CG11412.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BERKELEY;
 RA MEDLINE:20196006; PubMed:10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazer V., Chapple M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Adayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotler P.,
 RA Burlis K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durkin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
 RA Palazzolo M., Pitman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spletter E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svitskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT The genome sequence of Drosophila melanogaster.*;
 RL Science 287:2185-2195(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Papapanagiotis G., Spanos L., Cox S., Siden-Kiamos I., Louis C.;
 RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
 RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.

DR EMBL: AE003420: AAF45605.1: -
 DR EMBL: AL022018: CAI17683.1: -
 DR FlyBase: FBgn0024362; EG:8D8.6.
 DR InterPro: IPR00182; Acetyltransf_GCN5.
 DR Pfam: PF00583; Acetyltransf_1.
 SQ SEQUENCE 402 AA; 45172 MW; 8F758605333E5E5E CRC64;

Query Match 73.7%; Score 42; DB 5; Length 402;
 Best Local Similarity 66.7%; Pred. No. 8.7;
 Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 RYLDGISAURL 12
 |||:|:|
 Db 386 RYLYNGVDALRL 397

RESULT 8
 ID Q91566 PRELIMINARY; PRT; 386 AA.
 AC Q91566;
 DT 01-MAR-2001 (TEMBLrel. 16, Created)
 DT 01-MAR-2001 (TEMBLrel. 16, Last sequence update)
 DT 01-JUN-2001 (TEMBLrel. 17, Last annotation update)
 DE PROBABLE ACYL-COA DEHYDROGENASE.
 GN PA0879.
 OS Pseudomonas aeruginosa.
 OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
 OC Pseudomonas.
 OX NCBI_TaxID=287;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=20437337; Pubmed=10984043;
 RA Stover C.K., Pham X.-O.T., Erwin A.L., Mizoguchi S.D., Warrenner P.,
 RA Hickey M.J., Brinkman F.S.T., Hufnagle W.O., Kowalik D.J., Lagrou M.,
 RA Garber R.L., Goltzy L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
 RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
 RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
 RA Reizer J., Saler M.H., Hancock R.E.W., Lory S., Olson M.V.;
 RA "Complete genome sequence of Pseudomonas aeruginosa PA01, an
 opportunistic pathogen.";
 RT Nature 406:959-964(2000).
 RL EMBL: AE004522; AAC04268.1; -
 DR InterPro: IPR001552; Acyl-CoA_dh.
 DR Pfam: PF00441; Acyl-CoA_dh; 2.
 DR PROSITE: PS00073; ACYL_COA_DH_2; UNKNOWN_1.
 KW Complete proteome.
 SQ SEQUENCE 386 AA; 42825 MW; B9FAC778EB359836 CRC64;

Query Match 71.9%; Score 41; DB 2; Length 386;
 Best Local Similarity 72.7%; Pred. No. 13;
 Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RYLDGISAURL 11
 |||||:|
 Db 235 RYLDGSLAER 245

RESULT 9
 ID Q46988 PRELIMINARY; PRT; 261 AA.
 AC Q46988;
 DT 01-NOV-1996 (TEMBLrel. 01, Created)
 DT 01-NOV-1996 (TEMBLrel. 01, Last sequence update)
 DT 01-JUN-2001 (TEMBLrel. 17, Last annotation update)
 DE OFB14 (FRAGMENT).
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 OX NCBI_TaxID=562;
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN-ATCC 11105.
 RX MEDLINE=96125235; Pubmed=8550403;
 RA Pileo M.A., Diaz E., Garcia J.L.;
 RA "Molecular characterization of the 4-hydroxyphenylacetate catabolic
 RT pathway of Escherichia coli W: engineering a mobile aromatic
 RT degradative cluster.";
 RL J. Bacteriol. 178:111-120(1996).
 DR EMBL: Z37980; CAA8052.1; -
 DR InterPro: IPR003495; CoBW.
 DR Pfam: PF02492; CoBW; 1.
 FT NON_TER 261
 SQ SEQUENCE 261 AA; 28672 MW; 7C957440C3422EAC CRC64;

Query Match 68.4%; Score 39; DB 2; Length 261;
 Best Local Similarity 70.0%; Pred. No. 20;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RYLDGISAURL 10
 |||:|:|
 Db 148 RYLDGVIAL 157

RESULT 10
 ID Q9FU95 PRELIMINARY; PRT; 641 AA.
 AC Q9FU95;
 DT 01-MAR-2001 (TEMBLrel. 16, Created)
 DT 01-MAR-2001 (TEMBLrel. 16, Last sequence update)
 DT 01-MAR-2001 (TEMBLrel. 16, Last annotation update)
 DE P0019D06.6 PROTEIN.
 GN P0019D06.6
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzae; Oryza.
 OX NCBI_TaxID=4530;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CV, NIPPONBARE;
 RA Sasaki T., Matsumoto T., Yamamoto K.;
 RA "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
 RT clone:P0019D06.";
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AP002483; BAB16449.1; -
 SQ SEQUENCE 641 AA; 72807 MW; B37CD89FF5B200AF CRC64;

Query Match 68.4%; Score 39; DB 10; Length 641;
 Best Local Similarity 66.7%; Pred. No. 56;
 Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 RYLDGISAURL 12
 |||||:|
 Db 211 RYLDGSKLQI 222

RESULT 11
 ID Q912L1 PRELIMINARY; PRT; 787 AA.
 AC Q912L1;
 DT 01-MAR-2001 (TEMBLrel. 16, Created)
 DT 01-MAR-2001 (TEMBLrel. 16, Last sequence update)
 DT 01-JUN-2001 (TEMBLrel. 17, Last annotation update)
 DE DNA POLYMERASE II.
 GN POLB OR PA1886.
 OS Pseudomonas aeruginosa.
 OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
 OC Pseudomonas.
 OX NCBI_TaxID=287;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN-PA01;
RX MEDLINE=20437337; PubMed=10984043;
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,
Hickey M.J., Brinkman F.S.L., Huinagle W.O., Kowalik D.J., Lagrou M.,
Rader R.L., Goltzy L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
Brody L.L., Coulter S.N., Folger K.R., Kas A., Labbig K., Lam R.M.,
Smith K.A., Spencer D.H., Wong K.-S., Wu Z., Paulsen I.T.,
Reizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.,
RT "Complete genome sequence of *Pseudomonas aeruginosa* PA01, an
opportunistic pathogen.";
RT Nature 406:959-964(2000).
RL -1- CATALYTIC ACTIVITY: N-DEOXYNUCLEOSIDE TRIPHOSPHATE - N
CC PYROPHOSPHATE + DNA(N).
CC -1- SIMILARITY: BELONGS TO DNA POLYMERASE TYPE-B FAMILY.
CC EMBL, AF004614; AAC05275.1.
DR InterPro: IPR002064; DNA_POL_B.
DR Pfam: PF00136; DNA_POL_B.1.
DR PRINTS: PR00106; DNAPOLB.
DR SMART: SM00486; POLBc.1.
DR PROSITE: PS00116; DNA_POLYMERASE_B; 1.
KW Complete proteome; DNA replication; DNA-binding;
KW DNA-directed DNA polymerase.
SQ SEQUENCE 787 AA; 89722 MW; 73A594B5A8F9C44 CRC64;

Query Match 68.4%; Score 39; DB 2; Length 787;
Best Local Similarity 72.7%; Pred. No. 71;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 RYLDGISALR 11
| | | | |
DB 274 RYLDGISALR 284

RESULT 12
O9YAB3 PRELIMINARY; PRT; 124 AA.
AC O9YAB3;
DT 01-NOV-1999 (TREMblrel. 12, Created)
DT 01-NOV-1999 (TREMblrel. 12, Last sequence update)
DT 01-MAR-2001 (TREMblrel. 16, Last annotation update)
DE HYPOTHEETICAL 13.7 KDA PROTEIN APEZ026.
GN APEZ026.
OS Aeropyrum pernix.
OC Archaea; Crenarchaeota; Desulfurococcales; Desulfurococcaceae;
OC Aeropyrum.
OX NCBI_TaxID=56636;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-K1;
RX MEDLINE=99310339; PubMed=10382966;
RA Kawarabayashi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Y.,
Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankal A., Kosugi H.,
Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H.,
Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y.,
Yamazaki J., Kushiida N., Oguchi A., Aoki K.-I., Kubota K.,
Nakamura Y., Nomura N., Sako Y., Kikuchi H.,
RT "Complete genome sequence of an aerobic hyper-thermophilic
crenarchaeon, *Aeropyrum pernix* K1.";
RT DNA Res. 6:83-101(1999).
DR EMBL: AP000063; BAA81036.1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 124 AA; 13744 MW; 32260ADAA47A6566 CRC64;

Query Match 66.7%; Score 38; DB 1; Length 124;
Best Local Similarity 80.0%; Pred. No. 13;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 3 IUDGISALRL 12
| | | | |
DB 73 IUDGISALRL 82

RESULT 13
O67469 PRELIMINARY; PRT; 673 AA.
AC O67469;
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
DE ORF2.
OS *Feldmannia* sp. virus.
OC Viruses; dsDNA viruses, no RNA stage; Phycodnaviridae.
OX NCBI_TaxID=39420;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-FSV;
RA Henry E.C., Meints R.H.,
RL J. Phycol. 28:517-526(1992).
RL [2]
RP SEQUENCE FROM N.A.
RC STRAIN-FSV;
RX MEDLINE=93211912; PubMed=7681583;
RA Loverling R., Hanson I.M., Borden K.L., Martin S., O'Reilly N.J.,
Evan G.I., Rahman D., Pappin D.J., Trowsdale J., Freemont P.S.;
RT "Identification and preliminary characterization of a protein motif
related to the zinc finger.";
RT Proc. Natl. Acad. Sci. U.S.A. 90:2112-2116(1993).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-FSV;
RX MEDLINE=96204601; PubMed=8623545;
RA Krueger S.K., Ivey R.G., Henry E.C., Meints R.H.;
RT "A brown algal virus genome contains a 'RING' zinc finger motif.";
RL Virology 219:301-303(1996).
CC -1- SIMILARITY: CONTAINS A RING-TYPE ZINC FINGER.
DR EMBL: U22375; AAB03854.1.
DR InterPro: IPR001841; Znf_ring.
DR Pfam: PF00097; zf-C3HC4.1.
DR SMART: SM00184; RINGc.1.
KW Zinc-finger.
SQ SEQUENCE 673 AA; 75359 MW; CA1C24098C4ECC1 CRC64;

Query Match 66.7%; Score 38; DB 12; Length 673;
Best Local Similarity 50.0%; Pred. No. 93;
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

OY 1 RYLDGISALRL 12
| | | | |
DB 354 RYLDGISALRL 365

RESULT 14
O33257 PRELIMINARY; PRT; 699 AA.
AC O33257;
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
DE NADH DEHYDROGENASE SUBUNIT (FRAGMENT).
GN NDHF.
OS *Verbena bracteata* (prostrate vervain).
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Lamiales; Verbenaceae; Verbena.
OX NCBI_TaxID=39417;
RN [1]
RP SEQUENCE FROM N.A.
RA Olmstead R.G., Reeves P.A.;
RL Ann. Mo. Bot. Gard. 82:176-193(1995).
CC -1- CATALYTIC ACTIVITY: NADH + PLASTOQUINONE = NAD(+) + PLASTOQUINOL.
CC -1- SIMILARITY: TO NADH-UBIQUINONE/PLASTOQUINONE (COMPLEX I), VARIOUS
CHAINS.

DR EMBL: L36418; AAA84708.1; .
 DR Mendeil; 2530; Verbr;ndhr;2530.
 DR InterPro: IPR001750; Oxidored_q1.
 DR InterPro: IPR002128; Oxidored_q1_C.
 DR Pfam: PF00361; oxidored_q1; 1.
 DR Pfam: PF01010; oxidored_q1_C; 1.
 KW Chloroplast; MAD; Oxidoreductase; Plastoquinone.
 FT NON_TER 1
 FT 699 699
 SO SEQUENCE 699 AA; 78507 MW; 82153D31B3D46101 CRC64;

Query Match 66.7%; Score 38; DB 8; Length 699;
 Best Local Similarity 87.5%; Pred. No. 97;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RYIDG1S 8
 |||:||||
 Db 682 RYIDG1S 689

RESULT 15

09DM97 PRELIMINARY; PRT; 737 AA.
 ID 09DM97
 AC 09DM97;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE pr104.
 GN R104.
 OS Rat cytomegalovirus (strain Maastricht).
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 OC Betaherpesvirinae; Muromegalovirus.
 OX NCBI_TaxID=79700;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MAASTRICHT;
 RX MEDLINE=20366325; PubMed=10906222;
 RA Vink C., Beuken E., Bruggeman C.A.;
 RT "Complete DNA sequence of the rat cytomegalovirus genome."
 RL J Virol. 74:7656-7665(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MAASTRICHT;
 RX MEDLINE=20473137; PubMed=11018281;
 RA Gruijthuisen Y.K., Beuken E., Bruggeman C.A.;
 RT "Rat cytomegalovirus R89 is a highly conserved gene which expresses a
 RT spliced transcript."
 RL Virus Res. 69:119-130(2000).
 DR EMBL: AF232689; AAF9193.1; .
 DR InterPro: IPR002660; Herpes_UL6.
 DR Pfam: PF01763; Herpes_UL6; 1.
 DR ProDom: PD003210; Herpes_UL6; 1.
 SO SEQUENCE 737 AA; 83091 MW; 6DD147C3BF244187 CRC64;

Query Match 66.7%; Score 38; DB 12; Length 737;
 Best Local Similarity 58.3%; Pred. No. 1e+02;
 Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 RYIDG1SALRL 12
 |||:||||:|
 Db 100 RYIDG1SALRL 111

Search completed: December 19, 2001, 16:25:18
 Job time: 543 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: December 19, 2001, 16:14:15 ; Search time 78.52 Seconds
(without alignments)
3.439 Million cell updates/sec

Title: US-09-202-104A-1

Perfect score: 57

Sequence: 1 RYLDGISAURL 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapect 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/PCYUS.COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/Dackfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	53	93.0	12	US-08-591-438-17	Sequence 17, Appl
2	53	93.0	16	US-08-567-047-9	Sequence 9, Appl
3	53	93.0	16	US-08-567-048-9	Sequence 9, Appl
4	53	93.0	162	US-08-716-317-10	Sequence 10, Appl
5	53	93.0	163	US-08-716-317-15	Sequence 15, Appl
6	53	93.0	164	US-08-318-193-60	Sequence 60, Appl
7	53	93.0	167	US-08-246-427A-2	Sequence 2, Appl
8	53	93.0	167	US-08-766-620-2	Sequence 2, Appl
9	53	93.0	167	US-08-595-06094-2	Sequence 2, Appl
10	53	93.0	172	US-08-149-101A-21	Sequence 21, Appl
11	53	93.0	172	US-08-149-101A-21	Sequence 21, Appl
12	53	93.0	174	US-08-149-101A-20	Sequence 20, Appl
13	53	93.0	174	US-08-149-101A-20	Sequence 20, Appl
14	53	93.0	181	US-08-209-183C-4	Sequence 4, Appl
15	53	93.0	181	US-08-209-183C-4	Sequence 4, Appl
16	53	93.0	182	US-08-149-101A-25	Sequence 25, Appl
17	53	93.0	183	US-08-149-101A-25	Sequence 25, Appl
18	53	93.0	183	US-08-009-973-1	Sequence 1, Appl
19	53	93.0	184	US-08-567-047-2	Sequence 2, Appl
20	53	93.0	184	US-08-567-047-2	Sequence 2, Appl
21	53	93.0	184	US-08-567-048-2	Sequence 2, Appl
22	53	93.0	184	US-08-567-048-2	Sequence 2, Appl
23	53	93.0	184	US-08-149-101A-17	Sequence 17, Appl
24	53	93.0	184	US-08-149-101A-22	Sequence 22, Appl
25	53	93.0	184	US-08-149-101A-23	Sequence 23, Appl
26	53	93.0	184	US-08-149-101A-23	Sequence 23, Appl
27	53	93.0	184	US-08-149-101A-23	Sequence 23, Appl

28	53	93.0	184	5	PCT-US94-12873-23	Sequence 23, Appl
29	53	93.0	184	6	5186931-1	Patent No. 5186931
30	53	93.0	185	1	US-07-632-070B-1	Sequence 1, Appl
31	53	93.0	185	1	US-07-918-181A-2	Sequence 2, Appl
32	53	93.0	185	1	US-07-918-181A-4	Sequence 4, Appl
33	53	93.0	185	1	US-07-918-181A-6	Sequence 6, Appl
34	53	93.0	185	1	US-07-918-181A-8	Sequence 8, Appl
35	53	93.0	185	1	US-08-231-575-2	Sequence 2, Appl
36	53	93.0	185	1	US-08-231-575-4	Sequence 4, Appl
37	53	93.0	185	1	US-08-231-575-6	Sequence 6, Appl
38	53	93.0	185	1	US-08-231-575-8	Sequence 8, Appl
39	53	93.0	185	1	US-08-246-427A-5	Sequence 5, Appl
40	53	93.0	185	2	US-08-716-317-7	Sequence 7, Appl
41	53	93.0	185	2	US-08-766-620-5	Sequence 5, Appl
42	53	93.0	185	5	PCT-US92-05612-2	Sequence 2, Appl
43	53	93.0	185	5	PCT-US93-06928-2	Sequence 2, Appl
44	53	93.0	185	5	PCT-US93-06928-4	Sequence 4, Appl
45	53	93.0	185	5	PCT-US93-06928-8	Sequence 8, Appl

ALIGNMENTS

RESULT 1
US-08-591-438-17
Sequence 17, Application US/08591438
Patent No. 5939063
GENERAL INFORMATION:
APPLICANT: Vadas, Matthew A.
APPLICANT: Lopez, Angel F.
APPLICANT: Shannon, Mary F.
TITLE OF INVENTION: HAEMOPOIETIC GROWTH FACTOR ANTAGONISTS
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: USA
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentia Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/591,438
FILING DATE: 08-APR-1996
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Digilio Esq., Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 9972
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: polypeptide
US-08-591-438-17
Query Match 93.0%; Score 53; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.00014;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 RYLDGISAURL 11
|||||||

Db 1 RYLDG1SALR 11

RESULT 2

US-08-567-047-9
; Sequence 9, Application US/08567047
; Patent No. 5789552
; Patent No. 5789552 5789555
; GENERAL INFORMATION:
; APPLICANT: SAVINO, Rocco
; APPLICANT: LAHM, Armin
; APPLICANT: CILIBERTO, Gennaro
; TITLE OF INVENTION: METHOD FOR SELECTING SUPERAGONISTS,
; TITLE OF INVENTION: ANTAGONISTS AND SUPERANTAGONISTS FOR HORMONES HAVING
; TITLE OF INVENTION: GP 130 AS PART OF THEIR RECEPTOR COMPLEX
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/567,047
; FILING DATE: 04-DEC-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/387,924
; FILING DATE: 23-FEB-1995
; APPLICATION NUMBER: IT RM93A000409
; FILING DATE: 23-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: SAVINO-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEICAL: no
; FRAGMENT TYPE: internal
; IMMEDIATE SOURCE:
; LIBRARY: production in bacteria as recombinant protein
; FEATURE:
; NAME/KEY: wild type interleukin-6
; IDENTIFICATION METHOD: polyacrylamide gel
; OTHER INFORMATION: sequence of wild type of interleukin 6,
; OTHER INFORMATION: from position 27 to position 42
US-08-567-047-9

Query Match 93.0%; Score 53; DB 1; Length 16;

Best Local Similarity 100.0%; Pred. No. 0.0002;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RYLDG1SALR 11

Db 4 RYLDG1SALR 14

RESULT 3

US-08-567-048-9

; Sequence 9, Application US/08567048
; Patent No. 5891998
; GENERAL INFORMATION:
; APPLICANT: SAVINO, Rocco
; APPLICANT: LAHM, Armin
; APPLICANT: CILIBERTO, Gennaro
; TITLE OF INVENTION: METHOD FOR SELECTING SUPERAGONISTS,
; TITLE OF INVENTION: ANTAGONISTS AND SUPERANTAGONISTS FOR HORMONES HAVING
; TITLE OF INVENTION: GP 130 AS PART OF THEIR RECEPTOR COMPLEX
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/567,048
; FILING DATE: 04-DEC-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/387,924
; FILING DATE: 23-FEB-1995
; APPLICATION NUMBER: IT RM93A000409
; FILING DATE: 23-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: SAVINO-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEICAL: no
; FRAGMENT TYPE: internal
; IMMEDIATE SOURCE:
; LIBRARY: production in bacteria as recombinant protein
; FEATURE:
; NAME/KEY: wild type interleukin-6
; IDENTIFICATION METHOD: polyacrylamide gel
; OTHER INFORMATION: sequence of wild type of interleukin 6,
; OTHER INFORMATION: from position 27 to position 42
US-08-567-048-9

Query Match 93.0%; Score 53; DB 2; Length 16;

Best Local Similarity 100.0%; Pred. No. 0.0002;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RYLDG1SALR 11

Db 4 RYLDG1SALR 14

RESULT 4

US-08-716-317-10
; Sequence 10, Application US/08716317
; Patent No. 5919654
; GENERAL INFORMATION:
; APPLICANT: HAMA, YUKO

APPLICANT: TOHDA, HIDEKI
APPLICANT: TSUKAMOTO, HIROKO
APPLICANT: NIKAI, KIYOKAZU
APPLICANT: KUMAGAI, HIROMICHI
TITLE OF INVENTION: SECRETION SIGNAL GENE AND EXPRESSION
TITLE OF INVENTION: VECTOR CONTAINING IT
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: P. C. JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/716,317
FILING DATE: 02-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP96/00198
FILING DATE: 01-FEB-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 17167/1995
FILING DATE: 03-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 59-924-0 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 162 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-716-317-10

Query Match 93.0%; Score 53; DB 2; Length 162;
Best Local Similarity 100.0%; Pred. No. 0.003;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RYLDGISA LR 11
DB 15 RYLDGISA LR 25
RESULT 5
US-08-716-317-15
Sequence 15, Application US/08716317
Patent No. 5919654
GENERAL INFORMATION:
APPLICANT: HAMA, YUKO
APPLICANT: TOHDA, HIDEKI
APPLICANT: TSUKAMOTO, HIROKO
APPLICANT: NIKAI, KIYOKAZU
APPLICANT: KUMAGAI, HIROMICHI
TITLE OF INVENTION: SECRETION SIGNAL GENE AND EXPRESSION
TITLE OF INVENTION: VECTOR CONTAINING IT
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
P. C.
ADDRESS: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/716,317
FILING DATE: 02-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP96/00198
FILING DATE: 01-FEB-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 17167/1995
FILING DATE: 03-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 59-924-0 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 163 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-716-317-15

CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/716,317
FILING DATE: 02-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP96/00198
FILING DATE: 01-FEB-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 17167/1995
FILING DATE: 03-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 59-924-0 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 163 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-716-317-15
Query Match 93.0%; Score 53; DB 2; Length 163;
Best Local Similarity 100.0%; Pred. No. 0.003;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RYLDGISA LR 11
DB 16 RYLDGISA LR 26
RESULT 6
US-08-318-193-60
Sequence 60, Application US/08318193
Patent No. 5641663
GENERAL INFORMATION:
APPLICANT: GARVIN, Robert T.
APPLICANT: MAIER, Lawrence T.
TITLE OF INVENTION: AN EXPRESSION SYSTEM FOR THE SECRETION
TITLE OF INVENTION: OF BIOACTIVE HUMAN GRANULOCYTE MACROPHAGE COLONY
TITLE OF INVENTION: STIMULATING FACTOR (GM-CSF) AND OTHER HETEROLOGOUS
TITLE OF INVENTION: PROTEINS FROM STREPTOMYCES
NUMBER OF SEQUENCES: 91
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: Virginia
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/318,193
FILING DATE:
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,314
FILING DATE:
APPLICATION NUMBER: US 07/224,568
ATTORNEY/AGENT INFORMATION:
NAME: BERT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 18740/116 CACO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
LENGTH: 164 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-318-193-60

Query Match 93.0%; Score 53; DB 1; Length 164;
Best Local Similarity 100.0%; Pred. No. 0.003;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RYLDGISA LR 11
DB 10 RYLDGISA LR 20

RESULT 7
US-08-246-427A-2
Sequence 2, Application US/08246427A
Patent No. 5641657
GENERAL INFORMATION:
APPLICANT: RUBEN, ET AL.
TITLE OF INVENTION: Interleukin-6 Splice Variant
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
ADDRESS: CECCHI, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/246,427A
FILING DATE: Submitted herewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/246,427
FILING DATE: MAY 19, 1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: FERRARO, GREGORY D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1744
TELEFAX: 201-994-1700
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 167 AMINO ACIDS
TYPE: AMINO ACID
STRANDEDNESS:
TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN

US-08-246-427A-2

Query Match 93.0%; Score 53; DB 1; Length 167;
Best Local Similarity 100.0%; Pred. No. 0.0031;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RYLDGISA LR 11
DB 31 RYLDGISA LR 41

RESULT 8
US-08-766-620-2
Sequence 2, Application US/08766620
Patent No. 5958400
GENERAL INFORMATION:
APPLICANT: RUBEN, ET AL.
TITLE OF INVENTION: Interleukin-6 Splice Variant
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
ADDRESS: CECCHI, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/766,620
FILING DATE: December 12, 1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/246,427
FILING DATE: MAY 19, 1994
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: MULLINS, J.G.
REGISTRATION NUMBER: 33,073
REFERENCE/DOCKET NUMBER: 325800-593 (PFI20)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 167 AMINO ACIDS
TYPE: AMINO ACID
STRANDEDNESS:
TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN
US-08-766-620-2

Query Match 93.0%; Score 53; DB 2; Length 167;
Best Local Similarity 100.0%; Pred. No. 0.0031;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RYLDGISA LR 11
DB 31 RYLDGISA LR 41

RESULT 9
PCT-US95-06094-2
Sequence 2, Application PC/TUS9506094
GENERAL INFORMATION:
APPLICANT: RUBEN, ET AL.
TITLE OF INVENTION: Interleukin-6 Splice Variant

```

; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; ADDRESSEE: CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/06094
; FILING DATE: Submitted herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/246,427
; FILING DATE: MAY 19, 1994
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: FERRARO, GREGORY D.
; REGISTRATION NUMBER: 36,134
; REFERENCE/DOCKET NUMBER: 325800-
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 167 AMINO ACIDS
; TYPE: AMINO ACID
; STRANDEDNESS:
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
; PCT-US95-06094-2

Query Match          93.0%; Score 53; DB 5; Length 167;
Best Local Similarity 100.0%; Pred. No. 0.0031;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RYILDGISALR 11
Db 31 RYILDGISALR 41

RESULT 10
US-08-149-101A-21
; Sequence 21, Application US/08149101A
; Patent No. 6171824
; GENERAL INFORMATION:
; APPLICANT: Todaro, George J.
; APPLICANT: Leung, David W.
; APPLICANT: Rose, Timothy M.
; TITLE OF INVENTION: HYBRID CYTOKINES
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cell Therapeutics, Inc.
; STREET: 200 Elliott Avenue West, Suite 400
; CITY: Seattle
; STATE: Washington
; COUNTRY: U.S.A.
; ZIP: 98119
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" disk, 1.44MB, double side, high density
; COMPUTER: AST-IBM Compatible
; OPERATING SYSTEM: MS-DOS Version 6
; SOFTWARE: WORD for WINDOWS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/149,101A
; FILING DATE: 8-NO. 6171824-1993
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; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US08/097,869
; FILING DATE: 27-Jul-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Oster, Jeffrey B. and Faciszewski, Stephen
; REGISTRATION NUMBER: 32,585 and 36,131, respectively
; REFERENCE/DOCKET NUMBER: 0105A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)282-7100
; TELEFAX: (206)284-6206
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 172
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: no
; ANTI-SENSE: no
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM: homo sapien
; US-08-149-101A-21

Query Match          93.0%; Score 53; DB 4; Length 172;
Best Local Similarity 100.0%; Pred. No. 0.0032;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RYILDGISALR 11
Db 31 RYILDGISALR 41

RESULT 11
PCT-US94-12873-21
; Sequence 21, Application PC/TUS9412873
; GENERAL INFORMATION:
; APPLICANT:
; APPLICANT:
; APPLICANT:
; TITLE OF INVENTION: HYBRID CYTOKINES
; NUMBER OF SEQUENCES: 26
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" diskette, 1.44MB, double side, high density
; OPERATING SYSTEM: MS-DOS Version 6
; SOFTWARE: WORD for WINDOWS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/12873
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 172
; TYPE: amino acid
; TOPOLOGY: linear
; PCT-US94-12873-21

Query Match          93.0%; Score 53; DB 5; Length 172;
Best Local Similarity 100.0%; Pred. No. 0.0032;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RYILDGISALR 11
Db 31 RYILDGISALR 41

RESULT 12
US-08-149-101A-20
; Sequence 20, Application US/08149101A
; Patent No. 6171824
; GENERAL INFORMATION:
```


APPLICANT: Skelly, Susan M.
APPLICANT: Tackney, Charles T.
APPLICANT: Snouwaert, John N.
APPLICANT: Rowles, Dana M.
TITLE OF INVENTION: Cysteine Depleted IL-6 Mutelins
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Imclone Systems Incorporated
STREET: 180 Varick Street
CITY: New York
STATE: New York
COUNTRY: United States
ZIP: 10014
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05612
FILING DATE: 19920702
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Felt, Irving N.
REGISTRATION NUMBER: 28,601
REFERENCE/DOCKET NUMBER: SKE-1-PT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-645-1405
TELEFAX: 212-645-2054
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 181 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US92-05612-4

Query Match 93.0%; Score 53; DB 5; Length 181;
Best Local Similarity 100.0%; Pred. No. 0.0034;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RYLDGISAIR 11
|||||
DB 27 RYLDGISAIR 37

Search completed: December 19, 2001, 16:20:58
Job time: 403 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: December 19, 2001, 16:19:33 ; Search time 170.68 Seconds
(without alignments)
6.944 Million cell updates/sec

Title: US-09-202-104A-2
Perfect score: 75
Sequence: 1 STKVLIOFLQKAKNL 16

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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21: /SID8/gcgdata/geneseq/AA2000.DAT: *
22: /SID8/gcgdata/geneseq/AA2001.DAT: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	75	100.0	29	11	AA06541 Human B-cell stim
2	75	100.0	148	22	AA002910 Angiotensin conver
3	75	100.0	151	16	AA077393 Human mutant IL-6a
4	75	100.0	158	16	AA077392 Human mutant IL-6a
5	75	100.0	162	16	AA077391 Human mutant IL-6a
6	75	100.0	162	17	AA000131 Human interleukin-
7	75	100.0	163	17	AA000132 Human interleukin-
8	75	100.0	166	16	AA077390 Human IL-6 mutant
9	75	100.0	167	17	AA077649 Human interleukin-
10	75	100.0	169	16	AA077387 Human IL-6 mutant
11	75	100.0	173	16	AA077389 Human IL-6 mutant

12	75	100.0	174	16	AA075342 Hybrid human cytok
13	75	100.0	176	16	AA075341 Hybrid human cytok
14	75	100.0	177	16	AA077388 Human IL-6 mutant
15	75	100.0	179	16	AA075334 Human interleukin-
16	75	100.0	180	22	AA073405 Human CNF/IL-6 ch
17	75	100.0	181	14	AA031996 -4aa IL-6 SSSS mut
18	75	100.0	181	15	AA072211 Human interleukin-
19	75	100.0	181	17	AA055866 -4aa SSCC mutein o
20	75	100.0	181	22	AA073406 Human CNF/IL-6 ch
21	75	100.0	182	16	AA075346 Hybrid human cytok
22	75	100.0	183	15	AA060125 Human interleukin
23	75	100.0	184	9	AA081158 Polypeptide with B
24	75	100.0	184	10	AA094753 Sequence of varian
25	75	100.0	184	11	AA065332 Human B-cell stiml
26	75	100.0	184	11	AA003914 Polypeptide with h
27	75	100.0	184	13	AA020783 Interleukin-6. A
28	75	100.0	184	15	AA072219 Human interleukin-
29	75	100.0	184	15	AA054990 Mutant interleukin
30	75	100.0	184	15	AA055256 Interleukin-6. Ho
31	75	100.0	184	15	AA074659 Interleukin-6 for
32	75	100.0	184	16	AA068623 B-cell differentia
33	75	100.0	184	17	AA002609 Interleukin-6. Ho
34	75	100.0	184	17	AA002610 Interleukin-6 (Q75
35	75	100.0	184	17	AA002611 Interleukin-6 (F74
36	75	100.0	184	17	AA002612 Interleukin-6 (Q75
37	75	100.0	184	22	AA073404 Human CNF/IL-6 ch
38	75	100.0	185	9	AA081159 Polypeptide with B
39	75	100.0	185	10	AA090059 Human Ala B cell d
40	75	100.0	185	10	AA090536 Human B cell diffe
41	75	100.0	185	10	AA094754 Sequence of varian
42	75	100.0	185	10	AA091015 Synthetic interlev
43	75	100.0	185	11	AA052755 Segment of human B
44	75	100.0	185	11	AA05274 Segment of human B
45	75	100.0	185	12	AA010983 Recombinant human

ALIGNMENTS

RESULT 1
ID AAR06541 standard; protein; 29 AA.
XX
AC AAR06541;
XX
DT 04-JAN-1991 (first entry)
XX
DE Human B-cell stimulator 2 (BSF2) antagonist.
XX
KW Immunodeficiency; myeloma; chronic articular rheumatism;
KW endotoxin shock;
XX
OS Homo sapiens.
XX
PN JP02188600-A.
XX
PD 24-JUL-1990.
XX
PF 17-JAN-1989; 89JP-0007944.
XX
PR 17-JAN-1989; 89JP-0007944.
XX
PA (CHUS) CHUGAI PHARMACEUTICAL KK.
XX
DR WPI: 1990-266224/35.
XX
PT Polypeptide with antagonist against human B cell stimulator 2 -
PT comprises human B cell stimulator with deficiency of 2 or more
PT aminoacid(s) at N-and/or C-terminal.
XX
PS Claim 14; Page 968; 6pp; Japanese.
XX
CC BSF2 antagonists are useful in diagnosis and treatment of immuno-

CC deficiencies eg. myeloma, chronic articular rheumatism and endotoxin
 CC shock. Antagonist comprises Bsf2 peptide (pref. AAs 20-40) with
 CC substitutions of two or more C- and/or N-terminal AAs.
 SQ Sequence 29 AA;

Query Match 100.0%; Score 75; DB 11; Length 29;
 Best Local Similarity 100.0%; Pred. No. 2.7e-05;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 STKVLIQFLOKKAKNL 16
 |||||
 Db 13 stkvliqfllqkxaknl 28

RESULT 2

AAU02910
 ID AAU02910 standard; Protein: 148 AA.

AC AAU02910;

DT 12-SEP-2001 (first entry)

DE Angiotensin converting enzyme (ACEV) splice variant protein #10.

XX Angiotensin converting enzyme splice variant; ACEV; interleukin 6;
 KM granulocyte colony stimulating factor receptor; glucagon; hypertrophy;
 KM platelet-derived endothelial cell growth factor; cardiovascular disease;
 KM cellular tumour antigen p53; cyclin-dependent kinase inhibitor 1C;
 KM vasoactive intestinal polypeptide receptor 2; arteriosclerosis; cancer;
 KM myocardial infarction; coronary arterial thrombosis; renal disease;
 KM diabetic nephropathy; muscular disease; immune disorder; sarcoidosis;
 KM multiple sclerosis; immune complex nephritis; deep vein thrombosis;
 KM nonarctoidic pulmonary granulomatous disease; endothelial abnormality;
 KM vascular disorder; asbestosis.

OS Homo sapiens.

XX WO200136632-A2.

PN 25-MAY-2001.

PF 17-NOV-2000; 2000WO-1100766.

XX 17-NOV-1999; 99IL-0132978.

PR 10-DEC-1999; 99IL-0133455.

PA (COMP-) COMPUGEN LTD.

PI Levine Z, David A, Azar I, Khosravi R, Bernstein J;

DR WPI: 2001-336004/35.

XX N-PSDB; AAS06010.

PT Novel alternative splicing variants e.g. variant of angiotensin
 PT converting enzyme (ACEV), useful in identifying candidate compounds
 PT capable of binding to the variant and to detect anti-variant antibodies

PS Claim 4; Fig 10; 519pp; English.

XX The sequence represents an angiotensin converting enzyme splice variant
 CC (ACEV) polypeptide. The polypeptides of the invention include variants of
 CC granulocyte colony stimulating factor receptor, glucagon, interleukin 6,
 CC platelet-derived endothelial cell growth factor, cyclin-dependent kinase
 CC inhibitor 1C, cellular tumour antigen p53, and vasoactive intestinal
 CC polypeptide receptor 2. The polypeptides and their associated nucleic
 CC acids are useful for identification of variant sequences and detection of
 CC candidate compounds capable of binding the molecules. The sequences of
 CC the invention can be used in the treatment and diagnosis of various
 CC disorders including cardiovascular diseases such as arteriosclerosis,
 CC myocardial infarction and coronary arterial thrombosis, renal diseases

CC such as diabetic nephropathy, muscular diseases such as hypertrophy,
 CC immune disorders such as immune complex nephritis, multiple sclerosis,
 CC cancer, sarcoidosis, nonarctoidic pulmonary granulomatous diseases such
 CC as asbestosis and vascular pathologies involving an endothelial
 CC abnormality such as deep vein thrombosis.

XX Sequence 148 AA;

Query Match 100.0%; Score 75; DB 22; Length 148;
 Best Local Similarity 100.0%; Pred. No. 0.00013;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 STKVLIQFLOKKAKNL 16
 |||||
 Db 82 stkvliqfllqkxaknl 97

RESULT 3

AAU02910
 ID AAR77393 standard; Protein: 151 AA.

AC AAR77393;

DT 17-APR-1996 (first entry)

DE Human mutant IL-6a/C3 (amino acids 5-19, 44-50 and 73-83 deleted).

XX Human interleukin-6; IL-6a/C3 mutant; increased stability;
 KM recombinant; production; deletion mutant;
 KM amino acids 5-19, 44-50 and 73-83.

OS Homo sapiens.

XX JF07224097-A.

PN 22-AUG-1995.

PF 08-FEB-1994; 94JP-0014461.

PR 08-FEB-1994; 94JP-0014461.

PA (ASAG) ASAMI GLASS CO LTD.

DR WPI: 1995-325556/42.

XX N-PSDB; AAQ94348.

PT Interleukin-6 mutant, related DNA and expression vectors - has
 PT higher stability than natural interleukin-6

PS Claim 1; Pages 15-16; 18pp; Japanese.

XX AAQ94348 encodes AAR77393 the human IL-6 deletion mutant IL-6a/C3
 CC which lacks the amino acids Gly5-Leu19, Cys44-Cys50 and Cys73-Cys83
 CC of the wild type protein. The cDNA can be used for the recombinant
 CC prodn. of IL-6a/C3 which has increased stability compared to wild
 CC type IL-6.

XX Sequence 151 AA;

SQ

Query Match 100.0%; Score 75; DB 16; Length 151;
 Best Local Similarity 100.0%; Pred. No. 0.00013;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 STKVLIQFLOKKAKNL 16
 |||||
 Db 85 stkvliqfllqkxaknl 100

RESULT 4

AAU02910
 ID AAR77392 standard; Protein: 158 AA.


```

XX AC AAR77392;
XX XX 17-APR-1996 (first entry)
XX DT
XX DE Human mutant IL-6a/C2 (amino acids 5-19 and 73-83 deleted).
XX XX
XX KW Human interleukin-6; IL-6a/C2 mutant; increased stability;
XX KM recombinant; production; deletion mutant;
XX KW amino acids 5-19 and 73-83.
XX OS Homo sapiens.
XX PS
XX FT Key Location/Qualifiers
XX FT mat_peptide 1..474
XX FT /*tag= a
XX PN JP07224097-A.
XX PD 22-AUG-1995.
XX PF 08-FEB-1994; 94JP-0014461.
XX PR 08-FEB-1994; 94JP-0014461.
XX PA (ASAG ) ASahi GLASS CO LTD.
XX XX
XX DR WPI: 1995-325556/42.
XX DR N-PSDB; AA094347.
XX PT Interleukin-6 mutant; related DNA and expression vectors - has
XX PT higher stability than natural interleukin-6
XX PS Claim 1; Pages 14-15; 18pp; Japanese.
XX XX
XX CC AA094347 encodes AAR77392 the human IL-6 deletion mutant IL-6a/C2
XX CC which lacks the amino acids Gly5-Leu19 and Cys73-Cys83 of the
XX CC wild type protein. The cDNA can be used for the recombinant prodn.
XX CC of IL-6a/C2 which has increased stability compared to wild type
XX CC IL-6.
XX CC
XX SQ Sequence 158 AA;

```

```

PF 08-FEB-1994; 94JP-0014461.
XX XX
XX PR 08-FEB-1994; 94JP-0014461.
XX XX
XX PA (ASAG ) ASahi GLASS CO LTD.
XX DR WPI: 1995-325556/42.
XX DR N-PSDB; AA094346.
XX PT Interleukin-6 mutant; related DNA and expression vectors - has
XX PT higher stability than natural interleukin-6
XX PS Claim 1; Page 14; 18pp; Japanese.
XX XX
XX CC AA094346 encodes AAR77391 the human IL-6 deletion mutant IL-6a/C1,
XX CC which lacks the amino acids Gly5-Leu19 and Cys44-Cys50 of the
XX CC wild type protein. The cDNA can be used for the recombinant prodn.
XX CC of IL-6a/C1, which has increased stability compared to wild type
XX CC IL-6.
XX SQ Sequence 162 AA;

```

Query Match 100.0%; Score 75; DB 16; Length 162;
 Best Local Similarity 100.0%; Pred. No. 0.00014;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 1 STKVLIOFLQKRAKML 16
   |||||||
Db 96 sckvliqflqkkaknl 111

```

RESULT 6
 ID AAW00131 standard; Protein; 162 AA.
 XX
 XX AAW00131;
 AC
 XX DT 09-APR-1997 (first entry)
 DE Human interleukin-6 fragment.
 XX
 KW Secretory; signal peptide; P-factor; multicloning vector; PCR;
 KW animal protein; expression; production; recombinant; primer;
 KW fission yeast; human; serum albumin; interleukin-6;
 KW polymerase chain reaction; Schizosaccharomyces pombe;
 KW PO fragment.
 XX
 OS Homo sapiens.
 XX
 XX W09623890-A1.
 PN
 XX PD 08-AUG-1996.
 XX
 XX PF 01-FEB-1996; 96W0-JP00198.
 XX PR 03-FEB-1995; 95JP-0017167.
 XX PA (ASAG) ASahi GLASS CO LTD.
 XX
 XX Hama Y, Kumagai H, Nikaide K, Tohda H, Tsukamoto H;
 PI WPI: 1996-371438/37.
 DR
 XX Schizosaccharomyces pombe secretory signal peptide (P-factor) gene
 XX - for production of vectors for expression of animal proteins in a
 PT fission yeast, pref. S. pombe, host
 PT
 XX Example 4; Pages 28-29; 50pp; Japanese.
 PS
 XX A multicloning vector, comprising the human interleukin-6 (hIL-6)
 CC cDNA, a Schizosaccharomyces pombe secretory signal peptide
 CC fragment or P-factor fragment (PO fragment) DNA and preferably an

CC animal cell viral promoter sequence and a neomycin resistance gene,
 CC can be used for the efficient production of a hIL-6 fragment, i.e.,
 CC the present sequence, in a fission yeast host, preferably *S. pombe*,
 CC culture.
 XX
 SQ Sequence 162 AA;

Query Match 100.0%; Score 75; DB 17; Length 162;
 Best Local Similarity 100.0%; Pred. No. 0.00014;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 STKVLIQFLQKKAKNL 16
 |||||
 Db 96 stkvliqflqkkaknl 111

RESULT 7

AAW00132
 ID AAW00132 standard; Protein; 163 AA.

AC AAW00132;

DT 09-APR-1997 (first entry)

XX Human interleukin-6 fragment.

XX Secretory; signal peptide; P-factor; multicloning vector; PCR;

KW animal protein; expression; production; recombinant; primer;

KW fission yeast; human; serum albumin; Interleukin-6;

KW polymerase chain reaction; Schizosaccharomyces pombe;

KW PI fragment.

XX Homo sapiens.

XX W09622890-A1.

XX 08-AUG-1996.

XX 01-FEB-1996; 96WO-JP00198.

XX 03-FEB-1995; 95JP-0017167.

XX (ASAG) ASAH I GLASS CO LTD.

XX Hama Y, Kumagai H, Nikaido K, Tonda H, Tsukamoto H;

XX WPI: 1996-371438/37.

XX Schizosaccharomyces pombe secretory signal peptide (P-factor) gene

XX for production of vectors for expression of animal proteins in a

XX fission yeast, pref. *S. pombe*, host

XX Example 7; Pages 30-31; 50pp; Japanese.

XX A multicloning vector, comprising the human interleukin-6 (hIL-6)

XX cDNA, a Schizosaccharomyces pombe secretory signal peptide

XX fragment or P-factor fragment (PI fragment) DNA and preferably an

XX animal cell viral promoter sequence and a neomycin resistance gene,

XX can be used for the efficient production of a hIL-6 fragment, i.e.,

XX the present sequence, in a fission yeast host, preferably *S. pombe*,
 XX culture.
 SQ Sequence 163 AA;

Query Match 100.0%; Score 75; DB 17; Length 163;

Best Local Similarity 100.0%; Pred. No. 0.00014;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 STKVLIQFLQKKAKNL 16
 |||||
 Db 97 stkvliqflqkkaknl 112

RESULT 8

AAAR77390
 ID AAR77390 standard; Protein; 166 AA.

AC AAR77390;

DT 17-APR-1996 (first entry)

XX Human IL-6 mutant IL-6C3 (amino acids 44-50 and 73-83 deleted).

XX Human interleukin-6; IL-6C3 mutant; increased stability;

KW recombinant; production; deletion mutant;

KW amino acids 44-50 and 73-83.

XX Homo sapiens.

XX Key Location/Qualifiers

FT mat_peptide 1..498

FT /*tag= a

PN JPO7224097-A.

XX 22-AUG-1995.

XX 08-FEB-1994; 94JP-0014461.

XX 08-FEB-1994; 94JP-0014461.

XX (ASAG) ASAH I GLASS CO LTD.

XX WPI: 1995-32556/42.

XX N-PSDB; AAQ94345.

XX Interleukin-6 mutant, related DNA and expression vectors - has

XX higher stability than natural Interleukin-6

XX Claim 1; Page 13; 18pp; Japanese.

XX AAQ94345 encodes AAR77390 the human IL-6 deletion mutant IL-6C3,

XX which lacks the amino acids Cys44-Cys50 and Cys73-Cys83 of the

XX wild type protein. The cDNA can be used for the recombinant prodn.

XX of IL-6C3, which has increased stability compared to wild type

XX IL-6.
 SQ Sequence 166 AA;

Query Match 100.0%; Score 75; DB 16; Length 166;

Best Local Similarity 100.0%; Pred. No. 0.00015;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 STKVLIQFLQKKAKNL 16
 |||||
 Db 100 stkvliqflqkkaknl 115

RESULT 9

AAAR77649
 ID AAR77649 standard; Protein; 167 AA.

AC AAR77649;

DT 27-JUN-1996 (first entry)

XX Human interleukin-6 splice variant.

XX Human; interleukin-6; splice variant; IL-6SV; treatment;

XX immunotherapeutic; anti-inflammatory; bone marrow transplant;

XX chemotherapy; side effect; corneal damage; keratitis; ulcer;
 KW antagonist; Castleman's disease; multiple myeloma;
 KW cardiac myxoma; cervical cancer; rheumatoid arthritis;

```
KW autoimmune diabetes; sepsis.
XX
OS Homo sapiens.
XX
PN W09532282-A1.
XX
PD 30-NOV-1995.
XX
PE 17-MAY-1995; 95WO-US06094.
XX
PR 19-MAY-1994; 94US-0246427.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PI
PI Adams MD, Li H, Ruben S;
XX
DR WPI: 1996-020577/02.
DR N-PSDB: AAT08558.
XX
PT Polynucleotide encoding interleukin 6-splice variant - used for
PT treating auto-immune diseases and inflammation.
XX
PS Claim 1; Page 40; 54pp; English.
XX
CC The human interleukin-6 splice variant (IL-6SV) AAR77649 is encoded
CC by AAT08558 (which is derived from an activated macrophage cDNA
CC library), and may be used in immunotherapeutic and
CC anti-inflammatory comps., and for the treatment of patients
CC suffering from bone marrow transplant chemotherapy side effects,
CC corneal damage, keratitis and ulcers. Antagonists of IL-6SV may
CC be used to treat diseases caused by the up-regulated prodn. of
CC IL-6 (i.e. Castleman's disease, multiple myeloma, cardiac myxoma,
CC cervical cancer, rheumatoid arthritis and autoimmune diabetes),
CC and sepsis.
XX
SQ Sequence 167 AA;

Query Match 100.0%; Score 75; DB 17; Length 167;
Best Local Similarity 100.0%; Pred. No. 0.00015;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 STKVLIOFLOKRAKKNL 16
   |||||||
DB 101 stkvllqflqkxaknl 116

RESULT 10
AAR77387
ID AAR77387 standard; Protein; 169 AA.
XX
AC AAR77387;
XX
DT 17-APR-1996 (first entry)
XX
DE Human IL-6 mutant IL-6a (amino acids 5-19 deleted).
XX
XX Human interleukin-6; IL-6a mutant; increased stability;
KW recombinant; production; deletion mutant; amino acids 5-19.
XX
OS Homo sapiens.
XX
PN JP07224097-A.
XX
PD 22-AUG-1995.
XX
PE 08-FEB-1994; 94JP-0014461.
XX
PR 08-FEB-1994; 94JP-0014461.
XX
PA (ASAG ) ASAMI GLASS CO LTD.
XX
DR WPI: 1995-325556/42.
```

```
DR N-PSDB: AA094342.
XX
PT Interleukin-6 mutant, related DNA and expression vectors - has
PT higher stability than natural interleukin-6
XX
PS Claim 1; Page 10; 18pp; Japanese.
XX
CC AA094342 encodes AAR77387 the human IL-6 deletion mutant IL-6a, which
CC lacks the amino acids Gly5-Ileu19 of the wild type protein. The
CC cDNA can be used for the recombinant prodn. of IL-6a, which has
CC increased stability compared to wild type IL-6.
XX
SQ Sequence 169 AA;

Query Match 100.0%; Score 75; DB 16; Length 169;
Best Local Similarity 100.0%; Pred. No. 0.00015;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 STKVLIOFLOKRAKKNL 16
   |||||||
DB 103 stkvllqflqkxaknl 118

RESULT 11
AAR77389
ID AAR77389 standard; Protein; 173 AA.
XX
AC AAR77389;
XX
DT 17-APR-1996 (first entry)
XX
DE Human IL-6 mutant IL-6C2 (amino acids 73-83 deleted).
XX
XX Human interleukin-6; IL-6C2 mutant; increased stability;
KW recombinant; production; deletion mutant; amino acids 73-83.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FH FT mat_peptide 1..519
FH FT /*tag= a
XX
PN JP07224097-A.
XX
PD 22-AUG-1995.
XX
PE 08-FEB-1994; 94JP-0014461.
XX
PR 08-FEB-1994; 94JP-0014461.
XX
PA (ASAG ) ASAMI GLASS CO LTD.
XX
DR WPI: 1995-325556/42.
XX
DR N-PSDB: AA094344.
XX
PT Interleukin-6 mutant, related DNA and expression vectors - has
PT higher stability than natural interleukin-6
XX
PS Claim 1; Page 12; 18pp; Japanese.
XX
CC AA094344 encodes AAR77389 the human IL-6 deletion mutant IL-6C2,
CC which lacks the amino acids Cys73-Cys83 of the wild type protein.
CC The cDNA can be used for the recombinant prodn. of IL-6C2, which
CC has increased stability compared to wild type IL-6.
XX
SQ Sequence 173 AA;

Query Match 100.0%; Score 75; DB 16; Length 173;
Best Local Similarity 100.0%; Pred. No. 0.00015;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 1 STKVLIQFLOKKAKNL 16
 |||||
 Db 107 stkvliqfllqkknkl 122

RESULT 12

AA075342
 ID AAR75342 standard; Protein: 174 AA.

AC AAR75342;

DT 13-DEC-1995 (first entry)

DE Hybrid human cytokine IIIL.

KM Hybrid cytokine; tumour proliferation; cancer therapy.

OS Synthetic.

FT Key Location/Qualifiers

FT Misc-difference 173 /note= "site of stop codon"

PN MO9513393-A.

PD 18-MAY-1995.

PE 07-NOV-1994; 94MO-US12873.

PR 08-NOV-1993; 93US-0149101.

PA (HUTC-) HUTCHINSON CANCER RES CENTER FRED.

PI Leung DW, Rose TM, Todaro GJ;

DR WPI: 1995-194111/25.

DR N-PSDB; AA087161.

PT New hybrid cytokines with alpha helical sequences from different
 PT sources - also DNA encoding them, vectors and transformed cells,
 PT useful e.g. for treating cancer, remodelling bone etc.

PS Claim 11: Page 31; 52pp; English.

CC The cytokine encoding genes for leukemia inhibitory factor (L),
 CC granulocyte-colony stimulating factor (G), interleukin-6 (I),
 CC interleukin-11 (E), ciliary neurotrophic factor (C) and
 CC oncostatin-M (O) have been cloned and reported in the literature.
 CC I, G, L, E, C and O each comprise four alpha-helical sequences. In
 CC each cytokine, the four alpha-helical sequences are linked by non-
 CC alpha-helical 'linking' sequences of about 5-100 AAs. The invention
 CC provides a group of therapeutic hybrid cytokines, having a size ranging
 CC from about 10 to about 30 kDa. Each hybrid cytokine comprises three or
 CC four alpha-helical sequences and linking sequences, ranging from about
 CC 5-40 AAs in length. In the nomenclature of the hybrid cytokines,
 CC upper case letters designate alpha-helical sequences, lower case
 CC letters (whether Arabic numerals, alphabetic or symbolic) indicate
 CC a specific linking sequence. The first three alpha-helical
 CC sequences of IIL and IIL-alpha were derived from IL-6 and the
 CC fourth alpha-sequence was derived from LIF. IIL-alpha has two
 CC additional AAs inserted in a linking sequence between alpha-helices
 CC III and IV, as compared with IIL.

CC Sequence 174 AA;

Query Match 100.0%; Score 75; DB 16; Length 174;
 Best Local Similarity 100.0%; Pred. No. 0.00015;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STKVLIQFLOKKAKNL 16
 |||||
 Db 119 stkvliqfllqkknkl 134

RESULT 13

AA075341
 ID AAR75341 standard; Protein: 176 AA.

AC AAR75341;

DT 13-DEC-1995 (first entry)

DE Hybrid human cytokine IIL-alpha.

KM Hybrid cytokine; tumour proliferation; cancer therapy.

OS Synthetic.

FT Key Location/Qualifiers

FT Misc-difference 175 /note= "site of stop codon"

PN MO9513393-A.

PD 18-MAY-1995.

PE 07-NOV-1994; 94MO-US12873.

PR 08-NOV-1993; 93US-0149101.

PA (HUTC-) HUTCHINSON CANCER RES CENTER FRED.

PI Leung DW, Rose TM, Todaro GJ;

DR WPI: 1995-194111/25.

DR N-PSDB; AA087160.

PT New hybrid cytokines with alpha helical sequences from different
 PT sources - also DNA encoding them, vectors and transformed cells,
 PT useful e.g. for treating cancer, remodelling bone etc.

PS Claim 11: Page 30; 52pp; English.

CC The cytokine encoding genes for leukemia inhibitory factor (L),
 CC granulocyte-colony stimulating factor (G), interleukin-6 (I),
 CC interleukin-11 (E), ciliary neurotrophic factor (C) and
 CC oncostatin-M (O) have been cloned and reported in the literature.
 CC I, G, L, E, C and O each comprise four alpha-helical sequences. In
 CC each cytokine, the four alpha-helical sequences are linked by non-
 CC alpha-helical 'linking' sequences of about 5-100 AAs. The invention
 CC provides a group of therapeutic hybrid cytokines, having a size ranging
 CC from about 10 to about 30 kDa. Each hybrid cytokine comprises three or
 CC four alpha-helical sequences and linking sequences, ranging from about
 CC 5-40 AAs in length. In the nomenclature of the hybrid cytokines,
 CC upper case letters designate alpha-helical sequences, lower case
 CC letters (whether Arabic numerals, alphabetic or symbolic) indicate
 CC a specific linking sequence. The first three alpha-helical
 CC sequences of IIL and IIL-alpha were derived from IL-6 and the
 CC fourth alpha-sequence was derived from LIF. IIL-alpha has two
 CC additional AAs inserted in a linking sequence between alpha-helices
 CC III and IV, as compared with IIL.

CC Sequence 176 AA;

Query Match 100.0%; Score 75; DB 16; Length 176;
 Best Local Similarity 100.0%; Pred. No. 0.00015;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STKVLIQFLOKKAKNL 16
 |||||
 Db 119 stkvliqfllqkknkl 134

RESULT 14

AA077388
ID AAR77388 standard; Protein; 177 AA.
XX
AC AAR77388;
XX
DT 17-APR-1996 (first entry)
XX
DE Human IL-6 mutant IL-6C1 (amino acids 44-50 deleted).
XX
KW Human interleukin-6; IL-6C1 mutant; increased stability;
KW recombinant; production; deletion mutant; amino acids 44-50.
XX
OS Homo sapiens.
XX
PN JP07224097-A.
XX
PD 22-AUG-1995.
XX
PF 08-FEB-1994; 94JP-0014461.
XX
PR 08-FEB-1994; 94JP-0014461.
XX
PA (ASAG) ASahi GLASS CO LTD.
XX
DR WPI: 1995-325556/42.
XX N-PSDB; AA094343.
XX
PT Interleukin-6 mutant, related DNA and expression vectors - has
PT higher stability than natural Interleukin-6
XX
PS Claim 1; Page 11; 18pp; Japanese.
XX
CC AA094343 encodes AAR77388 the human IL-6 deletion mutant IL-6C1,
CC which lacks the amino acids Cys44-Cys50 of the wild type protein.
CC The cDNA can be used for the recombinant prodn. of IL-6C1, which
CC has increased stability compared to wild type IL-6.
XX
SQ Sequence 177 AA;

Query Match ~100.0%; Score 75; DB 16; Length 177;
Best Local Similarity 100.0%; Pred. No. 0.00016;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STKVLIQFIQKKAKNL 16
DB 111 stkvliqfiqkkaknl 126

RESULT 15
AAR75334
ID AAR75334 standard; Protein; 179 AA.
XX
AC AAR75334;
XX
DT 13-DEC-1995 (first entry)
XX
DE Human Interleukin-6 (IL-6).
XX
KW Cytokine; tumour proliferation; cancer therapy.
XX
OS Homo sapiens.
XX
PN WO9513393-A.
XX
PD 18-MAY-1995.
XX
PF 07-NOV-1994; 94WO-US12873.
XX
PR 08-NOV-1993; 93US-0149101.
XX
PA (HUTC-) HUTCHINSON CANCER RES CENTER FRED.
XX

PI Leung DW, Rose TM, Todaro GJ;
XX
DR WPI: 1995-194111/25.
DR N-PSDB; AA087153.
XX
PT New hybrid cytokines with alpha helical sequences from different
PT sources - also DNA encoding them, vectors and transformed cells,
PT useful e.g. for treating cancer, remodelling bone etc.
XX
PS Disclosure; Page 23-24; 52pp; English.
XX
XX The cytokine encoding genes for leukemia inhibitory factor (LIF),
CC granulocyte-colony stimulating factor (G-CSF), interleukin-6 (IL-6),
CC interleukin-11 (IL-11), ciliary neurotrophic factor (CNTF) and
CC oncostatin-M (OSM) have been cloned and reported in the literature.
CC IL-6, G-CSF, LIF, IL-11, CNTF and OSM each comprise four alpha-
CC helical sequences. In each cytokine, the four alpha-helical
CC sequences are linked by non-alpha-helical 'linking' sequences of
CC about 5-100 AAs, and in some cases the alpha-helices are maintained
CC in the proper conformation and geometry with respect to each other
CC through disulfide bridges. The invention provides a group of
CC therapeutic hybrid cytokines, having a size ranging from about 10
CC to about 30 kDa. Each hybrid cytokine comprises three or four
CC alpha-helical sequences and linking sequences, ranging from about
CC 5-40 AAs in length, selected from the linking sequences of the
CC above cytokines or other linking sequences.
XX
SQ Sequence 179 AA;

Query Match 100.0%; Score 75; DB 16; Length 179;
Best Local Similarity 100.0%; Pred. No. 0.00016;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STKVLIQFIQKKAKNL 16
DB 113 stkvliqfiqkkaknl 128

Search completed: December 19, 2001, 16:19:33
Job time: 358 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: December 19, 2001, 16:22:34 ; Search time 88.82 Seconds
(without alignments)
13.722 Million cell updates/sec

Title: US-09-202-104A-2
Perfect score: 75
Sequence: 1 STKVLQFLQKKAKNL 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues
Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 10%
Listing first 45 summaries

Database : PIR,68:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB ID	Description
1	75	100.0	212	1	IVHUB2
2	50	66.7	208	2	T09216
3	47	62.7	207	2	I46084
4	47	62.7	212	2	I46621
5	47	62.7	212	2	I46590
6	46	61.3	274	2	F81448
7	44	58.7	959	1	B71405
8	42	56.0	161	2	E84959
9	42	56.0	286	2	T33500
10	42	56.0	425	2	S76697
11	41	54.7	290	2	B83924
12	40	53.3	373	2	G70355
13	40	53.3	1168	2	T30935
14	39	52.0	153	2	PW0103
15	39	52.0	286	2	A70193
16	39	52.0	313	2	A34785
17	39	52.0	358	2	C42026
18	39	52.0	389	1	A39429
19	39	52.0	437	2	A54595
20	39	52.0	448	2	A42026
21	39	52.0	456	2	B42026
22	39	52.0	505	1	S05380
23	39	52.0	704	2	S25371
24	39	52.0	1240	2	T05162
25	38	50.7	89	2	C86073
26	38	50.7	89	2	S48004
27	38	50.7	130	1	R4BY24
28	38	50.7	130	2	S30003
29	38	50.7	130	2	S51385

ALIGNMENTS

30	38	50.7	278	2	E83773	transcription regu
31	38	50.7	365	2	S50409	hypothetical prote
32	38	50.7	474	1	A32386	protein-tyrosine-p
33	38	50.7	657	2	B72034	exonuclease ABC,
34	38	50.7	657	2	G86590	exonuclease ABC su
35	38	50.7	144	2	A46068	Huntington disease
36	37	49.3	187	2	D64160	hypothetical prote
37	37	49.3	220	2	G86837	cytidylate kinase
38	37	49.3	250	2	E85487	hypothetical prote
39	37	49.3	291	2	C71877	hypothetical prote
40	37	49.3	415	2	H84718	hypothetical prote
41	37	49.3	423	2	I38056	nicotinic acetylch
42	37	49.3	436	2	D64056	branched-chain ami
43	37	49.3	575	2	JC4554	ABC-type transport
44	37	49.3	693	2	T33251	hypothetical prote
45	37	49.3	723	2	H85092	hypothetical prote

RESULT 1
IVHUB2
Interleukin-6 precursor [validated] - human
N.Alternate names: B-cell differentiation factor; B-cell hybridoma growth factor; B-c
on factor
C.Species: Homo sapiens (man)
C.Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 08-Dec-2000
C.Accession: A32648; A26966; A3515; A25801; A25921; I52193; I56003; A27601;
R.Yasukawa, K.; Hirano, T.; Watanabe, Y.; Muratani, K.; Matsuda, T.; Nakai, S.; Kishi
EMBO J. 6, 2939-2945, 1987
A.Title: Structure and expression of human B cell stimulatory factor-2 (BSF-2/IL-6) g
A.Reference number: A32648; MUID:88082664
A.Accession: A32648
A.Molecule type: DNA
A.Residues: 1-212 <YAS>
A.Cross-references: GB:Y00081; NID:929494; PIDN:CA68278.1; PID:q29495
A.Note: the authors translated the codon CAG for residue 130 as Glu
R.Zilberstein, A.; Ruggieri, R.; Korn, J.H.; Revel, M.
EMBO J. 5, 2529-2537, 1986
A.Title: Structure and expression of cDNA and genes for human interferon-beta-2, a di
A.Reference number: A91051; MUID:87053818
A.Accession: A25692
A.Molecule type: mRNA
A.Residues: 1-212 <ZIL>
A.Cross-references: GB:X04430; NID:932673; PIDN:CA28026.1; PID:q32674
R.Hirano, T.; Yasukawa, K.; Harada, H.; Tega, T.; Watanabe, Y.; Matsuda, T.; Kashiwam
I, T.; Kishimoto, T.
Nature 324, 73-76, 1986
A.Title: Complementary DNA for a novel human interleukin (BSF-2) that induces B lymph
A.Reference number: A93387; MUID:87065033
A.Accession: A26966
A.Molecule type: mRNA
A.Residues: 1-212 <HIR>
A.Cross-references: GB:X04602; NID:933849; PIDN:CA28268.1; PID:q33850
R.Tonouchi, N.; Miwa, K.; Karasuyama, H.; Matsui, H.
Biochem. Biophys. Res. Commun. 163, 1056-1062, 1989
A.Title: Deletion of 3' untranslated region of human BSF-2 mRNA causes stabilization
A.Reference number: A33515; MUID:89391958
A.Accession: A33515
A.Molecule type: mRNA
A.Residues: 1-212 <TON>
A.Cross-references: GB:M29150; NID:9186349; PIDN:AA59154.1; PID:q307063
R.Haeghebaert, G.; Content, J.; Volckaert, G.; Derynck, R.; Tavernier, J.; Piers, W.
Eur. J. Biochem. 159, 625-632, 1986
A.Title: Structural analysis of the sequence coding for an inducible 26-kDa protein 1
A.Reference number: A25801; MUID:87004683
A.Accession: A25801
A.Molecule type: DNA; mRNA
A.Residues: 1-212 <HAE>
A.Cross-references: GB:X04403
A.Experimental source: fibroblast
R.May, L.T.; Helfgott, D.C.; Seigal, P.B.

Proc. Natl. Acad. Sci. U.S.A. 83, 8957-8961, 1986
 A:Title: Anti-beta-interferon antibodies inhibit the increased expression of HLA-B7 mRNA
 A:Reference number: A25921; MVID:87067433
 A:Accession: A25921
 A:Molecule type: mRNA
 A:Residues: 1-212 <MAY>
 A:Cross-references: GB:M14584; NID:g184628; PIDN:AA52728.1; PID:g306910
 R:Mong, G.G.; Witek-Giamotti, J.; Hewick, R.M.; Clark, S.C.; Ogawa, M.
 Behring Inst. Mitt. 83, 40-47, 1988
 A:Title: Interleukin 6: identification as a hematopoietic colony-stimulating factor.
 A:Reference number: I52193; MVID:89193317
 A:Accession: I52193
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-212 <MON>
 A:Cross-references: GB:M54894; NID:g186351; PIDN:AAC41704.1; PID:g186352
 R:Brakenhoff, J.P.; de Groot, E.R.; Evers, R.F.; Pannekoek, H.; Aarden, L.A.
 J. Immunol. 139, 4116-4121, 1987
 A:Title: Molecular cloning and expression of hybridoma growth factor in *Escherichia coli*
 A:Reference number: I56003; MVID:88088768
 A:Accession: I56003
 A>Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-212 <BRA>
 A:Cross-references: GB:M18403; NID:g184631; PIDN:AA52729.1; PID:g306911
 R:Van Damme, J.; Van Beeumen, J.; Decock, B.; Van Snick, J.; De Ley, M.; Billiau, A.
 J. Immunol. 140, 1534-1541, 1988
 A:Title: Separation and comparison of two monokines with lymphocyte-activating factor ad
 A:Reference number: A92816; MVID:88154445
 A:Accession: A27601
 A:Molecule type: protein
 A:Residues: 28-51, 'X', 53-57, 'X', 59, 'X', 61 <VAN1>
 A:Accession: B27601
 A:Molecule type: protein
 A:Residues: 30-56, 'XX', 59-61, 'X', 63 <VA2>
 R:Yamamoto, R.; Lin, L.S.; Lowe, R.; Warren, M.K.; White, T.J.
 J. Immunol. 144, 1808-1816, 1990
 A:Title: The human lung fibroblast cell line, MRC-5, produces multiple factors involved
 A:Reference number: A60400; MVID:90171574
 A:Accession: A60400
 A:Molecule type: protein
 A:Residues: 30-43 <YAM>
 R:Hirano, T.; Taga, T.; Yasukawa, K.; Nakajima, K.; Nakano, N.; Takatsuki, F.; Shimizu, Proc. Natl. Acad. Sci. U.S.A. 84, 228-231, 1987
 A:Title: Human beta-cell differentiation factor defined by an anti-peptide antibody and
 A:Reference number: A29085; MVID:87092370
 A:Accession: A29085
 A:Molecule type: protein
 A:Residues: 29-42 <HIR2>
 R:Noda, M.; Takeda, K.; Sugimoto, H.; Hosoi, T.; Takechi, K.; Hara, T.; Ishikawa, H.; Anticancer Res. 11, 961-968, 1991
 A:Title: Purification and characterization of human fibroblast derived differentiation f
 A:Reference number: A61159; MVID:91280765
 A:Accession: A61159
 A:Molecule type: protein
 A:Residues: 30-42 <MOD>
 A:Experimental source: fibroblast
 R:Ming, J.E.; Cernetti, C.; Steinman, R.M.; Granelli-Piperno, A.
 J. Mol. Cell. Immunol. 4, 203-212, 1989
 A:Title: Interleukin 6 is the principal cytolytic T lymphocyte differentiation factor fo
 A:Reference number: A61462; MVID:90121567
 A:Accession: A61462
 A:Molecule type: protein
 A:Residues: 28-48 <MIN>
 A:Experimental source: leukocyte-conditioned medium
 R:May, L.T.; Shaw, J.E.; Khanna, A.K.; Zabriske, J.B.; Sehgal, P.B.
 Cytokine 3, 204-211, 1991
 A:Title: Marked cell-type-specific differences in glycosylation of human interleukin-6.
 A:Reference number: A48419; MVID:91355644
 A:Accession: A48419
 A:Molecule type: protein
 A:Residues: 30-37, 'X', 39-40 <MAY2>
 A:Experimental source: FS-4 fibroblasts

A:Note: sequence extracted from NCBI backbone
 A:Note: this 28-30k form contained both N-linked and O-linked carbohydrate: a 25k for
 A:Accession: C48419
 A:Molecule type: protein
 A:Residues: 28-40 <MAY3>
 A:Experimental source: FS-4 fibroblasts
 A:Note: sequence extracted from NCBI backbone (NCBI:63787)
 A:Note: this 23-25k form contained O-linked but not N-linked carbohydrate
 R:Ohta, T.; Oheida, M.; Hasegawa, M.; Kubonawa, H.; Esaki, K.; Ochi, N.
 J. Biochem. 115, 345-350, 1994
 A:Title: Polypeptide and carbohydrate structure of recombinant human interleukin-6 pr
 A:Reference number: JX0305; MVID:94266765
 A:Contents: annotation; modified sites in recombinant protein from CHO cells
 R:Clogston, C.L.; Boone, T.C.; Crandall, C.; Mendiaz, E.A.; Lu, H.S.
 Arch. Biochem. Biophys. 272, 144-151, 1989
 A:Title: Disulfide structures of human interleukin-6 are similar to those of human gr
 A:Reference number: S04981; MVID:89286115
 A:Contents: annotation; disulfide bonds in recombinant protein
 R:Rock, F.L.; Li, X.; Chong, P.; Ida, N.; Klein, M.
 Biochemistry 33, 5146-5154, 1994
 A:Title: Roles of disulfide bonds in recombinant human interleukin 6 conformation.
 A:Reference number: A54253; MVID:94227044
 A:Contents: annotation; lability and functional significance of each disulfide bond
 C:Comment: Produced by both lymphoid and nonlymphoid tissue in response to growth fac
 C:Comment: This protein plays a regulatory role in various host defense mechanisms an
 C:Genetics:
 A:Gene: GDB:IL6
 A:Cross-references: GDB:120748; OMIM:147620
 A:Map position: 7p21-7p21
 A:Introns: 7/1; 70/3; 108/3; 157/3
 C:Superfamily: Interleukin-6
 C:Keywords: Castleman's disease; cytokine; extracellular protein; glycoprotein; growt
 F:1-27/Domain: signal sequence #status predicted <SIG>
 F:28-212/Product: interleukin-6, long form #status experimental <MATS>
 F:30-212/Product: interleukin-6, short form #status experimental <MATS>
 F:72-78,101-111/Disulfide bonds: #status experimental
 F:73/Binding site: carbohydrate (Asn) (covalent) (partial) #status experimental
 F:166/Binding site: carbohydrate (Thr) (covalent) #status experimental
 F:172/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 75; DB 1; Length 212;
 Best Local Similarity 100.0%; Pred. No. 1.6e-05;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STKVLIQFLOKRAKRL 16
 DB 146 STKVLIQFLOKRAKRL 161

RESULT 2
 T09216
 Interleukin-6 precursor - horse
 C:Species: Equus caballus (domestic horse)
 C>Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 23-Jul-1999
 C:Accession: T09216
 R:Swiderski, C.E.; Horohov, D.W.
 submitted to the EMBL Data Library, July 1996
 A:Reference number: Z16613
 A:Accession: T09216
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-208 <SWI>
 A:Cross-references: EMBL:U64794; NID:g2654387; PID:g2654388
 C:Genetics:
 A:Gene: IL-6
 C:Superfamily: Interleukin-6
 C:Keywords: cytokine; growth factor

Query Match 66.7%; Score 50; DB 2; Length 208;
 Best Local Similarity 66.7%; Pred. No. 0.31;

Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 STKVLIOFLQKRAKN 15
|||||:|:|:|
DB 143 STKVLIOFLQKRAKN 157

RESULT 3
146084
Interleukin 6 - cat
C:Species: Fells silvestris catus (domestic cat)
C:Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 16-Jul-1999
C:Accession: 146084
R:Bradley, W.G.; Gibbs, C.; Kraus, L.; Good, R.A.; Day, N.K.
Proc. Soc. Exp. Biol. Med. 204, 301-305, 1993
A:Title: Molecular cloning and characterization of a cDNA encoding feline Interleukin-6.
A:Reference number: 146084; MUID:94052249
A:Accession: 146084
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-207 <BBR>
A:Cross-references: GB:146914; NID:9438519; PIDN:AA16620.1; PID:9438520
C:Superfamily: Interleukin-6

Query Match 62.7%; Score 47; DB 2; Length 207;
Best Local Similarity 60.0%; Pred. No. 1;
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 1 STKVLIOFLQKRAKN 15
|||:|:|:|
DB 142 STKVLIOFLQKRAKN 156

RESULT 4
146621
proInterleukin 6 - pig
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 16-Jul-1999
C:Accession: 146621
R:Richards, C.; Saklatva, J.
Cytokine 3, 269-276, 1991
A:Title: Molecular Cloning and Sequence of Porcine Interleukin 6 cDNA and Expression of
A:Reference number: 146621; MUID:91338547
A:Accession: 146621
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-212 <RIC>
A:Cross-references: GB:M86722; NID:9164624; PIDN:AAC37333.1; PID:9164625
C:Genetics:
A:Gene: IL6
C:Superfamily: Interleukin-6

Query Match 62.7%; Score 47; DB 2; Length 212;
Best Local Similarity 66.7%; Pred. No. 1;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 STKVLIOFLQKRAKN 15
|||:|:|:|
DB 146 STKVLIOFLQKRAKN 160

RESULT 5
146590
Interleukin 6 - pig
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 16-Jul-1999
C:Accession: 146590
R:Mathialagan, N.; Bixby, J.; Roberts, M.R.
Mol. Reprod. Dev. 32, 324-330, 1992
A:Title: Expression of Interleukin-6 in porcine, ovine, and bovine preimplantation conce
A:Reference number: 146590; MUID:92360284

A:Accession: 146590
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-212 <MAT>
A:Cross-references: GB:M80258; NID:9164514; PIDN:AAC27127.1; PID:9164515
C:Genetics:
A:Gene: IL-6
C:Superfamily: Interleukin-6

Query Match 62.7%; Score 47; DB 2; Length 212;
Best Local Similarity 66.7%; Pred. No. 1;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 STKVLIOFLQKRAKN 15
|||:|:|:|
DB 146 STKVLIOFLQKRAKN 160

RESULT 6
F81448
3-methyl-2-oxobutanoate hydroxymethyltransferase (EC 2.1.2.11) Cj0298c [imported] - C
C:Species: Campylobacter jejuni
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-May-2000
C:Accession: F81448
R:Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chl
C.W.; Quail, M.; Rajandream, K.A.; Rutherford, K.M.; VanVleet, A.; Whitehead, S.; Ba
Nature 403, 665-668, 2000
A:Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals
A:Reference number: A81250; MUID:20150912
A:Accession: F81448
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-274 <PAR>
A:Cross-references: GB:AL139074; GB:AL111168; NID:96967505; PIDN:CA872765.1; PID:9696
A:Experimental source: serotype O2, strain NCTC 11168
C:Genetics:
A:Gene: panB; Cj0298c
C:Superfamily: 3-methyl-2-oxobutanoate hydroxymethyltransferase
C:Keywords: coenzyme A biosynthesis; transferase

Query Match 61.3%; Score 46; DB 2; Length 274;
Best Local Similarity 69.2%; Pred. No. 1.9;
Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 3 KVLIOFLQKRAKN 15
|:|:|:|:|
DB 3 KSWISFLKRAKN 15

RESULT 7
B71405
probable kinesin - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
A:Variety: columbia
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
C:Accession: B71405
R:Bevan, M.; Bancroft, I.; Bent, E.; Love, K.; Goodman, H.; Dean, C.; Bergkamp, R.; D
P.; Medler, H.; Medler, E.; Wambutt, R.; Welzenegger, T.; Pohl, T.M.; Terry, N.; G
avanah, T.; Hempel, S.; Kotter, P.; Eutian, K.D.; Rieger, M.; Schaeffer, M.; Funk, B
Nature 391, 485-488, 1998
A:Authors: Mueller-Auer, S.; Silvey, M.; James, R.; Montfort, A.; Pons, A.; Pulgaden
ernolt, A.; Moores, T.; Jones, J.D.G.; Eneva, T.; Palme, K.; Benes, V.; Rechman, S.;
C.; Chalwatzis, N.
A:Title: Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of Arabidopsis t
A:Reference number: A71400; MUID:98121113
A:Accession: B71405
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-959 <BEV>
A:Cross-references: GB:Z97336; NID:92244788; PIDN:CA810212.1; PID:92244790
C:Genetics:

A:Map position: 4COP9-463845
 C:Superfamily: Arbidloopsis thaliana 107.5K kinesin-related protein; kinesin motor domain
 F:49-379/Domain: kinesin motor domain homology <KNOT>

Query Match 58.7%; Score 44; DB 1; Length 959;
 Best Local Similarity 60.0%; Pred. No. 14;
 Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 1 STKVLFLOKRAKN 15
 ||||| : : |||||
 DB 201 STKVLFLEVMGKRAKN 215

RESULT 8
 E84959
 hypothetical protein yfnc [imported] - Buchnera sp. (strain APS)

C:Species: Buchnera sp.
 C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001
 C:Accession: E84959
 R:Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H.

A:Title: Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp. A
 A:Reference number: AB4930; MUID:20445173

A:Accession: E84959
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-161 <STO>
 A:Cross-references: GB:AP000398; GSPDB:GN00144
 A:Experimental source: strain APS
 C:Genetics:
 A:Gene: yfnc; BU255
 C:Superfamily: hypothetical protein yaaJ

Query Match 56.0%; Score 42; DB 2; Length 161;
 Best Local Similarity 66.7%; Pred. No. 5.7;
 Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 4 VLIQFLOKRAKN 15
 :||| |||||
 DB 142 ILINFFOKRKKN 153

RESULT 9
 T33500
 hypothetical protein C50E10.6 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans
 C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
 C:Accession: T33500
 R:Nelson, J.; Klink, B.; Wohlmann, P.; Bauer, C.
 A:Description: The sequence of C. elegans cosmid C50E10.
 A:Reference number: Z21359
 A:Accession: T33500

A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA

A:Residues: 1-286 <NBL>
 A:Cross-references: EMBL:AF098988; PIDN:AAC67437.1; GSPDB:GN00020; CESP:C50E10.6
 A:Experimental source: strain Bristol N2; clone C50E10
 C:Genetics:
 A:Gene: CESP:C50E10.6
 A:Map position: 2
 A:Introns: 202/3; 241/3

Query Match 56.0%; Score 42; DB 2; Length 286;
 Best Local Similarity 64.3%; Pred. No. 9.3;
 Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 3 KVLIOFLOKRAKN 16
 ||: || |||||
 DB 207 KIMOFGOKRAKN 220

RESULT 10
 S76697
 precorrin-6Y methylase - Synechocystis sp. (strain PCC 6803)
 N:Alternate names: protein sll0099
 C:Species: Synechocystis sp.
 A:Variety: PCC 6803
 C>Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999
 C:Accession: S76697
 R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, O.; K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Mada, T.; Watanabe, A.; Yamada, M.; Yas

DNA Res. 3; 109-136, 1996
 A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis.
 A:Reference number: S74322; MUID:97061201
 A:Accession: S76697
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-425 <KAN>
 A:Cross-references: EMBL:D64004; GB:AB001339; NID:91001701; PIDN:BA10641.1; PID:dl01
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
 C:Genetics:
 A:Gene: cb1e

Query Match 56.0%; Score 42; DB 2; Length 425;
 Best Local Similarity 62.5%; Pred. No. 14;
 Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 1 STKVLFLOKRAKN 16
 ||: ||||| |||||
 DB 130 SNEILLQALQKRAKN 145

RESULT 11
 B83924

hypothetical protein BH2194 [imported] - Bacillus halodurans (strain C-125)
 C:Species: Bacillus halodurans
 C>Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 31-Dec-2000
 C:Accession: B83924

R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; H
 Nucleic Acids Res. 28, 4317-4331, 2000
 A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans a
 A:Reference number: AB3650; MUID:20263314
 A:Accession: B83924
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-290 <STO>
 A:Cross-references: GB:AP001514; GB:BA000004; NID:910174613; PIDN:BA05913.1; GSPDB:G

A:Experimental source: strain C-125
 C:Genetics:
 A:Gene: BH2194
 C:Superfamily: Aeropyrum pernix hypothetical protein APE1388

Query Match 54.7%; Score 41; DB 2; Length 290;
 Best Local Similarity 66.7%; Pred. No. 15;
 Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 3 KVLIOFLOKRAKN 14
 ||: ||||| |||||
 DB 278 RVFSPFLOKRAKN 289

RESULT 12
 G70355

8-aminio-7-oxononanoate synthase (EC 2.3.1.47) - Aquifex aeolicus
 C:Species: Aquifex aeolicus
 C>Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 05-May-2000
 C:Accession: G70355
 R:Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; V.

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OM protein - protein search, using sw model

Run on: December 19, 2001, 16:26:13 ; Search time 48.45 seconds
(without alignments)
12.108 Million cell updates/sec

Title: US-09-202-104A-2
Perfect score: 75
Sequence: 1 STKVLQFLQKKAKNL 16

Scoring table: BIOSUM62
Gapop 10.0, Gapext 0.5

Searched: 100059 seqs, 36664827 residues
Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: SwissProt_39:*

Prod. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	75	100.0	212	1 IL6_HUMAN	P05231 homo sapien
2	75	100.0	212	1 IL6_MACFA	P79341 macaca fasc
3	75	100.0	212	1 IL6_MACMU	P51494 macaca mula
4	69	92.0	212	1 IL6_CERPTO	P46650 cercopithec
5	50	66.7	207	1 IL6_CANFA	P41323 canis famill
6	50	66.7	208	1 IL6_HORSE	P05181 equus caball
7	47	62.7	208	1 IL6_FELCA	P41683 felis silve
8	47	62.7	209	1 IL6_PHOVI	P28819 phoca vitul
9	47	62.7	212	1 IL6_PIG	P26893 sus scrofa
10	42	56.0	161	1 Y255_BUCAL	P57343 buchnera ap
11	40	53.3	205	1 IL6_ORCOR	P02847 orcinus orc
12	40	53.3	373	1 BIOF_AQUAE	P06675 aquilifex aeo
13	39	52.0	437	1 E2F2_HUMAN	P01409 homo sapien
14	39	52.0	487	1 ATRF2_CHICK	P03602 gallus gall
15	39	52.0	487	1 ATRF2_HUMAN	P15336 homo sapien
16	39	52.0	487	1 ATRF2_MOUSE	P16851 mus musculu
17	39	52.0	487	1 ATRF2_RAT	P00869 rattus norv
18	39	52.0	704	1 DBF4_YEAST	P32325 saccharomyc
19	39	52.0	757	1 MLH1_RAT	P97679 rattus norv
20	38	50.7	89	1 Y1HD_ECOLI	P32126 escherichia
21	38	50.7	129	1 RS22_YEAST	P04648 saccharomyc
22	38	50.7	130	1 RS22_KLUMA	P33553 kluyveromyc
23	38	50.7	365	1 YNZ7_YEAST	P28625 saccharomyc
24	38	50.7	657	1 UVRB_CHLPN	P92745 chlamydia p
25	38	50.7	3144	1 HD_HUMAN	P42858 homo sapien
26	37.5	50.0	1081	1 DPOD_ARATH	P01427 arabidopsis
27	37.5	50.0	1105	1 DPOD_ORYSA	P01566 oryza sativ
28	37	49.3	96	1 SY20_HUMAN	P78556 homo sapien
29	37	49.3	187	1 YGRA_HAEIN	P44905 haemophilus
30	37	49.3	220	1 KCY_LACLA	P09671 lactococcus
31	37	49.3	346	1 MG84_HUMAN	P01581 haemophilus
32	37	49.3	436	1 BRNO_HAEIN	P71345 haemophilus
33	37	49.3	458	1 ACHO_HUMAN	P005901 homo sapien

34	37	49.3	1049	1	POL_HV2G1
35	37	49.3	1073	1	POL_HV2D1
36	37	49.3	1142	1	POL_HV2BE
37	36.5	48.7	212	1	R1A_MYCPN
38	36	48.0	158	1	FABZ_ZYMMO
39	36	48.0	227	1	Y053_METUA
40	36	48.0	246	1	PSA6_SOYBN
41	36	48.0	246	1	PSA6_TOBAC
42	36	48.0	374	1	HSP5_ARATH
43	36	48.0	856	1	CLPB_HELPY
44	36	48.0	856	1	YOR1_YEAST
45	36	48.0	1477	1	P53049 saccharomyc

ALIGNMENTS

RESULT 1	ID	IL6_HUMAN	STANDARD;	PRT;	212 AA.
AC	P05231;				
DT	13-AUG-1987	(rel. 05, Created)			
DT	13-AUG-1987	(rel. 05, Last sequence update)			
DT	20-AUG-2001	(rel. 40, Last annotation update)			
DE	INTERLEUKIN-6 PRECURSOR (IL-6) (B-CELL STIMULATORY FACTOR 2) (BSF-2)				
DE	(INTERFERON BETA-2) (HYBRIDOMA GROWTH FACTOR).				
GN	IL6 OR IFNB2.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
OX	NCBI_Taxid=9606;				
RP	SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.				
RX	MEDLINE=87063033; PubMed=3491322;				
RA	Hirano T., Yasukawa K., Harada H., Taga T., Watanabe Y., Matsuda T.,				
RA	Kashimawara S.-I., Nakajima K., Koyama K., Iwamatsu A., Tsunashima S.,				
RA	Sakiyama F., Matsui H., Takahara Y., Taniguchi T., Kishimoto T.;				
RT	Complementary DNA for a novel human interleukin (BSF-2) that induces				
RT	B lymphocytes to produce immunoglobulin.";				
RL	Nature 324:73-76(1986).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=88082664; PubMed=3500852;				
RA	Yasukawa K., Hirano T., Watanabe Y., Muratani K., Matsuda T.,				
RT	Nakai S., Kishimoto T.;				
RT	"Structure and expression of human B cell stimulatory factor-2				
RL	(BSF-2/IL-6) gene.";				
RL	EMBO J. 6:2939-2945(1987).				
RN	[3]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=87067433; PubMed=3538015;				
RA	May L.T., Hellgott D.C., Sehgal P.B.;				
RT	"Anti-beta-interferon antibodies inhibit the increased expression of				
RT	HLA-B7 mRNA in tumor necrosis factor-treated human fibroblasts:				
RT	structural studies of the beta 2 interferon involved.";				
RL	Proc. Natl. Acad. Sci. U.S.A. 83:8957-8961(1986).				
RN	[4]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=87053818; PubMed=3023045;				
RA	Zilberstein A., Ruggieri R., Korn J.H., Revel M.;				
RT	"Structure and expression of cDNA and genes for human				
RT	interferon-beta-2, a distinct species inducible by growth-stimulatory				
RT	cytokines.";				
RL	EMBO J. 5:2529-2537(1986).				
RN	[5]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=88088768; PubMed=3320204;				
RA	Brakenhoff J.P.J., de Groot E.R., Evers R.F., Pannekoek H.,				
RA	Aarden L.A.;				
RT	"Molecular cloning and expression of hybridoma growth factor in				
RT	Escherichia coli.";				
RL	J. Immunol. 139:4116-4121(1987).				
RN	[6]				

RP SEQUENCE FROM N.A.
 RX MEDLINE-89391958; PubMed-2789513;
 RA Tonouchi N., Mitsu K., Karasuyama H., Matsui H.;
 RT "Deletion of 3' untranslated region of human BSF-2 mRNA causes
 RT stabilization of the mRNA and high-level expression in mouse NIH3T3
 RT cells.";
 RL Biochem. Biophys. Res. Commun. 163:1056-1062(1989).
 RN [17]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Fibroblast;
 RX MEDLINE-87004683; PubMed-3758081;
 RA Hegeman G., Content J., Volckaert G., Derynck R., Tavernier J.,
 RA Piers W.;
 RT "Structural analysis of the sequence coding for an inducible 26-kDa
 RT protein in human fibroblasts.";
 RL Eur. J. Biochem. 159:625-632(1986).
 RN [18]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-89193317; PubMed-3266463;
 RA Wong G., Witek-Glannon J., Hewick R., Clark S., Ogawa M.;
 RT "Interleukin 6: Identification as a hematopoietic colony-stimulating
 RT factor.";
 RL Behring Inst. Mitt. 83:40-47(1988).
 RN [19]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-93178270; PubMed-1291290;
 RA Chen Q.Y.;
 RT "Stable and efficient expression of human interleukin-6 cDNA in
 RT mammalian cells after gene transfer.";
 RL Chung-Hua Chung Liu Tsa Chih 14:340-344(1992).
 RN [10]
 RP SEQUENCE OF 30-63.
 RX MEDLINE-88154445; PubMed-3279116;
 RA van Damme J., van Beeumen J., Decock B., van Snick J., de Ley M.,
 RA Billiau A.;
 RT "Separation and comparison of two monokines with
 RT lymphocyte-activating factor activity: IL-1 beta and hybridoma growth
 RT factor (HGF). Identification of leukocyte-derived HGF as IL-6.";
 RL J. Immunol. 140:1534-1541(1988).
 RN [11]
 RP SEQUENCE OF 50-212 OF RECOMBINANT FORM LACKING 1ST DISULFIDE BOND.
 RX MEDLINE-95154344; PubMed-7851440;
 RA Breton J., la Flura A., Bertolero F., Orsini G., Valsasina B.,
 RA Zilio R., de Filippis V., Polverino de Lauro P., Fontana A.;
 RT "Structure, stability and biological properties of a N-terminally
 RT truncated form of recombinant human interleukin-6 containing a single
 RT disulfide bond.";
 RL Eur. J. Biochem. 227:573-581(1995).
 RN [12]
 RP DISULFIDE BONDS.
 RX MEDLINE-89286115; PubMed-2472117;
 RA Clogston C.L., Boone T.C., Crandall B.C., Mendiaz E.A., Lu H.S.;
 RT "Disulfide structures of human interleukin-6 are similar to those of
 RT human granulocyte colony stimulating factor.";
 RL Arch. Biochem. Biophys. 272:144-151(1989).
 RN [13]
 RP MUTAGENESIS.
 RX MEDLINE-91243808; PubMed-2037043;
 RA Lueticken C., Krutigen A., Moeller C., Heinrich P.C., Rose-John S.;
 RT "Evidence for the importance of a positive charge and an
 RT alpha-helical structure of the C-terminus for biological activity of
 RT human IL-6.";
 RL FEBS Lett. 282:265-267(1991).
 RN [14]
 RP STRUCTURE BY NMR.
 RX MEDLINE-96134845; PubMed-8555185;
 RA Nishimura C., Watanabe A., Gouda H., Shimada I., Arata Y.;
 RT "Folding topologies of human interleukin-6 and its mutants as studied
 RT by NMR spectroscopy.";
 RL Biochemistry 35:273-281(1996).
 RN [15]
 RP STRUCTURE BY NMR.
 RX MEDLINE-97303053; PubMed-9159484;

RA Xu G.-Y., Yu H.-A., Hong J., Stahl M., McDonagh T., Kay L.E.,
 RA Cumming D.A.;
 RT "Solution structure of recombinant human interleukin-6.";
 RL J. Mol. Biol. 268:468-481(1997).
 RN [16]
 RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
 RX MEDLINE-97224126; PubMed-9118960;
 RA Somers W., Stahl M., Seehra J.S.;
 RT "1.9-A crystal structure of interleukin 6: implications for a novel
 RT mode of receptor dimerization and signaling.";
 RL EMBL J. 16:989-997(1997).
 CC -1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
 CC OF B-CELLS INTO IS-SECRETING CELLS. IT INDUCES MYELOMA AND
 CC PLASMACYTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN
 CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS.
 CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: X04430; CAA28026.1; -
 DR EMBL: M14584; AAA52728.1; -
 DR EMBL: X04602; CAA28268.1; -
 DR EMBL: Y00081; CAA68278.1; -
 DR EMBL: M18403; AAA52729.1; -
 DR EMBL: M29150; AAA59154.1; -
 DR EMBL: X04402; CAA27990.1; -
 DR EMBL: X04403; CAA27991.1; -
 DR EMBL: M54894; AAC41704.1; -
 DR EMBL: S56892; AAD13886.1; -
 DR EMBL: A09363; CAA00839.1; -
 DR PIR: A32648; IYHUR2.
 DR PIR: A25921; A25921.
 DR PDB: 1IL6; 04-FEB-98.
 DR PDB: 2IL6; 04-FEB-98.
 DR PDB: 1ALD; 03-JUN-98.
 DR MIM: 147620; -
 DR InterPro: IPR003573; IL6_MGF_GCSF.
 DR InterPro: IPR003574; Interleukin_6.
 DR Pfam: PF00489; IL6; 1.
 DR PRINTS: PR00433; IL6GCSFNGF.
 DR PRINTS: PR00434; INTERLEUKIN6.
 DR PRODOM: PD004356; Interleukin_6; 1.
 DR SMART: SM00126; IL6; 1.
 DR PROSITE: PS00254; INTERLEUKIN_6; 1.
 KW Cytokine; Glycoprotein; Growth factor; Signal; 3D-structure.
 FT SIGNAL 1 29
 FT CHAIN 30 212
 FT DISULFID 72 78
 FT DISULFID 101 111
 FT CARBOHYD 73 73
 FT MUTAGEN 173 173
 FT MUTAGEN 185 185
 FT MUTAGEN 204 204
 FT MUTAGEN 210 210
 FT MUTAGEN 212 212
 FT MUTAGEN 212 212
 FT SEQUENCE 212 AA; 23718 MW; 1FIED1FELB734079 CRC64;

Query Match 100.0%; Score 75; DR 1; Length 212;
 Best Local Similarity 100.0%; Pred. NO. 3.8e-06; Indels 0; Gaps 0;
 Matches 16; Conservative 0; Mismatches 0;
 Oy 1 STKVLIQFLQKKAKNL 16
 |||
 Db 146 STKVLIQFLQKKAKNL 161

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RESULT 2
IL6_MACFA STANDARD; PRT; 212 AA.
AC PV9341;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DE 15-JUL-1998 (Rel. 36, Last annotation update)
DE INTERLEUKIN-6 PRECURSOR (IL-6).
GN IL6.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RA Tatsumi M.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
CC FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
CC OF B-CELLS INTO IG-SECRETING CELLS, IT INDUCES MELOMA AND
CC PLASMACYTES GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN
CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
CC -----
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CC -----
DR EMBL; AB000554; BAA19148.1; -.
DR HSP; P05231; 21L6.
DR InterPro; IPR003573; IL6_MGF_GCSF.
DR InterPro; IPR003574; Interleukin_6.
DR Pfam; PF00489; IL6; 1.
DR PRINTS; PRO0433; IL6GCSFMGF.
DR PRINTS; PRO0434; INTERLEUKIN6.
DR ProDom; PD004356; Interleukin_6; 1.
DR SMART; SM00126; IL6; 1.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
DR CYTOKINE; Glycoprotein; Growth factor; Signal.
FT SIGNAL 1 29 BY SIMILARITY.
FT CHAIN 30 212 INTERLEUKIN-6.
FT DISULFID 72 78 POTENTIAL.
FT DISULFID 101 111 POTENTIAL.
FT CARBOYD 73 73 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOYD 172 172 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 212 AA; 23654 MW; CFB173FCBF0B0389 CMC64;

Query Match 100.0%; Score 75; DB 1; Length 212;
Best Local Similarity 100.0%; Pred. No. 3.8e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STKVLIQFLQKKAKNL 16
DB 146 STKVLIQFLQKKAKNL 161

RESULT 3
IL6_MACMU STANDARD; PRT; 212 AA.
AC PS1494;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE INTERLEUKIN-6 PRECURSOR (IL-6).
GN IL6.
OS Macaca mulatta (Rhesus macaque).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RAC 2;
RX MEDLINE=96003435; PubMed=7561102;
RA Vulliamier F.J., Brar S.S., Wayne A.E., Chikkala N., Ansari A.A.;
RT "Comparative sequence analysis of cytokine genes from human and
  nonhuman primates";
RL J. Immunol. 155:3946-3954(1995).
CC -!- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
  FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
  OF B-CELLS INTO Ig-SECRETING CELLS, IT INDUCES MYELOID AND
  PLASMACYTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN
  HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; L26028; AAA99978.1; -.
CC HSSP; P05231; IALU.
CC InterPro; IPR003573; IL6_MGF_GCSF.
CC InterPro; IPR003574; Interleukin_6.
CC Pfam; PF00489; IL6; 1.
CC PRINTS; PR00433; IL6GCSFMGF.
CC PRINTS; PR00434; INTERLEUKIN6.
CC ProDom; PD004356; Interleukin_6; 1.
CC SMART; SM00126; IL6; 1.
CC PROSITE; PS00254; INTERLEUKIN_6; 1.
CC Cytokine; Glycoprotein; Growth factor; Signal.
CC FT SIGNAL 1 29 BY SIMILARITY.
CC FT CHAIN 30 212 INTERLEUKIN-6.
CC FT DISULFID 72 78 POTENTIAL.
CC FT DISULFID 101 111 POTENTIAL.
CC FT CARBOHYD 73 73 POTENTIAL.
CC FT CARBOHYD 172 172 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 172 172 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 212 AA; 23728 MW; 4130FDE0CF0BCAD CRC64;

Query Match 100.0%; Score 75; DB 1; Length 212;
Best Local Similarity 100.0%; Pred. No. 3,8e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STKVLIQFLQKKAKNL 16
DB 146 STKVLIQFLQKKAKNL 161

RESULT 4
IL6_CERTO STANDARD; PRT; 212 AA.
AC P46630;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE INTERLEUKIN-6 PRECURSOR (IL-6).
GN IL6.
OS Cercopithecus torquatus atys (Red-crowned mangabey) (Sooty mangabey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Cercopithecus.
OX NCBI_TaxID=9531;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FUJ;

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RA MEDLINE-96003435; PubMed-7561102;
RA Villinger F.J., Brar S.S., Mayne A.E., Chikala N., Ansari A.A.;
RT "Comparative sequence analysis of cytokine genes from human and
RT nonhuman primates."
CC J. Immunol. 155:3946-3954 (1995).
CC -1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
CC FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
CC OF B-CELLS INTO IG-SECRETING CELLS. IT INDUCES MYELOMA AND
CC PLASMACYTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN
CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
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CC -----
CC EMBL: L26032; AAA99972.1; -
CC HSSP: P05231; 1ALU.
CC InterPro: IPR003573; IL6_MGF_GCSF.
CC InterPro: IPR003574; Interleukin_6.
CC Pfam: PF00489; IL6; 1.
CC PRINTS: PR00433; IL6GCSFMGF.
CC PRINTS: PR00434; INTERLEUKIN6.
CC ProDom: PD004356; Interleukin_6; 1.
CC SMART: SM00126; IL6; 1.
CC PROSITE: PS00254; INTERLEUKIN_6; 1.
CC CYTOKINE; Glycoprotein; Growth factor; Signal.
CC SIGNAL 1 29 BY SIMILARITY.
CC CHAIN 30 212 INTERLEUKIN-6.
CC DISULFID 72 78 POTENTIAL.
CC DISULFID 101 111 POTENTIAL.
CC CARBOHYD 73 73 N-LINKED (GLCNAC...) (POTENTIAL).
CC CARBOHYD 172 172 N-LINKED (GLCNAC...) (POTENTIAL).
CC SEQUENCE 212 AA; 23668 MW; C73C035226B4B9F CRC64;
SQ
Query Match 92.0%; Score 69; DB 1; Length 212;
Best Local Similarity 93.8%; Pred. No. 4.4e-05;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 STKVLIQFLQKKAKNL 16
DB 146 STKVLIQFLQKKAKNL 161
RESULT 5
IL6_CANFA 4
ID IL6_CANFA STANDARD; PRT; 207 AA.
AC P41323;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE INTERLEUKIN-6 PRECURSOR (IL-6).
GN IL6.
OS Canis familiaris (Dog)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MONGREL;
RX MEDLINE-94303924; PubMed-7913298;
RA Kujala G.L., Youker K.A., Hawkins H.K., Perrard J.L.,
RA Michael L.H., Ballantyne C.M., Smith C.W., Eutman M.L.;
RT "Regulation of ICAM-1 and IL-6 in myocardial ischemia: effect of
RT reperfusion."
RL Ann. N.Y. Acad. Sci. 723:258-270 (1994).
CC -1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
CC FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION

CC OF B-CELLS INTO IG-SECRETING CELLS. IT INDUCES MYELOMA AND
CC PLASMACYTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN
CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS.
CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
CC -----
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CC -----
CC EMBL: U12234; AAA83030.1; -
CC HSSP: P05231; 2IL6.
CC InterPro: IPR003573; IL6_MGF_GCSF.
CC InterPro: IPR003574; Interleukin_6.
CC Pfam: PF00489; IL6; 1.
CC PRINTS: PR00433; IL6GCSFMGF.
CC PRINTS: PR00434; INTERLEUKIN6.
CC ProDom: PD004356; Interleukin_6; 1.
CC SMART: SM00126; IL6; 1.
CC PROSITE: PS00254; INTERLEUKIN_6; 1.
CC CYTOKINE; Glycoprotein; Growth factor; Signal.
CC SIGNAL 1 29 BY SIMILARITY.
CC CHAIN 30 212 INTERLEUKIN-6.
CC DISULFID 72 78 POTENTIAL.
CC DISULFID 101 111 POTENTIAL.
CC CARBOHYD 73 73 N-LINKED (GLCNAC...) (POTENTIAL).
CC CARBOHYD 172 172 N-LINKED (GLCNAC...) (POTENTIAL).
CC SEQUENCE 207 AA; 22945 MW; 45540154EA9C0F50 CRC64;
SQ
Query Match 66.7%; Score 50; DB 1; Length 207;
Best Local Similarity 60.0%; Pred. No. 0.097;
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
OY 1 STKVLIQFLQKKAKNL 15
DB 141 STKVLIQFLQKKAKNL 155
RESULT 6
IL6_HORSE
ID IL6_HORSE STANDARD; PRT; 208 AA.
AC Q95181; Q19007; Q46568;
DT 01-NOV-1997 (Rel. 35, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE INTERLEUKIN-6 PRECURSOR (IL-6).
GN IL6.
OS Equus caballus (Horse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RA Swiderski C.E., Horohov D.W.;
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Leutenegger C.M., Huder J.B., von Rechenberg B., Akens M., Auer J.;
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Lai A.C.K.;
RT "Cloning and expression of equine interleukin-6."
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
CC FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
CC OF B-CELLS INTO IG-SECRETING CELLS. IT INDUCES MYELOMA AND
CC PLASMACYTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN
CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
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DR EMBL: U64794; AAB87703.1; -
 DR EMBL: AF005227; AAB62246.1; -
 DR EMBL: AF041975; AAC04574.1; -
 DR HSSP: P05231; 1ALU.
 DR InterPro: IPR003573; IL6_MGF_GCSF.
 DR InterPro: IPR003574; Interleukin_6.
 DR Pfam: PF00489; IL6; 1.
 DR PRINTS: PR00433; IL6GCSFMGF.
 DR PRINTS: PR00434; INTERLEUKIN_6.
 DR ProDom: PD004356; Interleukin_6; 1.
 DR SMART: SM00126; IL6; 1.
 DR PROSITE: PS00254; INTERLEUKIN_6; 1.
 DR Cytokine; Glycoprotein; Growth factor; Signal.
 FT SIGNAL 1 27
 FT CHAIN 28 208
 FT DISULFID 69 75
 FT DISULFID 98 108
 FT CARBOHYD 71 71
 FT CARBOHYD 184 184
 FT CONFLICT 4 5
 FT CONFLICT 8 8
 FT CONFLICT 137 137
 FT CONFLICT 205 205
 FT CONFLICT 208 AA; 23325 MM; A62F4C234056H66 CRC64;
 SQ SEQUENCE

Query Match 66.7%; Score 50; DB 1; Length 208;
 Best Local Similarity 66.7%; Pred. No. 0.097;
 Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 STKVLIQFLOKRRKN 15
 DB 143 STKVLIQFLOKRRKN 157

RESULT 7
 IL6_FELCA STANDARD; PRT; 208 AA.
 AC P41683;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE INTERLEUKIN-6 PRECURSOR (IL-6).
 GN IL6.
 OS Felis silvestris catus (Cat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
 CX NCBI_TaxID=9685;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94162386; PubMed=8117820;
 RA Ohashi T., Matsumoto Y., Watarai T., Gotsuka R., Tsujimoto H.,
 RA Hasegawa A.;
 RT "Molecular cloning of feline interleukin-6 cDNA.";
 RL J. Vet. Med. Sci. 55:941-944(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lymphocytes;
 RX MEDLINE=94052249; PubMed=8234373;
 RA Bradley W.G., Gibbs C., Kraus L., Good R.A., Day N.K.;
 RT "Molecular cloning and characterization of a cDNA encoding feline
 RT interleukin-6.";
 RL Proc. Soc. Exp. Biol. Med. 204:301-305(1993).
 CC -I- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
 CC FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION

CC OF B-CELLS INTO IG-SECRETING CELLS, IT INDUCES MYELOMA AND
 CC PLASMACYTOMA GROWTH. IT INDUCES NERVE CELLS DIFFERENTIATION, IN
 CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS.
 CC -I- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.

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DR EMBL: L16914; AAA16620.1; -
 DR EMBL: D13227; BAA02507.1; -
 DR HSSP: P05231; 2IL6.
 DR InterPro: IPR003573; IL6_MGF_GCSF.
 DR InterPro: IPR003574; Interleukin_6.
 DR Pfam: PF00489; IL6; 1.
 DR PRINTS: PR00433; IL6GCSFMGF.
 DR PRINTS: PR00434; INTERLEUKIN_6.
 DR ProDom: PD004356; Interleukin_6; 1.
 DR SMART: SM00126; IL6; 1.
 DR PROSITE: PS00254; INTERLEUKIN_6; 1.
 DR Cytokine; Glycoprotein; Growth factor; Signal.
 FT SIGNAL 1 27
 FT CHAIN 28 208
 FT DISULFID 68 74
 FT DISULFID 97 107
 FT CONFLICT 2 2
 FT CONFLICT 45 45
 FT CONFLICT 133 133
 FT CONFLICT 173 187
 FT CONFLICT 200 201
 FT CONFLICT 208 AA; 23401 MM; 93B4456B2989CA4C CRC64;
 SQ SEQUENCE

Query Match 62.7%; Score 47; DB 1; Length 208;
 Best Local Similarity 60.0%; Pred. No. 0.33;
 Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 1 STKVLIQFLOKRRKN 15
 DB 142 STKVLIQFLOKRRKN 156

RESULT 8
 IL6_PROVI STANDARD; PRT; 209 AA.
 AC Q28619;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE INTERLEUKIN-6 PRECURSOR (IL-6) (FRAGMENT).
 GN IL6.
 OS Phoca vitulina (Harbor seal).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Carnivora; Plinipedia; Phocidae; Phoca.
 CX NCBI_TaxID=9720;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96163018; PubMed=8575817;
 RA King D.P., Schrenzel M.D., McKnight M.L., Reidarson T.H., Hanni K.D.,
 RA Stolt J.L., Ferrick D.A.;
 RT "Molecular cloning and sequencing of interleukin 6 cDNA fragments from
 RT the harbor seal (Phoca vitulina), killer whale (Orcinus orca), and
 RT Southern sea otter (Enhydra lutris nereis).";
 RL Immunogenetics 43:190-195(1996).
 CC -I- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
 CC FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
 CC OF B-CELLS INTO IG-SECRETING CELLS, IT INDUCES MYELOMA AND
 CC PLASMACYTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN

HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS (BY SIMILARITY).

CC -1- SUBCELLULAR LOCATION: SECRETED.

CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.

CC -----

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CC -----

DR EMBL: L46802; AAB01430.1; -.

DR HSSP: P05231; 21L6.

DR InterPro: IPR003573; IL6_MGF_GCSF.

DR Pfam: PF00489; IL6; 1.

DR SMART: SM00126; IL6; 1.

DR PROSITE: PS00254; INTERLEUKIN_6; 1.

KW Cytokine; Glycoprotein; Growth factor; Signal.

FT NON_TER 1 1

FT SIGNAL <1 26 BY SIMILARITY.

FT CHAIN 27 209 INTERLEUKIN-6.

FT DISULFID 69 75 BY SIMILARITY.

FT DISULFID 98 108 BY SIMILARITY.

FT SEQUENCE 209 AA; 23483 MW; 75144922E43B4BE9 CRC64;

QY 1 STKVLIOFLQKAKN 15

Db 143 STKLVQMLMKKVS 157

Query Match 62.7%; Score 47; DB 1; Length 209;

Best Local Similarity 60.0%; Pred. No. 0.33;

Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

RESULT 9

ID IL6_PIG STANDARD; PRT; 212 AA.

AC P26893;

DT 01-AUG-1992 (Rel. 23, Created)

DT 01-AUG-1992 (Rel. 23, Last sequence update)

DT 15-DEC-1998 (Rel. 37, Last annotation update)

DE INTERLEUKIN-6 PRECURSOR (IL-6).

GN IL6.

OS Sus scrofa (Pig).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.

OC NCBI_TaxID=9823;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=91338547; PubMed=1873476;

RA Richards C., Saklatvala J.;

RT "Molecular cloning and sequence of porcine interleukin 6 cDNA and

RT expression of mRNA in synovial fibroblasts in vitro."

RL Cytokine 3:269-276(1991).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=92360284; PubMed=1497880;

RA Mathialagan N., Bixby J.A., Roberts M.R.;

RT "Expression of interleukin-6 in porcine, ovine, and bovine

RT preimplantation conceptuses."

RL Mol. Reprod. Dev. 32:324-330(1992).

-1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL

CC FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION

CC OF B-CELLS INTO IG-SECRETING CELLS. IT INDUCES MYELOMA AND

CC PLASMACTOMA GROWTH. IT INDUCES NERVE CELLS DIFFERENTIATION, IN

CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS.

CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.

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CC -----

DR EMBL: M86722; AAC37333.1; -.

DR EMBL: M80258; AAC27127.1; -.

DR HSSP: P05231; 1ALU.

DR InterPro: IPR003573; IL6_MGF_GCSF.

DR Pfam: PF00489; IL6; 1.

DR PRINTS: PR00433; IL6GCSFMGF.

DR PRINTS: PR00434; INTERLEUKIN_6.

DR PRODOM: PD004356; Interleukin_6; 1.

DR SMART: SM00126; IL6; 1.

DR PROSITE: PS00254; INTERLEUKIN_6; 1.

KW Cytokine; Glycoprotein; Growth factor; Signal.

FT SIGNAL 1 29 BY SIMILARITY.

FT CHAIN 30 212 INTERLEUKIN-6.

FT DISULFID 72 78 BY SIMILARITY.

FT DISULFID 101 111 BY SIMILARITY.

FT CONFLICT 30 30 G -> E (IN REF. 2).

FT SEQUENCE 212 AA; 23880 MW; EF100ED030B6FDD0 CRC64;

QY 1 STKVLIOFLQKAKN 15

Db 146 STKALIQTLRQKGN 160

Query Match 62.7%; Score 47; DB 1; Length 212;

Best Local Similarity 66.7%; Pred. No. 0.33;

Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

RESULT 10

ID Y255_BUCAI STANDARD; PRT; 161 AA.

AC P57343;

DT 20-AUG-2001 (Rel. 40, Created)

DT 20-AUG-2001 (Rel. 40, Last sequence update)

DT 20-AUG-2001 (Rel. 40, Last annotation update)

DE HYPOTHETICAL PROTEIN BU255.

GN BU255.

OS Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum

OS symbiotic bacterium).

OC Bacteria; Proteobacteria; gamma; subdivision; Buchnera.

OC NCBI_TaxID=118099;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-TOKYO 1998;

RA Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.;

RT "Genome sequence of the endocellular bacterial symbiont of aphids

RT Buchnera sp. Aps."

RL Nature 407:81-86(2000).

CC -1- COFACTOR: ZINC (BY SIMILARITY).

CC -1- SIMILARITY: BELONGS TO THE CYTIDINE AND DEOXYCYTIDYLATE DEAMINASES

CC FAMILY. STRONG, TO E.COLI AND B.SUBTILIS RIBG. STRONG, TO E.COLI

CC YPHC.

CC -----

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CC -----

DR EMBL: AP001118; BAB12965.1; -.

DR InterPro: IPR002125; dCMP_cyt_deam.

DR Pfam: PF00383; dCMP_cyt_deam; 1.

DR PROSITE: PS00903; Cyt_dCMP_DEAMINASES; 1.

KM Hypothetical protein; Hydrolase; Zinc; Complete proteome.
 FT METL 55 55 ZINC (BY SIMILARITY).
 FT METL 85 85 ZINC (BY SIMILARITY).
 FT METL 88 88 ZINC (BY SIMILARITY).
 SQ SEQUENCE 161 AA; 18663 MW; 018DE825D8D7CC CRC64;

Query Match 56.0%; Score 42; DB 1; Length 161;
 Best Local Similarity 66.7%; Pred. No. 1.9;
 Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 4 VLIOFLOKRAKN 15
 DB 142 ILINFEQKRRKN 153

RESULT 11
 ID IL6_ORCOR STANDARD; PRT: 205 AA.
 AC 028747;
 DT 30-MAY-2000 (rel. 39, Created)
 DT 30-MAY-2000 (rel. 39, Last sequence update)
 DT 30-MAY-2000 (rel. 39, Last annotation update)
 DE INTERLEUKIN-6 PRECURSOR (IL-6) (FRAGMENT).
 GN IL6.
 OS Orcinus orca (Killer whale).
 OC Eukaryota; Metazoa; Chordata; Craniata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti; Delphinidae;
 OC Orcinus.
 OX NCBI_TaxID=9733;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96163018; PubMed=8575817;
 RA King D.P., Schrenzel M.D., McKnight M.L., Reidarson T.H., Hanni K.D.,
 RA Stolt J.L., Petrick D.A.;
 RT "Molecular cloning and sequencing of interleukin 6 cDNA fragments from
 RT the harbor seal (Phoca vitulina), killer whale (Orcinus orca), and
 RT Southern sea otter (Enhydra lutris nereis).";
 RL Immunogenetics 43:190-195(1996).
 CC -1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
 CC FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
 CC OF B-CELLS INTO IG-SECRETING CELLS, IT INDUCES MYELOMA AND
 CC PLASMACYTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN
 CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: SECRETED.
 CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
 CC
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 CC
 CC EMBL: L46803; AAB01429.1; -
 CC HSSP: P05231; IALU.
 DR InterPro: IPR003573; IL6_MGF_GCSF.
 DR InterPro: IPR003574; Interleukin_6.
 DR Pfam: PF00489; IL6; 1.
 DR SMART: SM00126; IL6; 1.
 DR PROSITE: PS00254; INTERLEUKIN_6; 1.
 KW Cytokine; Glycoprotein; Growth factor; Signal.
 FT NON_TER 1
 FT SIGNAL <1 21 BY SIMILARITY.
 FT CHAIN 22 205 INTERLEUKIN-6.
 FT DISULFID 64 70 BY SIMILARITY.
 FT DISULFID 93 103 BY SIMILARITY.
 FT CARBOHYD 164 164 N-LINKED (GLCNAC...) (POTENTIAL).
 SQ SEQUENCE 205 AA; 23266 MW; 630BF3A457960832 CRC64;

Query Match 53.3%; Score 40; DB 1; Length 205;

Best Local Similarity 53.3%; Pred. No. 5.6;
 Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 1 STKVLIQFLOKRAKN 15
 DB 138 SSRKLAQILROKVK 152

RESULT 12
 ID B1OF_AOUAE STANDARD; PRT: 373 AA.
 AC 066875;
 DT 30-MAY-2000 (rel. 39, Created)
 DT 30-MAY-2000 (rel. 39, Last sequence update)
 DT 20-AUG-2001 (rel. 40, Last annotation update)
 DE 8-AMINO-7-OXONONANOATE SYNTHASE (EC 2.3.1.47) (AONS) (8-AMINO-7-
 DE KETOPELARGONATE SYNTHASE) (7-KETO-8-AMINO-PELARGONIC ACID SYNTHETASE)
 DE (7-KAP SYNTHETASE) (L-ALANINE--PIMELYL COA LIGASE).
 GN B1OF OR NO.626.
 OS Aquifex aeolicus.
 OC Bacteria; Aquificales; Aquificaceae; Aquifex.
 OX NCBI_TaxID=63363;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=VE5;
 RX MEDLINE=98196666; PubMed=9537320;
 RA Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
 RA Graham D.E., Overbeek R., Sneed M.A., Keller M., Anjay M., Huber R.,
 RA Feldman R.A., Short J.M., Olson G.O., Swanson R.V.;
 RT "The complete genome of the hyperthermophilic bacterium Aquifex
 RT aeolicus.";
 RL Nature 392:353-358(1998).
 CC -1- CATALYTIC ACTIVITY: 6-CARBOXYHEXANOYL-COA + L-ALANINE -
 CC 8-AMINO-7-OXONONANOATE + COA + CO(2).
 CC -1- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).
 CC -1- PATHWAY: FIRST STEP IN BIOTIN BIOSYNTHESIS.
 CC -1- SIMILARITY: BELONGS TO CLASS-II OF PYRIDOXAL-PHOSPHATE-DEPENDENT
 CC AMINOTRANSFERASES.
 CC
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 CC
 CC EMBL: AEO00699; AAC06836.1; -
 DR InterPro: IPR001917; Aminotransf_2.
 DR Pfam: PF00222; aminotran_2; 1.
 DR PROSITE: PS00599; AA_TRANSFR_CLASS_2; 1.
 KW Biotin biosynthesis; Transferase; Pyridoxal phosphate;
 KW Complete proteome.
 FT BINDING 223
 SQ SEQUENCE 373 AA; 42532 MW; 536B34A5D584401 CRC64;

Query Match 53.3%; Score 40; DB 1; Length 373;
 Best Local Similarity 53.3%; Pred. No. 10;
 Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

OY 2 TKVLIQFLOKRAKNL 16
 DB 235 TKLLIDYLVNKRSL 249

RESULT 13
 ID E2F2_HUMAN STANDARD; PRT: 437 AA.
 AC 014209;
 DT 01-NOV-1997 (rel. 35, Created)
 DT 01-NOV-1997 (rel. 35, Last sequence update)
 DT 30-MAY-2000 (rel. 39, Last annotation update)

TRANSCRIPTION FACTOR E2F2 (E2F-2).
GN E2F2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI:TaxID:9606;
RN [1]
RP
RP SEQUENCE FROM N.A.
RA MEDLINE:94067141; Pubmed:8246995;
RX Ivey-Hoyte M., Conroy R., Huber H.E., Goodhart P.J., Olfiff A.,
RA Helmbrook D.C.;
RT "Cloning and characterization of E2f-2, a novel protein with the
RT biochemical properties of transcription factor E2F";
RT Mol. Cell. Biol. 13:7802-7812(1993).
RN [2]
RP
RP SEQUENCE FROM N.A.
RA Pearce A.;
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
CC
CC -1- FUNCTION: TRANSCRIPTION ACTIVATOR THAT BINDS DNA COOPERATIVELY
CC WITH DP PROTEINS THROUGH THE E2 RECOGNITION SITE. TTTC/GGCC,
CC FOUND IN THE PROMOTER REGION OF A NUMBER OF GENES WHOSE PRODUCTS
CC ARE INVOLVED IN CELL CYCLE REGULATION OR IN DNA REPLICATION. THE
CC DREF1/EPZ COMPLEX FUNCTIONS IN THE CONTROL OF CELL-CYCLE
CC PROGRESSION FROM G1 TO S PHASE. E2F-2 BINDS SPECIFICALLY TO RB1
CC PROTEIN, IN A CELL-CYCLE DEPENDENT MANNER.
CC
CC -1- SUBUNIT: COMPONENT OF THE DREF1/E2F TRANSCRIPTION FACTOR COMPLEX.
CC FORMS HETERODIMERS WITH DP FAMILY MEMBERS. THE E2F-2 COMPLEX BINDS
CC SPECIFICALLY HYPOPHOSPHORYLATED RETINOBLASTOMA PROTEIN RB1. DURING
CC THE CELL CYCLE, RB1 BECOMES PHOSPHORYLATED IN MID-TO-LATE G1
CC PHASE. DETACHES FROM THE DREF1/EPZ COMPLEX, RENDERING E2F
CC TRANSCRIPTIONALLY ACTIVE. VITAL ONCOPROTEINS, NOTABLY E1A, T-
CC ANTIGEN AND HPV E7, ARE CAPABLE OF SEQUESTERING RB PROTEIN, THUS
CC RELEASING THE ACTIVE COMPLEX.
CC
CC -1- SUBCELLULAR LOCATION: NUCLEAR.
CC
CC -1- TISSUE SPECIFICITY: HIGHEST LEVEL OF EXPRESSION IS FOUND IN
CC PLACENTA, LOW LEVELS ARE FOUND IN LUNG. FOUND ALSO IN MANY
CC IMMORTALIZED CELL LINES DERIVED FROM TUMOR SAMPLES.
CC
CC -1- PM: PHOSPHORYLATED BY CDK2 AND CYCLIN A-CDK2 IN THE S-PHASE (BY
CC SIMILARITY).
CC
CC -1- SIMILARITY: BELONGS TO THE E2F/DP FAMILY.
CC
CC -----
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CC
CC EMBL: L22846; AAL16890.1; -
DR EMBL: AL021154; CAA15949.1; -
DR MIM: 600426; -
DR InterPro: IPR003316; E2F_TDP.
DR Pfam: PF03319; E2F_TDP; 1.
KW Transcription regulation; Activator; DNA-binding; Nuclear protein;
KW Phosphorylation; Cell cycle.
FT DOMAIN 65 105 CYCLIN A/CDK2 BINDING (POTENTIAL).
FT DNAS_BIND 107 196 POTENTIAL.
FT FT 155 176 LEUCINE-ZIPPER.
FT DOMAIN 160 196 DEF BOX.
FT DOMAIN 197 289 DIMERIZATION (POTENTIAL).
FT DOMAIN 359 437 TRANSACTIVATION (POTENTIAL).
FT DOMAIN 360 363 POLY-PRO.
FT DOMAIN 410 427 RETINOBLASTOMA PROTEIN ASSOCIATION
FT (POTENTIAL).
SQ SEQUENCE 437 AA; 47505 MW; 60541f4235507005 CRC64;

Query Match	52.0%;	Score 39;	DB 1;	Length 437;
Best Local Similarity	62.5%;	Pred. No. 18;		
Matches 10;	Conservative	2;	Mismatches	2;
			Indels	2;
			Gaps	1
QY	2	TKVL--IOPLOKKAKN	15	

Db 173 T N V L E G I Q L I R K K A K N 188

SEQUENCE	487 AA:	52406 MM:	ATP42734D9C6A146 CRC64:
ATF2_CHECK	14		
ID	ATF2_CHECK	STANDARD:	ERT: 487 AA.
AC	093602;		
DT	30-MAY-2000 (Rel. 39, Created)		
DT	30-MAY-2000 (Rel. 39, Last sequence update)		
DT	30-MAY-2000 (Rel. 39, Last annotation update)		
DE	CYCLO-AMP-DEPENDENT TRANSCRIPTION FACTOR ATF-2 (ACTIVATING TRANSCRIPTION FACTOR 2).		
GN	ATF2.		
OS	Gallus gallus (chicken).		
OC	Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi;		
OC	Archosauromorpha; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;		
OC	Gallus.		
OX	NCBI_TaxID=9031;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Hugnier S., Baguet J., Perez S., van Dam H., Castellazzi M.;		
RT	"transcription factor ATF2 cooperates with v-Jun to promote growth-factor independent proliferation in vitro and tumor formation in vivo";		
RL	Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.		
CC	-1- FUNCTION: A TRANSCRIPTIONAL ACTIVATOR, PROBABLY CONSTITUTIVE, WHICH BINDS TO THE CAMP RESPONSIVE REGION (CRE) (CONSENSUS: 5'GTGACG(A/C)(A/G)-3'); A SEQUENCE PRESENT IN MANY VIRAL AND CELLULAR PROMOTERS (BY SIMILARITY).		
CC	-1- SUBUNIT: BINDS DNA AS A DIMER.		
CC	-1- SUBCELLULAR LOCATION: NUCLEAR.		
CC	-1- SIMILARITY: BELONGS TO THE BZIP FAMILY. ATF SUBFAMILY.		
CC	-----		
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CC	-----		
DR	EMBL; Y17724; CAA76838.1; -		
DR	HSSP; P08047; ISP2.		
DR	InterPro; IPR000822; znf-C2H2.		
DR	InterPro; IPR001871; bZIP.		
DR	Pfam; PF00170; bZIP. 1.		
DR	Pfam; PF00096; zf-C2H2; 1.		
DR	SMART; SM00338; BRLZ. 1.		
DR	SMART; SM00355; znf-C2H2; 1.		
DR	PROSITE; PS00036; bZIP_BASIC. 1.		
DR	PROSITE; PS00028; ZINC_FINGER_C2H2_2; 1.		
KW	Transcription regulation; DNA-binding; Activator; Nuclear protein;		
KW	Zinc-finger; Metal-binding.		
FT	ZN_FING 7 31		
FT	C2H2-TYPE.		
FT	BASIC MOTIF.		
FT	DNA_BIND 333 356		
FT	LEUCINE-ZIPPER.		
FT	DNA_BIND 362 390		
SEQUENCE	487 AA: 52406 MM:		

Query Match	52.0%;	Score 39;	DB 1;	Length 487;
Best Local Similarity	57.1%;	Pred. No. 20;		
Matches	8;	Conservative	4;	Mismatches 2;
				Indels 0;
				Gaps 0;
QY	3	KVLIQFLQKKANKL	16	
		: : : : :		
DB	356	KYVQSLERKAEDL	369	
RESULT 15				
ATF2_HUMAN				
ID	ATF2_HUMAN	STANDARD;	PRT:	487 AA.

1
2
3
4

ID	Q97TH4	PRELIMINARY;	PRT;	1/5 AA.
AC	Q97TH4;			
DT	01-MAY-2000 (TEMBLrel. 13, Created)			
DT	01-MAY-2000 (TEMBLrel. 13, Last sequence update)			
DT	01-JUN-2001 (TEMBLrel. 17, Last annotation update)			
DE	INTERLEUKIN-6 (FRAGMENT).			
GN	IL-6.			
OS	Aotus nigriceps (black-headed night monkey).			
OC	Eukaryota; Metacoa; Chordata; Cranialta; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.			
OX	NCBI_Taxid=57175;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Murillo L.A., Hernandez E., Echeverry S.J., Mendez J.A.,			
RA	Patarroyo M.E.;			
RT	"Aotus nigriceps gene for IL-6."			
RL	Submitted (CCT-1998) to the EMBL/GenBank/DBJ databases.			
RL	EMBL: AF097322; AAF21297.1; -			
DR	HSSP: P05231; 1A1U			
DR	InterPro: IPR003573; IL6_MGF_GCSF.			
DR	Pfam: PF00489; IL6; 1.			
DR	PRINTS: PR00433; IL6GCSFMGF.			
DR	SMART: SM00126; IL6; 1.			
DR	PROSITE: PS00254; INTERLEUKIN_6; 1.			
FT	NON_TER	1		
SO	SEQUENCE	175 AA;	19205 MW;	28CCE574CBB9B109 CRC64;

[illegible]

	RESULT	3	
	09JTH3		
ID	09JTH3	PRELIMINARY;	PRT; 209 AA.
AC	Q9TTH3;		
DT	01-MAY-2000 (TrEMBLrel. 13,	Created)	
DT	01-MAY-2000 (TrEMBLrel. 13,	Last sequence update)	
DT	01-JUN-2001 (TrEMBLrel. 17,	Last annotation update)	
DE	INTERLEUKIN-6 (FRAGMENT).		
CN	IL-6.		
OS	Aotus lemurinus (Northern gray-necked night monkey),		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;		
CC	Mammalia; Eutheria; Primates; Platyrrhini; Cebidae;		
OX	NCBI_TaxID=43147;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Morillo L.A., Hernandez F., Echeverry S.J., Mendez J.A.,		
PA	Palatroyo M.E.;		
RT	"Aotus lemurinus gene for IL-6.";		
RL	Submitted (Oct-1998) to the EMBL/Genbank/DDBJ databases.		
DR	EMBL: AF097323; AAF21298.1; -.		
DR	HSSP: P05231; IAUU		
DR	InterPro: IPRO03573; IL6_MGF_GCSF.		
DR	Pfam: PF00489; IL6; 1.		
DR	PRINTS: PR00433; IL6GCSFMFG.		
DR	SMART: SM00126; IL6; 1.		
DR	PROSITE: PS00254; INTERLEUKIN_6; 1.		
FT	NON_TER 1		
FT	NON_TER 1		
FT	NON_TER 1		
SQ	SEQUENCE 209 AA; 23115 MW; AD03DFAABF56GCC CRC64;		

Query Match	80.0%	Score 60;	Length 209;
Best Local Similarity	87.5%	Pred. No. 0.014;	
Matches 14;	Conservative	0;	Mismatches 2;
			Indels 0;
			Gaps 0;
1	STKVLIQFLQKKAKNL	16	

Db 146 STKGLIQSLQKKAKNL 161

RESULT	4			
OS	Q9MYZ7			
AC	Q9MYZ7;	PRELIMINARY;	PRT;	207 AA.
DT	01-OCT-2000 (TREMBLrel. 15, Created)			
DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)			
DT	01-JUN-2001 (TREMBLrel. 17, Last annotation update)			
DE	INTERLEUKIN-6.			
GN	IL-6.			
OS	Canis familiaris (Dog).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.			
OX	NCBI_TaxID=9615;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Youn H.-Y., Shin I.-S.;			
RT	"Canine IL-6 mRNA.";			
RL	Submitted (JUN-2000) to the EMBL/Genbank/DBJ databases.			
DR	EMBL: AF275796; AAF86275.1; -.			
DR	InterPro: IPR003573; IL6_MGF_GCSF.			
DR	Pfam: PF00489; IL6; 1.			
DR	PRINTS; PR00433; IL6GCSFMGF.			
DR	SMART; SM00126; IL6; 1.			
DR	PROSITE: PS00254; INTERLEUKIN_6; 1.			
SO	SEQUENCE	207 AA; 23042 MW; 45541AE011CB0F50 CRC64;		

[illegible]

	RESULT	5		
	062775			
ID	062775	PRELIMINARY;	PRT;	94 AA.
AC	062775:			
DT	01-AUG-1998	(TREMBLrel. 07, Created)		
PT	01-AUG-1998	(TREMBLrel. 07, Last sequence update)		
DT	01-JUN-2001	(TREMBLrel. 17, Last annotation update)		
DE	INTERLEUKIN 6 (FRAGMENT).			
OS	Felis silvestris catus (Cat).			
CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.			
OX	NCBI_TaxId=9685;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Hartley R., Helps C.R., Gruffydd-Jones T.J., Day M.J., Harbour D.A.;			
RL	Submitted (MAR-1998) to the EMBL/Genbank/DDBJ databases.			
DR	EMBL; AF054603; AAC15976.1; -.			
DR	HSSP; P05231; 1ALU.			
DR	InterPro; IPR003573; IL6_MGF_GCSF.			
DR	Pfam; PF00489; IL6; 1.			
FT	SMART; SMO0126; IL6; 1.			
FT	NON_TER	1		
SQ	SEQUENCE	94 AA;	11099 MW;	12B473B69EE94861 CRC64; .

	Query Match	62.7%	Score 47	DB 6	Length 94:
	Best Local Similarity	60.0%	Pred. No. 1.1:		
	Matches	9;	Conservative	3;	Mismatches
				3;	Indels
				0;	Gaps
OY	1	SMKVLIOFLQKKRN	15		
		: :			
Db	28	STNVLLQMLKRKGKN	42		


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RESULT 6
ID 09PIK1 PRELIMINARY: PRT: 274 AA.
AC 09PIK1:
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE 3-METHYL-2-OXOBUTANOATE HYDROXYMETHYLTRANSFERASE (EC 2.1.2.11).
GN PABN OR C00296.
OS Campylobacter jejuni.
OC Bacteria; Proteobacteria; epsilon subdivision; Campylobacter group;
OC Campylobacter.
OX NCBI_TaxID=197;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NCIC 11168;
RX MEDLINE=20150912; PubMed=10688204;
RA Parkhill J., Wren B.W., Mungall K., Ketley J.M., Churcher C.,
RA Basham D., Chillingworth T., Davies R.M., Feltham T., Holtroyd S.,
RA Jagers K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,
RA Quail M.A., Rajadream M.A., Rutherford K.M., Van Vliet A.H.M.,
RA Whitehead S., Barrett B.G.;
RT "The genome sequence of the food-borne pathogen Campylobacter jejuni
RT reveals hypervariable sequences."
RL Nature 403:665-668(2000).
DR EMBL: AL139074; CAB72765.1; -.
DR InterPro: IPR003700; Pantoate_transf.
DR Pfam: PF02548; Pantoate_transf; 1.
KW Complete proteome.
SQ SEQUENCE 274 AA; 30202 MW; 9B3CACB32EFDE0C7 CRC64;

Query Match 61.3%; Score 46; DB 2; Length 274;
Best Local Similarity 69.2%; Pred. No. 4.3;
Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 KYLQFLOKKAKN 15
|:|:|:|:|:|:|
DB 3 KSMISFLEKKAKN 15

RESULT 7
ID 023291 PRELIMINARY: PRT: 959 AA.
AC 023291:
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE KINESIN HOMOLOG (KINESIN LIKE PROTEIN).
GN ATG414330.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Euphorbiaceae; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Bevan M., Stiekema W., Murphy G., Wambutt R., Pohl T., Terryn N.,
RA Kreis M., Kavanagh T., Entlan K.D., Rieger M., James R.,
RA Puidomenech P., Hatzopoulos P., Obermaier B., Duesterhoft A.,
RA Jones J., Palme K., Ansgore W., Delseny M., Bancroft I., Mewes H.W.,
RA Scheller C., Chalwatzis N.;
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: Z97336; CAB10212.1; -.
DR EMBL: AL161538; CAB78475.1; -.
DR HSSP: P17119; 3KAR.
DR InterPro: IPR001752; kinesin.
DR Pfam: PF00225; kinesin; 2.

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DR PRINTS: PR00380; KINESINHEAVY.
DR SMART: SM00129; KISC; 1.
DR PROSITE: PS50067; KINESIN_MOTOR_DOMAIN2; 1.
KW ATP-binding; Coiled coil; Microtubules; Motor protein.
SQ SEQUENCE 959 AA; 107515 MW; A2DFD86F6D704FDA CRC64;

Query Match 58.7%; Score 44; DB 10; Length 959;
Best Local Similarity 60.0%; Pred. No. 29;
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 STKVLQFLOKKAKN 15
|:|:|:|:|:|:|
DB 201 STKRLQVKKKKAKN 215

RESULT 8
ID 09Y4J9 PRELIMINARY: PRT: 1199 AA.
AC 09Y4J9:
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE HYPOTHETICAL 135.2 KDA PROTEIN.
GN A-36266.1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Adams M.D.;
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Adams M.D., Loftus B.J., Zhou L., La Bombard M., Kim U.J.,
RA Venter J.C.;
RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Adams M.D.;
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: U95740; AAC31662.1; -.
DR InterPro: IPR000504; RRM.
DR Pfam: PF00076; rrm; 1.
DR PROSITE: PS50102; RRM; 1.
DR SMART: SM00360; RRM; 1.
KW Hypothetical protein.
SQ SEQUENCE 1199 AA; 135203 MW; 6BEBF653D7CDF57 CRC64;

Query Match 57.3%; Score 43; DB 4; Length 1199;
Best Local Similarity 57.1%; Pred. No. 53;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 3 KYLQFLOKKAKN 16
|:|:|:|:|:|:|
DB 994 QVYVQFLOKNGKEL 1007

RESULT 9
ID 09TZJ8 PRELIMINARY: PRT: 286 AA.
AC 09TZJ8:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE C50E10.6 PROTEIN.
GN C50E10.6.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;

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RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN-BRISTOL N2.
RX  MEDLINE=94150718; PubMed=7906398;
RA  WILSON R., Ainscough R., Anderson K., Baynes C., Berks M.,
RA  Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
RA  Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
RA  Gardner A., Green P., Hawken T., Hillier L., Jier M., Johnston L.,
RA  Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
RA  Lightning J., Lloyd C., McMurray A., Morlmore B., O'Callaghan M.,
RA  Parsons J., Percy C., Rinken L., Roopra A., Saunders D., Showkeen R.,
RA  Smaldon N., Smith A., Sonhammer E., Staden R., Sulston J.,
RA  Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
RA  Watson A., Weinstock L., Wilkinson-Sproat J., Woldman P.,
RT  *2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT  elegans.*;
RL  Nature 368:32-38(1994).
RN  [2]
RP  SEQUENCE FROM N.A.
RC  STRAIN-BRISTOL N2.
RX  NELSON J., Klinke B., Wohlmann P., Bauer C.;
RT  The sequence of C. elegans cosmid C50E10.*;
RL  Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
RN  [3]
RP  SEQUENCE FROM N.A.
RC  STRAIN-BRISTOL N2.
RX  WATERTON R.;
RL  Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
DR  EMBL: AF098988; AAC67437.1;
DR  InterPro: IPR002106; AA:RNA_Ligase_II.
DR  PROSITE: PS00339; AA:TRNA_LIGASE_II.2; UNKNOWN_1.
SQ  SEQUENCE 286 AA; 33227 MW; 66333B3046BC9010 CRC64;

Query Match          56.0%; Score 42; Length 286;
Best Local Similarity 64.3%; Pred. No. 21;
Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY  3 KVLVLIQLOKRAKRL 16
DB  207 KIMROFGOKPAKRL 220

RESULT 10
ID  Q55879          PRELIMINARY;      PRT;      425 AA.
AC  Q55879;
DT  01-NOV-1996 (TREMBlrel. 01, Created)
DT  01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DE  01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE  PRECORIN-6r METHYLASE.
GN  CAIE OR SLT0099.
OS  Synechocystis sp. (strain PCC 6803).
OC  Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
CX  NCBI_TaxID=1148;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  MEDLINE=96127529; PubMed=8590279;
RX  KANEKO T., Tanaka A., Sato S., Kotani H., Sazuka T., Miyajima N.,
RA  Sugitani M., Tabata S.;
RT  *sequence analysis of the genome of the unicellular cyanobacterium
RT  Synechocystis sp. strain PCC6803. I. Sequence features in the 1 Mb
RT  region from map positions 64k to 92k of the genome.*;
RL  DNA Res. 2:153-166(1995).
RN  [2]
RP  SEQUENCE FROM N.A.
RC  MEDLINE=97061201; PubMed=8905231;
RX  KANEKO T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
RA  Miyajima N., Hirosewa M., Sugitani M., Sasamoto S., Kimura T.,
RA  Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Nario K., Okumura S.,
RA  Shimpō S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
RA  Tabata S.;
RT  *Sequence analysis of the genome of the unicellular cyanobacterium

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RT  Synechocystis sp. strain PCC6803. II. Sequence determination of the
RT  entire genome and assignment of potential protein-coding regions.*;
RL  DNA Res. 3:109-136(1996).
RN  [1]
RP  EMBL: D64004; BAA10641.1;
DR  InterPro: IPR000878; Corrin_porph_methyltrnf.
DR  InterPro: IPR000051; SAM_bind.
DR  InterPro: IPR000531; TonB_boxC.
DR  Pfam: PF00590; TP_methylase; 1.
DR  PROSITE: PS00430; TONB_DEPENDENT_REC_1; UNKNOWN_1.
KW  Methyltransferase; Complete proteome.
SQ  SEQUENCE 425 AA; 46276 MW; 759AC9B32C435852 CRC64;

Query Match          56.0%; Score 42; DB 2; Length 425;
Best Local Similarity 62.5%; Pred. No. 30;
Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY  1 STKVLVLIQLOKRAKRL 16
DB  130 SNELLIQALQKRAKRL 145

RESULT 11
ID  Q9FT05          PRELIMINARY;      PRT;      517 AA.
AC  Q9FT05;
DT  01-MAR-2001 (TREMBlrel. 16, Created)
DT  01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DE  01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE  P0665D10.11 PROTEIN.
GN  P0665D10.11.
OS  Oryza sativa (Rice).
OC  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC  Ehrhartoideae; Oryzaceae; Oryza.
CX  NCBI_TaxID=4530;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN-CV. NIPPONBARE;
RX  SASAKI T., Matsumoto T., Yamamoto K.;
RT  *Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
RT  clone:P0665D10.*;
RL  Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR  EMBL: AP002861; BAA16486.1;
DR  InterPro: IPR002818; ThiJ.
DR  Pfam: PF01965; ThiJ; 2.
SQ  SEQUENCE 517 AA; 55153 MW; FF1BD618A12AD8AD CRC64;

Query Match          56.0%; Score 42; DB 10; Length 517;
Best Local Similarity 53.3%; Pred. No. 36;
Matches 8; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY  1 STKVLVLIQLOKRAKRL 15
DB  415 STKVLVLDLKKRAKRL 429

RESULT 12
ID  Q23055          PRELIMINARY;      PRT;      822 AA.
AC  Q23055;
DT  01-JAN-1998 (TREMBlrel. 05, Created)
DT  01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DE  01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE  HYPOTHEICAL 92.6 KDA PROTEIN.
GN  YUP8H12.27.
OS  Arabidopsis thaliana (Mouse-ear cress).
OC  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC  eurosids II; Brassicales; Brassicaceae; Arabidopsis.
CX  NCBI_TaxID=3702;
RN  [1]

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RP SEQUENCE FROM N.A.
 RC STRAIN-CV. COLUMBIA;
 RA Theologis A., Osbourne B.I., Vysotskaya V.S., Federspiel N.A.,
 RA Toriumi M., Yu G., Oji O., Araujo R., Chung R., Dewart K., Dietrich F.,
 RA Ecker J.R., Marzalli A., Oefner P., Davis R.W.;
 RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RN SEQUENCE FROM N.A.
 RC STRAIN-CV. COLUMBIA;
 RA Theologis A.;
 RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: CONTAINS A RING-TYPE ZINC FINGER.
 DR EMBL: AC000098; AAB71467.1; -
 DR Interpro: IPR001410; DEAD.
 DR Interpro: IPR000330; SNF2_N.
 DR Interpro: IPR001841; ZnF_ring.
 DR Pfam: PF00176; SNF2_N; 2.
 DR Pfam: PF00097; zf-C3HC4; 1.
 DR SMART: SM00487; DEXDC; 1.
 DR SMART: SM00184; RING; 1.
 DR PROSITE: PS00518; ZINC_FINGER_C3HC4; UNKNOWN_1.
 DR Zinc_Finger.
 KW ZINC_FINGER.
 SQ SEQUENCE 822 AA; 92580 MW; ED4ED7DC87ACF611 CRC64;

Query Match 56.0%; Score 42; DB 10; Length 822;
 Best Local Similarity 56.2%; Pred. No. 55;
 Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 OY 1 STKVLIOFLQKAKKL 16
 ID 220 STKVLVYHGAKRAKNI 235

RESULT 13
 ID 09JG27 PRELIMINARY; PRT; 75 AA.
 AC 09JG27;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE ORF1 (FRAGMENT).
 OS TT virus.
 OC Viruses; ssDNA viruses; unclassified ssDNA viruses.
 OX NCBI_TaxID=68887;
 RN [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN-T12Y005;
 RA Ukita M., Okamoto H., Nishizawa T., Tawara A., Takahashi M.,
 RA Itzuka H., Miyakawa Y., Mayumi M.;
 RT "The entire nucleotide sequences of two distinct TT virus (TTV)
 RT isolates (TJN01 and TJN02) remotely related to the original TTV
 RT isolates.";
 RL Arch. Virol. 0:0-0(2000).
 DR EMBL: AB028703; BAA94912.1; -
 FT NON_TER 1 75
 FT NON_TER 1 75
 KW COMPLETE PROTEOME.
 SQ SEQUENCE 75 AA; 8643 MW; 4A4546A2FC94D0C8 CRC64;

Query Match 54.7%; Score 41; DB 12; Length 75;
 Best Local Similarity 56.2%; Pred. No. 9.3;
 Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 1 STKVLIOFLQKAKKL 16
 ID 1 STKPTTQFLQKAKCL 16
 AC 09JH26 PRELIMINARY; PRT; 264 AA.
 AC 09JH26;

DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE ORF1 (FRAGMENT).
 OS TT virus.
 OC Viruses; ssDNA viruses; unclassified ssDNA viruses.
 OX NCBI_TaxID=68887;
 RN [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN-M193-5;
 RA Ukita M., Okamoto H., Nishizawa T., Tawara A., Takahashi M.,
 RA Itzuka H., Miyakawa Y., Mayumi M.;
 RT "The entire nucleotide sequences of two distinct TT virus (TTV)
 RT isolates (TJN01 and TJN02) remotely related to the original TTV
 RT isolates.";
 RL Arch. Virol. 0:0-0(2000).
 DR EMBL: AB028674; BAA94883.1; -
 FT NON_TER 1 264
 FT NON_TER 1 264
 KW COMPLETE PROTEOME.
 SQ SEQUENCE 264 AA; 31024 MW; BE35CCA928B2EDF CRC64;

Query Match 54.7%; Score 41; DB 12; Length 264;
 Best Local Similarity 56.2%; Pred. No. 29;
 Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 OY 1 STKVLIOFLQKAKKL 16
 ID 190 STKPTTQFLQKAKCL 205

RESULT 15
 ID 09KAU2 PRELIMINARY; PRT; 290 AA.
 AC 09KAU2;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE BH2194 PROTEIN.
 GN BH2194.
 OS Bacillus halodurans.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group;
 OC Bacillus/staphylococcus group; Bacillus.
 OX NCBI_TaxID=6665;
 RN [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN-C-125 / JCM 9153;
 RX MEDLINE-20512582; PubMed-11058132;
 RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
 RA Fujii F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
 RA Horikoshi K.;
 RT "Complete genome sequence of the alkaliphilic bacterium Bacillus
 RT halodurans and genomic sequence comparison with Bacillus subtilis.";
 RL Nucleic Acids Res. 28:4317-4331(2000).
 DR EMBL: AF001514; BAB05913.1; -
 FT NON_TER 1 290
 FT NON_TER 1 290
 KW COMPLETE PROTEOME.
 SQ SEQUENCE 290 AA; 31713 MW; 83688C587514129 CRC64;

Query Match 54.7%; Score 41; DB 2; Length 290;
 Best Local Similarity 66.7%; Pred. No. 32;
 Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 3 KVLIOFLQKAKK 14
 ID 278 RYVFSFLQKAKK 289

Search completed: December 19, 2001, 16:25:19
 Job time: 544 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: December 19, 2001, 16:20:58 ; Search time 78.52 seconds
(without alignments)
4.585 Million cell updates/sec

Title: US-09-202-104A-2
Perfect score: 75
Sequence: 1 STKVLIQFLQKKAKNL 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/PCYOS.COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	75	100.0	162	2	US-08-716-317-10
2	75	100.0	163	2	US-08-716-317-15
3	75	100.0	164	1	US-08-318-193-60
4	75	100.0	167	1	US-08-246-427A-2
5	75	100.0	167	2	US-08-766-620-2
6	75	100.0	167	5	PCT-US95-06094-2
7	75	100.0	172	4	US-08-149-101A-21
8	75	100.0	172	5	PCT-US94-12873-21
9	75	100.0	174	4	US-08-149-101A-20
10	75	100.0	174	5	PCT-US94-12873-20
11	75	100.0	181	1	US-08-209-182C-4
12	75	100.0	181	5	PCT-US92-05612-4
13	75	100.0	182	4	US-08-149-101A-25
14	75	100.0	183	5	PCT-US94-12873-25
15	75	100.0	183	1	US-08-009-973-1
16	75	100.0	184	1	US-08-567-047-2
17	75	100.0	184	2	US-08-693-182-2
18	75	100.0	184	2	US-08-567-046-2
19	75	100.0	184	4	US-09-008-482-2
20	75	100.0	184	4	US-08-149-101A-17
21	75	100.0	184	4	US-08-149-101A-22
22	75	100.0	184	5	PCT-US94-12873-17
23	75	100.0	184	5	PCT-US94-12873-22
24	75	100.0	184	6	5186931-1
25	75	100.0	185	1	US-07-632-070B-1
26	75	100.0	185	1	US-07-918-181A-2
27	75	100.0	185	1	US-07-918-181A-4

28	75	100.0	185	1	US-07-918-181A-6	Sequence 6, Appl1
29	75	100.0	185	1	US-07-918-181A-8	Sequence 8, Appl1
30	75	100.0	185	1	US-08-231-575-2	Sequence 2, Appl1
31	75	100.0	185	1	US-08-231-575-4	Sequence 4, Appl1
32	75	100.0	185	1	US-08-231-575-6	Sequence 6, Appl1
33	75	100.0	185	1	US-08-231-575-8	Sequence 8, Appl1
34	75	100.0	185	1	US-08-246-427A-5	Sequence 5, Appl1
35	75	100.0	185	2	US-08-716-317-7	Sequence 7, Appl1
36	75	100.0	185	2	US-08-766-620-5	Sequence 5, Appl1
37	75	100.0	185	5	PCT-US92-05612-2	Sequence 2, Appl1
38	75	100.0	185	5	PCT-US93-06928-2	Sequence 2, Appl1
39	75	100.0	185	5	PCT-US93-06928-4	Sequence 4, Appl1
40	75	100.0	185	5	PCT-US93-06928-6	Sequence 6, Appl1
41	75	100.0	185	5	PCT-US93-06928-8	Sequence 8, Appl1
42	75	100.0	185	6	5186931-2	Patent No. 5186931
43	75	100.0	186	1	US-07-632-070B-2	Sequence 2, Appl1
44	75	100.0	186	1	US-07-745-382-20	Sequence 20, Appl1
45	75	100.0	186	1	US-07-921-848-20	Sequence 20, Appl1

ALIGNMENTS

RESULT 1
US-08-716-317-10
Sequence 10, Application US/08716317
Patent No. 5919654
GENERAL INFORMATION:
APPLICANT: HAMA, YUKO
APPLICANT: TOHDA, HIDEKI
APPLICANT: TSUKAMOTO, HIROKO
APPLICANT: NIKAIKO, KIYOKAZU
APPLICANT: KIMAGAI, HIROMICHI
TITLE OF INVENTION: SECRETION SIGNAL GENE AND EXPRESSION
TITLE OR INVENTION: VECTOR CONTAINING IT
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MATER & NEUSTADT,
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/716,317
FILING DATE: 02-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP96/00198
FILING DATE: 01-FEB-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 17167/1995
FILING DATE: 03-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 59-924-0 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 162 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-716-317-10

Query Match 100.0%; Score 75; DB 2; Length 162;
Best Local Similarity 100.0%; Pred. No. 5.4e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STKVLIQFLOKKAKNL 16
|||||
DB 96 STKVLIQFLOKKAKNL 111

RESULT 2

US-08-716-317-15
; Sequence 15, Application US/08716317
; Patent No. 5919654
; GENERAL INFORMATION:
; APPLICANT: HAMA, YUKO
; APPLICANT: TOHDA, HIDEKI
; APPLICANT: TSUKAMOTO, HIROKO
; APPLICANT: NIKAIIDO, KIYOKAZU
; APPLICANT: KUMAGAI, HIROMICHI
; TITLE OF INVENTION: SECRETION SIGNAL GENE AND EXPRESSION
; TITLE OF INVENTION: VECTOR CONTAINING IT
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,
; ADDRESS: P.C.
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/716,317
; FILING DATE: 02-OCT-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP96/00198
; FILING DATE: 01-FEB-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 17167/1995
; FILING DATE: 03-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 59-924-0 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 163 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-716-317-15

Query Match 100.0%; Score 75; DB 2; Length 163;
Best Local Similarity 100.0%; Pred. No. 5.5e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STKVLIQFLOKKAKNL 16
|||||
DB 97 STKVLIQFLOKKAKNL 112

RESULT 3

US-08-318-193-60
; Sequence 60, Application US/08318193
; Patent No. 5641663
; GENERAL INFORMATION:
; APPLICANT: GARVIN, Robert T.
; APPLICANT: MALEK, Lawrence T.
; TITLE OF INVENTION: AN EXPRESSION SYSTEM FOR THE SECRETION
; TITLE OF INVENTION: OF BIOACTIVE HUMAN GRANULOCYTE MACROPHAGE COLONY
; TITLE OF INVENTION: STIMULATING FACTOR (GM-CSF) AND OTHER HETEROLOGOUS
; TITLE OF INVENTION: PROTEINS FROM STREPTOMYCES
; NUMBER OF SEQUENCES: 91
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/318,193
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,314
; FILING DATE:
; APPLICATION NUMBER: US/07/224,568
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 18740/116 CACO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 60:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 164 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-318-193-60

Query Match 100.0%; Score 75; DB 1; Length 164;
Best Local Similarity 100.0%; Pred. No. 5.5e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STKVLIQFLOKKAKNL 16
|||||
DB 98 STKVLIQFLOKKAKNL 113

RESULT 4

US-08-246-427A-2
; Sequence 2, Application US/08246427A
; Patent No. 5641657
; GENERAL INFORMATION:
; APPLICANT: RUBEN, ET AL.
; TITLE OF INVENTION: Interleukin-6 Splice Variant
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; ADDRESS: CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY

COUNTRY: USA
 ZIP: 07068
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 INCH DISKETTE
 COMPUTER: IBM PS/2
 OPERATING SYSTEM: MS-DOS
 SOFTWARE: WORD PERFECT 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/246,427A
 FILING DATE: Submitted herewith
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/246,427
 FILING DATE: MAY 19, 1994
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: FERRARO, GREGORY D.
 REGISTRATION NUMBER: 36,134
 REFERENCE/DOCKET NUMBER: 325800-
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 201-994-1700
 TELEFAX: 201-994-1744
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 167 AMINO ACIDS
 TYPE: AMINO ACID
 STRANDEDNESS:
 TOPOLOGY: LINEAR
 MOLECULE TYPE: PROTEIN
 US-08-246-427A-2

Query Match 100.0%; Score 75; DB 1; Length 167;
 Best Local Similarity 100.0%; Pred. No. 5.6e-05;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 STKVLIOFLQKKAKNL 16
 Db 101 STKVLIOFLQKKAKNL 116

RESULT 5
 US-08-766-620-2
 Sequence 2, Application US/08766620
 Patent No. 5958400
 GENERAL INFORMATION:
 APPLICANT: RUBEN, ET AL.
 TITLE OF INVENTION: Interleukin-6 splice variant
 NUMBER OF SEQUENCES: 5
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
 ADDRESSEE: CECCHI, STEWART & OLSTEIN
 STREET: 6 BECKER FARM ROAD
 CITY: ROSELAND
 STATE: NEW JERSEY
 COUNTRY: USA
 ZIP: 07068
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 INCH DISKETTE
 COMPUTER: IBM PS/2
 OPERATING SYSTEM: MS-DOS
 SOFTWARE: WORD PERFECT 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/766,620
 FILING DATE: December 12, 1996
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/246,427
 FILING DATE: MAY 19, 1994
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: MULLINS, J.G.
 REGISTRATION NUMBER: 33,073

REFERENCE/DOCKET NUMBER: 325800-593 (PFI20)
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 201-994-1700
 TELEFAX: 201-994-1744
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 167 AMINO ACIDS
 TYPE: AMINO ACID
 STRANDEDNESS:
 TOPOLOGY: LINEAR
 MOLECULE TYPE: PROTEIN
 US-08-766-620-2

Query Match 100.0%; Score 75; DB 2; Length 167;
 Best Local Similarity 100.0%; Pred. No. 5.6e-05;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 STKVLIOFLQKKAKNL 16
 Db 101 STKVLIOFLQKKAKNL 116

RESULT 6
 PCT-US95-06094-2
 Sequence 2, Application PC/TUS9506094
 GENERAL INFORMATION:
 APPLICANT: RUBEN, ET AL.
 TITLE OF INVENTION: Interleukin-6 Splice variant
 NUMBER OF SEQUENCES: 4
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
 ADDRESSEE: CECCHI, STEWART & OLSTEIN
 STREET: 6 BECKER FARM ROAD
 CITY: ROSELAND
 STATE: NEW JERSEY
 COUNTRY: USA
 ZIP: 07068
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 INCH DISKETTE
 COMPUTER: IBM PS/2
 OPERATING SYSTEM: MS-DOS
 SOFTWARE: WORD PERFECT 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US95/06094
 FILING DATE: Submitted herewith
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/246,427
 FILING DATE: MAY 19, 1994
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: FERRARO, GREGORY D.
 REGISTRATION NUMBER: 36,134
 REFERENCE/DOCKET NUMBER: 325800-
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 201-994-1700
 TELEFAX: 201-994-1744
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 167 AMINO ACIDS
 TYPE: AMINO ACID
 STRANDEDNESS:
 TOPOLOGY: LINEAR
 MOLECULE TYPE: PROTEIN
 PCT-US95-06094-2

Query Match 100.0%; Score 75; DB 5; Length 167;
 Best Local Similarity 100.0%; Pred. No. 5.6e-05;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 STKVLIOFLQKKAKNL 16

Db 101 STKVLIQFLOKRAKML 116

RESULT 7

US-08-149-101A-21
Sequence 21, Application US/08149101A
Patent No. 6171824
GENERAL INFORMATION:
APPLICANT: Todaro, George J.
APPLICANT: Leung, David W.
APPLICANT: Rose, Timothy M.
TITLE OF INVENTION: HYBRID CYTOKINES
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cell Therapeutics, Inc.
STREET: 200 Elliott Avenue West, Suite 400
CITY: Seattle
STATE: Washington
COUNTRY: U.S.A.
ZIP: 98119
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" disk, 1.44mb, double side, high density
COMPUTER: AST-IBM Compatible
OPERATING SYSTEM: MS-DOS Version 6
SOFTWARE: WORD for WINDOWS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/149,101A
FILING DATE: 8-NO. 6171824-1993
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US08/097,869
FILING DATE: 27-Jul-1993
ATTORNEY/AGENT INFORMATION:
NAME: Oster, Jeffrey B. and Paciszewski, Stephen
REGISTRATION NUMBER: 32,585 and 36,131, respectively
REFERENCE/DOCKET NUMBER: 0105A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)282-7100
TELEFAX: (206)284-6206
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 172
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: no
ANTI-SENSE: no
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM: homo sapien
US-08-149-101A-21

Query Match 100.0%; Score 75; DB 4; Length 172;
Best Local Similarity 100.0%; Pred. No. 5.7e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 STKVLIQFLOKRAKML 16
Db 119 STKVLIQFLOKRAKML 134

RESULT 8

PCT-US94-12873-21
Sequence 21, Application PC/TUS9412873
GENERAL INFORMATION:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
TITLE OF INVENTION: HYBRID CYTOKINES
NUMBER OF SEQUENCES: 26

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" diskette, 1.44mb, double side, high density
COMPUTER: AST-IBM Compatible
OPERATING SYSTEM: MS-DOS Version 6
SOFTWARE: WORD for WINDOWS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/12873
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 172
TYPE: amino acid
TOPOLOGY: linear
PCT-US94-12873-21

Query Match 100.0%; Score 75; DB 5; Length 172;
Best Local Similarity 100.0%; Pred. No. 5.7e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 STKVLIQFLOKRAKML 16
Db 119 STKVLIQFLOKRAKML 134

RESULT 9

US-08-149-101A-20
Sequence 20, Application US/08149101A
Patent No. 6171824
GENERAL INFORMATION:
APPLICANT: Todaro, George J.
APPLICANT: Leung, David W.
APPLICANT: Rose, Timothy M.
TITLE OF INVENTION: HYBRID CYTOKINES
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cell Therapeutics, Inc.
STREET: 200 Elliott Avenue West, Suite 400
CITY: Seattle
STATE: Washington
COUNTRY: U.S.A.
ZIP: 98119
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" disk, 1.44mb, double side, high density
COMPUTER: AST-IBM Compatible
OPERATING SYSTEM: MS-DOS Version 6
SOFTWARE: WORD for WINDOWS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/149,101A
FILING DATE: 8-NO. 6171824-1993
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US08/097,869
FILING DATE: 27-Jul-1993
ATTORNEY/AGENT INFORMATION:
NAME: Oster, Jeffrey B. and Paciszewski, Stephen
REGISTRATION NUMBER: 32,585 and 36,131, respectively
REFERENCE/DOCKET NUMBER: 0105A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)282-7100
TELEFAX: (206)284-6206
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 174
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: no
ANTI-SENSE: no
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM: homo sapien
US-08-149-101A-20

Db 115 STKVLIQFLOKKAKNL 130

RESULT 13

US-08-149-101A-25

Sequence 25, Application US/08149101A

Patent No. 6171824

GENERAL INFORMATION:

APPLICANT: Todaro, George J.

APPLICANT: Leung, David W.

APPLICANT: Rose, Timothy M.

TITLE OF INVENTION: HYBRID CYTOKINES

NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:

ADDRESSEE: Cell Therapeutics, Inc.

STREET: 200 Elliott Avenue West, Suite 400

CITY: Seattle

STATE: Washington

COUNTRY: U.S.A.

ZIP: 98119

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" disk, 1.44Mb, double side, high density

COMPUTER: AST-IBM Compatible

OPERATING SYSTEM: MS-DOS Version 6

SOFTWARE: WORD for WINDOWS

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/149,101A

FILING DATE: 8-No. 6171824-1993

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US08/097,869

FILING DATE: 27-Jul-1993

ATTORNEY/AGENT INFORMATION:

NAME: Ostler, Jeffrey B. and Faciszewski, Stephen

REGISTRATION NUMBER: 32,585 and 36,131, respectively

REFERENCE/DOCKET NUMBER: 0105A

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206)282-7100

TELEFAX: (206)284-6206

INFORMATION FOR SEQ ID NO: 25:

SEQUENCE CHARACTERISTICS:

LENGTH: 182

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

HYPOTHETICAL: no

ANTI-SENSE: no

FRAGMENT TYPE:

ORIGINAL SOURCE: homo sapien

US-08-149-101A-25

Query Match 100.0%; Score 75; DB 4; Length 182;

Best Local Similarity 100.0%; Pred. No. 6,1e-05; Mismatches 0; Indels 0; Gaps 0;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STKVLIQFLOKKAKNL 16

Db 119 STKVLIQFLOKKAKNL 134

RESULT 14

PCT-US94-12873-25

Sequence 25, Application PC/TUS9412873

GENERAL INFORMATION:

APPLICANT:

APPLICANT:

APPLICANT:

TITLE OF INVENTION: HYBRID CYTOKINES

NUMBER OF SEQUENCES: 26

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" diskette, 1.44Mb, double side, high density

COMPUTER: AST-IBM Compatible

OPERATING SYSTEM: MS-DOS Version 6

SOFTWARE: WORD for WINDOWS

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US94/12873

INFORMATION FOR SEQ ID NO: 25:

SEQUENCE CHARACTERISTICS:

LENGTH: 182

TYPE: amino acid

TOPOLOGY: linear

PCT-US94-12873-25

Query Match 100.0%; Score 75; DB 5; Length 182;

Best Local Similarity 100.0%; Pred. No. 6,1e-05; Mismatches 0; Indels 0; Gaps 0;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STKVLIQFLOKKAKNL 16

Db 119 STKVLIQFLOKKAKNL 134

RESULT 15

US-08-009-973-1

Sequence 1, Application US/08009973

Patent No. 533834

GENERAL INFORMATION:

APPLICANT: WILLIAMS, Ashley M.

TITLE OF INVENTION: Ultrapure Human Interleukin-6

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESSEE: Foley & Lardner

STREET: 3000 K Street, N.W., Suite 500

CITY: Washington, D.C.

COUNTRY: USA

ZIP: 20007-5109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/009,973

FILING DATE: 19930126

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: BENT, Stephen A.

REGISTRATION NUMBER: 29,768

REFERENCE/DOCKET NUMBER: 16777/199 ALLE

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202)672-5300

TELEFAX: (202)672-5399

TELEX: 904136

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 183 amino acids

TYPE: AMINO ACID

TOPOLOGY: linear

US-08-009-973-1

Query Match 100.0%; Score 75; DB 1; Length 183;

Best Local Similarity 100.0%; Pred. No. 6,1e-05; Mismatches 0; Indels 0; Gaps 0;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STKVLIQFLOKKAKNL 16

Db 117 STKVLIQFLOKKAKNL 132

Search completed: December 19, 2001, 16:20:58

Job time: 403 sec

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OM protein - protein search, using sw model

Run on: December 19, 2001, 16:19:33 ; Search time 170.68 Seconds
(without alignments)
8.246 Million cell updates/sec

Title: US-09-202-104A-3

Perfect score: 88
Sequence: 1 ILRSFKEFLQSSLRALRQW 19

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Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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15: /SIDSB/gcgdata/geneseq/geneseq/AA1994.DAT.*
16: /SIDSB/gcgdata/geneseq/geneseq/AA1995.DAT.*
17: /SIDSB/gcgdata/geneseq/geneseq/AA1996.DAT.*
18: /SIDSB/gcgdata/geneseq/geneseq/AA1997.DAT.*
19: /SIDSB/gcgdata/geneseq/geneseq/AA1998.DAT.*
20: /SIDSB/gcgdata/geneseq/geneseq/AA1999.DAT.*
21: /SIDSB/gcgdata/geneseq/geneseq/AA2000.DAT.*
22: /SIDSB/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	88	100.0	19	AAW52203	Interleukin-6 anta
2	88	100.0	65	AAW00402	Interleukin-6 anta
3	88	100.0	148	AAU02910	Angiotensin conver
4	88	100.0	151	AAW77393	Human mutant IL-6a
5	88	100.0	158	AAW77392	Human mutant IL-6a
6	88	100.0	162	AAW77391	Human mutant IL-6a
7	88	100.0	162	AAW00131	Human interleukin-
8	88	100.0	163	AAW00132	Human interleukin-
9	88	100.0	166	AAW77390	Human IL-6 mutant
10	88	100.0	167	AAW77649	Human interleukin-
11	88	100.0	169	AAW77387	Human IL-6 mutant

12	88	100.0	173	AAW77389	Human IL-6 mutant
13	88	100.0	177	AAW77388	Human IL-6 mutant
14	88	100.0	179	AAW75334	Human interleukin-
15	88	100.0	181	AAW31996	-4aa IL-6 SSSS mut
16	88	100.0	181	AAW72211	Human interleukin-
17	88	100.0	181	AAW05586	-4aa SSCC mutleu o
18	88	100.0	183	AAW60125	Human interleukin
19	88	100.0	184	AAW81158	Polypeptide with B
20	88	100.0	184	AAW94753	Sequence of varian
21	88	100.0	184	AAW05895	Human B-cell diffe
22	88	100.0	184	AAW06532	Human B-cell simul
23	88	100.0	184	AAW03914	Polypeptide with h
24	88	100.0	184	AAW20783	Interleukin-6. A
25	88	100.0	184	AAW72219	Human interleukin-
26	88	100.0	184	AAW54990	Mutant interleukin-
27	88	100.0	184	AAW55256	Interleukin 6. Ho
28	88	100.0	184	AAW75344	Hybrid human cyto
29	88	100.0	184	AAW74659	Interleukin-6 for
30	88	100.0	184	AAW68623	B-cell differentia
31	88	100.0	184	AAW07199	Human interleukin
32	88	100.0	184	AAW07197	Human interleukin
33	88	100.0	184	AAW07198	Human interleukin
34	88	100.0	184	AAW02609	Interleukin-6. Ho
35	88	100.0	185	AAW81159	Polypeptide with B
36	88	100.0	185	AAW90059	Human Ala B cell d
37	88	100.0	185	AAW94754	Sequence of varian
38	88	100.0	185	AAW94015	Synthetic interen
39	88	100.0	185	AAW05275	Segment of human B
40	88	100.0	185	AAW05274	Segment of human B
41	88	100.0	185	AAW05311	Segment of B-cell
42	88	100.0	185	AAW10983	Recombinant human
43	88	100.0	185	AAW31995	IL-6 SSCC mutleu.
44	88	100.0	185	AAW72210	Human interleukin-
45	88	100.0	185	AAW73403	Human mature inter

ALIGNMENTS

RESULT 1
ID AAW52203 standard; peptide; 19 AA.
XX AAW52203;
AC AAW52203;
XX
DT 09-JUN-1998 (first entry)
XX
DE Interleukin-6 antagonist peptide.
XX
KW Interleukin-6; IL-6; antagonist; IL-6 related disease; multiple myeloma;
KW acquired immune deficiency syndrome-related lymphoma; immune response;
KW rheumatoid arthritis; psoriasis; sepsis; osteoporosis; therapy;
XX Alzheimer's disease.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN W09748728-A1.
XX
PD 24-DEC-1997.
XX
PF 19-JUN-1997; 97WO-NL00345.
XX
PR 20-JUN-1996; 96EP-0201720.
XX
PA (KOST/) KOSTER H W.
XX
PI Hoebe KHN, Van Leeengoed LAMG;
XX
DR WPI: 1998-063080/06.
XX
PT New peptide(s) with interleukin-6 agonist or antagonist activity -
useful for treatment, prevention and diagnosis of IL-6 associated

PT diseases
 XX
 PS Claim 6; Page 17; 28pp; English.
 XX
 CC This sequence represents a interleukin-6 (IL-6) antagonist peptide. This
 CC sequence is a peptide of the invention, which are of 5-30 amino acids
 CC and have antagonistic activity against: (a) IL-6; (b) the alpha chain
 CC and/or beta chain of the IL-6 receptor (IL-6R); or (c) IL-6 activity. The
 CC antagonists are used to treat or prevent IL-6 related diseases (typical
 CC of many exemplified are multiple myeloma, acquired immune deficiency
 CC syndrome-related lymphoma, rheumatoid arthritis, psoriasis, sepsis,
 CC osteoporosis, Alzheimer's disease etc.), also to remove IL-6 or IL-6R
 CC from extracorporeal blood. They may also be used diagnostically for such
 CC diseases and IL-6 agonists are additives for cell cultures. Antibodies
 CC specific for the antagonists may be administered to subjects previously
 CC treated with the antagonists to counter their effects, also in
 CC extracorporeal dialysis and diagnosis. The antagonists are too small to
 CC induce an immune response and have minimal side effects (they are not
 CC lytic for erythrocytes nor toxic for polymorphonuclear cells or
 CC hepatocytes); contrast no-human anti-IL-6 antibodies. The mixtures, or
 CC multimers, have greater activity (acting on both IL-6 and its receptor)
 CC and the peptides can be engineered to increase half-life or to target
 CC organs by incorporating unnatural aa or altering the
 CC hydrophilic/lipophilic balance.
 XX
 SQ Sequence 19 AA;
 XX
 QY 1 ILRSFKEFLQSSIRALRQM 19
 Db 1 ILRSFKEFLQSSIRALRQM 19
 XX
 RESULT 2
 AAM00402
 ID AAM00402 standard; peptide; 65 AA.
 XX
 AC AAM00402;
 XX
 DT 29-AUG-1996 (first entry)
 XX
 DE Interleukin-6 antagonist peptide.
 XX
 KM IL-6; antagonist; autoimmune disease.
 XX
 OS Synthetic.
 XX
 PN JF07324097-A.
 PD 12-DEC-1995.
 XX
 PF 30-MAY-1994; 94JP-0117259.
 XX
 PR 30-MAY-1994; 94JP-0117259.
 XX
 PA (DAILEY) DAILEY CHEM IND LTD.
 PA (FUJII) FUJISAWA PHARM CO LTD.
 XX
 DR WPI; 1996-065476/07.
 XX
 PT Interleukin 6 antagonist - useful for treating autoimmune diseases
 XX
 PS Claim 1; Page 2; 19pp; Japanese.
 XX
 CC New IL-6 antagonists are provided which are of formula X-W-Y, in
 CC which X is H or an amino-protecting group, Y is OH or a carboxy-
 CC protecting group, and W is a peptide containing all or part of the
 CC sequence as given in AAM00401, AAM00402 (the present sequence), AAM00403
 CC or AAM00404, where any free mercapto groups in the sequence are

CC optionally protected. Specifically preferred partial peptides from the
 CC present sequence (AAM00412 AAM00427) are claimed as new chemical
 CC compounds. The IL-6 antagonists are useful for treating autoimmune
 CC diseases.
 XX
 SQ Sequence 65 AA;
 XX
 QY 1 ILRSFKEFLQSSIRALRQM 19
 Db 47 ILRSFKEFLQSSIRALRQM 65
 XX
 RESULT 3
 AAU02910
 ID AAU02910 standard; protein; 148 AA.
 XX
 AC AAU02910;
 XX
 DT 12-SEP-2001 (first entry)
 XX
 DE Angiotensin converting enzyme (ACEV) splice variant protein #10.
 XX
 KM Angiotensin converting enzyme splice variant; ACEV; interleukin 6;
 KM granulocyte colony stimulating factor receptor; glucagon; hypertrophy;
 KM platelet-derived endothelial cell growth factor; cardiovascular disease;
 KM cellular tumour antigen P53; cyclin-dependent kinase inhibitor 1c;
 KM vasoactive intestinal polypeptide receptor 2; arteriosclerosis; cancer;
 KM myocardial infarction; coronary arterial thrombosis; renal disease;
 KM diabetic nephropathy; muscular disease; immune disorder; sarcoidosis;
 KM multiple sclerosis; immune complex nephritis; deep vein thrombosis;
 KM nonarcoliotic pulmonary granulomatous disease; endothelial abnormality;
 KM vascular disorder; asbestosis.
 XX
 OS Homo sapiens.
 XX
 PN WO200136632-A2.
 PD 25-MAY-2001.
 XX
 PF 17-NOV-2000; 2000WO-IL00766.
 XX
 PR 17-NOV-1999; 99IL-0132978.
 PR 10-DEC-1999; 99IL-0133455.
 XX
 PA (COMP-) COMPUGEN LTD.
 XX
 PI Levine Z, David A, Azar I, Khosravi R, Bernstein J;
 XX
 DR WPI; 2001-336004/35.
 DR N-PSDB; AAS06010.
 XX
 PT Novel alternative splicing variants e.g. variant of angiotensin
 PT converting enzyme (ACEV), useful in identifying candidate compounds
 PT capable of binding to the variant and to detect anti-variant antibodies
 XX
 PS Claim 4; Fig 10; 51pp; English.
 XX
 CC The sequence represents an angiotensin converting enzyme splice variant
 CC (ACEV) polypeptide. The polypeptides of the invention include variants of
 CC granulocyte colony stimulating factor receptor, glucagon, interleukin 6,
 CC platelet-derived endothelial cell growth factor, cyclin-dependent kinase
 CC inhibitor 1c, cellular tumour antigen P53, and vasoactive intestinal
 CC polypeptide receptor 2. The polypeptides and their associated nucleic
 CC acids are useful for identification of variant sequences and detection of
 CC candidate compounds capable of binding the molecules. The sequences of
 CC the invention can be used in the treatment and diagnosis of various
 CC disorders including cardiovascular diseases such as arteriosclerosis,

CC myocardial infarction and coronary arterial thrombosis, renal diseases
 CC such as diabetic nephropathy, muscular diseases such as hypertrophy,
 CC immune disorders such as immune complex nephritis, multiple sclerosis,
 CC cancer, sarcoidosis, noncardiotoxic pulmonary granulomatous diseases such
 CC as asbestosis and vascular pathologies involving an endothelial
 CC abnormality such as deep vein thrombosis.
 XX
 XX Sequence 148 AA;

Query Match 100.0%; Score 88; DB 22; Length 148;
 Best Local Similarity 100.0%; Pred. No. 1.3e-06;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ILRSKFLQSSLRALROM 19
 DB 130 ILRSKFLQSSLRALROM 148

RESULT 4

AAR77393
 ID AAR77393 standard; Protein: 151 AA.

XX
 AC AAR77393;

DT 17-APR-1996 (first entry)

XX Human mutant IL-6a/C3 (amino acids 5-19, 44-50 and 73-83 deleted).

XX Human Interleukin-6; IL-6a/C3 mutant; increased stability;
 KW recombinant; production; deletion mutant;
 KW amino acids 5-19, 44-50 and 73-83.

XX Homo sapiens.

XX JP07224097-A.

XX 22-AUG-1995.

XX 08-FEB-1994; 94JP-0014461.

XX 08-FEB-1994; 94JP-0014461.

XX (ASAG) ASAHI GLASS CO LTD.

XX WPI; 1995-325556/42.

XX N-PSDB; AAQ94348.

XX Interleukin-6 mutant, related DNA and expression vectors - has
 PT higher stability than natural Interleukin-6

XX Claim 1; Pages 15-16; 18pp; Japanese.

XX AAQ94348 encodes AAR77393 the human IL-6 deletion mutant IL-6a/C3
 CC which lacks the amino acids Gly5-Leu19, Cys44-Cys50 and Cys73-Cys83
 CC of the wild type protein. The cDNA can be used for the recombinant
 CC prodn. of IL-6a/C3 which has increased stability compared to wild
 CC type IL-6.

XX Sequence 151 AA;

Query Match 100.0%; Score 88; DB 16; Length 151;
 Best Local Similarity 100.0%; Pred. No. 1.3e-06;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ILRSKFLQSSLRALROM 19
 DB 133 ILRSKFLQSSLRALROM 151

RESULT 5

AAR77392

ID AAR77392 standard; Protein: 158 AA.

XX AAR77392;

DT 17-APR-1996 (first entry)

XX Human mutant IL-6a/C2 (amino acids 5-19 and 73-83 deleted).

XX Human Interleukin-6; IL-6a/C2 mutant; increased stability;
 KW recombinant; production; deletion mutant;
 KW amino acids 5-19 and 73-83.

XX Homo sapiens.

XX Key Location/Qualifiers
 FT mat_peptide 1..474
 FT /*tag= a

XX JP07224097-A.

XX 22-AUG-1995.

XX 08-FEB-1994; 94JP-0014461.

XX 08-FEB-1994; 94JP-0014461.

XX (ASAG) ASAHI GLASS CO LTD.

XX WPI; 1995-325556/42.

XX N-PSDB; AAQ94347.

XX Interleukin-6 mutant, related DNA and expression vectors - has
 PT higher stability than natural interleukin-6

XX Claim 1; Pages 14-15; 18pp; Japanese.

XX AAQ94347 encodes AAR77392 the human IL-6 deletion mutant IL-6a/C2
 CC which lacks the amino acids Gly5-Leu19 and Cys73-Cys83 of the
 CC wild type protein. The cDNA can be used for the recombinant prodn.
 CC of IL-6a/C2 which has increased stability compared to wild type
 CC IL-6.

XX Sequence 158 AA;

Query Match 100.0%; Score 88; DB 16; Length 158;
 Best Local Similarity 100.0%; Pred. No. 1.3e-06;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ILRSKFLQSSLRALROM 19
 DB 140 ILRSKFLQSSLRALROM 158

RESULT 6

AAR77391
 ID AAR77391 standard; Protein: 162 AA.

XX AAR77391;

DT 17-APR-1996 (first entry)

XX Human mutant IL-6a/C1 (amino acids 5-19 and 44-50 deleted).

XX Human Interleukin-6; IL-6a/C1 mutant; increased stability;
 KW recombinant; production; deletion mutant;
 KW amino acids 5-19 and 44-50.

XX Homo sapiens.

XX JP07224097-A.

XX 22-AUG-1995.

XX 08-FEB-1994; 94JP-0014461.
 PF 08-FEB-1994; 94JP-0014461.
 PR 08-FEB-1994; 94JP-0014461.
 XX
 PA (ASAG) ASahi GLASS CO LTD.
 XX
 XX WPI; 1995-325556/42.
 DR N-PSDB; AA094346.
 XX
 PT Interleukin-6 mutant, related DNA and expression vectors - has
 PT higher stability than natural Interleukin-6
 XX
 PS Claim 1; Page 14; 18pp; Japanese.
 XX
 CC AA094346 encodes AAR77391 the human IL-6 deletion mutant IL-6a'Cl,
 CC which lacks the amino acids Gly5-Leu19 and Cys44-Cys50 of the
 CC wild type protein. The cDNA can be used for the recombinant prodn.
 CC of IL-6a'Cl, which has increased stability compared to wild type
 CC IL-6.
 CC
 SO Sequence 162 AA;

Query Match 100.0%; Score 88; DB 16; Length 162;
 Best Local Similarity 100.0%; Pred. No. 1.4e-06;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ILRSKFELQSSLRALRQ 19
 |||||
 Db 144 ILRSKFELQSSLRALRQ 162

RESULT 7

AAW00131
 ID AAW00131 standard; Protein; 162 AA.

AC AAW00131;

DT 09-APR-1997 (first entry)

XX Human Interleukin-6 fragment.

DE Secretary; signal peptide; P-factor; multicloning vector; PCR;

XX animal protein; expression; production; recombinant; primer;

KM fission yeast; human; serum albumin; Interleukin-6;

KW polymerase chain reaction; Schizosaccharomyces pombe;

KM PO fragment.

OS Homo sapiens.

XX WO9623890-A1.

PN 08-AUG-1996.

XX 01-FEB-1996; 96WO-JP00198.

XX 03-FEB-1995; 95JP-0017167.

XX (ASAG) ASahi GLASS CO LTD.

PI Hama Y, Kumagai H, Nikaido K, Tohda H, Tsukamoto H;

XX WPI; 1996-371438/37.

DR Schizosaccharomyces pombe secretory signal peptide (P-factor) gene

PT - for production of vectors for expression of animal proteins in a

PS fission yeast, pref. S. pombe, host

XX Example 4; Pages 28-29; 50pp; Japanese.

CC A multicloning vector, comprising the human interleukin-6 (hIL-6)

CC cDNA, a Schizosaccharomyces pombe secretory signal peptide

CC fragment or P-factor fragment (PO fragment) DNA and preferably an
 CC animal cell viral promoter sequence and a neomycin resistance gene,
 CC can be used for the efficient production of a hIL-6 fragment, i.e.
 CC the present sequence, in a fission yeast host, preferably S. pombe,
 CC culture.
 CC
 SO Sequence 162 AA;

Query Match 100.0%; Score 88; DB 17; Length 162;
 Best Local Similarity 100.0%; Pred. No. 1.4e-06;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ILRSKFELQSSLRALRQ 19
 |||||
 Db 144 ILRSKFELQSSLRALRQ 162

RESULT 8

AAW00132
 ID AAW00132 standard; Protein; 163 AA.

AC AAW00132;

DT 09-APR-1997 (first entry)

XX Human Interleukin-6 fragment.

DE Secretary; signal peptide; P-factor; multicloning vector; PCR;

KW animal protein; expression; production; recombinant; primer;

KM fission yeast; human; serum albumin; Interleukin-6;

KW polymerase chain reaction; Schizosaccharomyces pombe;

KM PI fragment.

OS Homo sapiens.

XX WO9623890-A1.

PN 08-AUG-1996.

XX 01-FEB-1996; 96WO-JP00198.

XX 03-FEB-1995; 95JP-0017167.

XX (ASAG) ASahi GLASS CO LTD.

PI Hama Y, Kumagai H, Nikaido K, Tohda H, Tsukamoto H;

XX WPI; 1996-371438/37.

DR Schizosaccharomyces pombe secretory signal peptide (P-factor) gene

PT - for production of vectors for expression of animal proteins in a

PT fission yeast, pref. S. pombe, host

XX Example 7; Pages 30-31; 50pp; Japanese.

XX A multicloning vector, comprising the human interleukin-6 (hIL-6)

CC cDNA, a Schizosaccharomyces pombe secretory signal peptide

CC fragment or P-factor fragment (PI fragment) DNA and preferably an

CC animal cell viral promoter sequence and a neomycin resistance gene,

CC can be used for the efficient production of a hIL-6 fragment, i.e.

CC the present sequence, in a fission yeast host, preferably S. pombe,

CC culture.

SO Sequence 163 AA;

Query Match 100.0%; Score 88; DB 17; Length 163;
 Best Local Similarity 100.0%; Pred. No. 1.4e-06;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ILRSKFELQSSLRALRQ 19
 |||||

Db 145 l1rsfkeflqsslrqlrqn 163

RESULT 9

AA077390
ID AAR77390 standard; Protein; 166 AA.

AC AAR77390;

DT 17-APR-1996 (first entry)

DE Human IL-6 mutant IL-6C3 (amino acids 44-50 and 73-83 deleted).

KN Human interleukin-6; IL-6C3 mutant; increased stability;

KV recombinant; production; deletion mutant;

OS Homo sapiens.

PH Key Location/Qualifiers

FT mat_peptide 1..498

FT /*tag= a

PN JP07224097-A.

PD 22-AUG-1995.

PE 08-FEB-1994; 94JP-0014461.

PR 08-FEB-1994; 94JP-0014461.

PA (ASAG) ASAMI GLASS CO LTD.

DR WPI: 1995-325556/42.

DR N-PSDB; AA094345.

PT Interleukin-6 mutant, related DNA and expression vectors - has

PS Claim 1; Page 13; 18pp; Japanese.

CC AA094345 encodes AAR77390 the human IL-6 deletion mutant IL-6C3,

CC which lacks the amino acids CYS44-CYS50 and CYS73-CYS83 of the

CC wild type protein. The cDNA can be used for the recombinant prodn.

CC of IL-6C3, which has increased stability compared to wild type

CC IL-6.

CC Sequence 166 AA;

QY 1 l1rsfkeflqsslrqlrqn 19

DB 148 l1rsfkeflqsslrqlrqn 166

RESULT 10

AA077649
ID AAR77649 standard; Protein; 167 AA.

AC AAR77649;

DT 27-JUN-1996 (first entry)

DE Human interleukin-6 splice variant.

KN Human; interleukin-6; splice variant; IL-6SV; treatment;

KV immunotherapeutic; anti-inflammatory; bone marrow transplant;

KN chemotherapy; side effect; corneal damage; keratitis; ulcer;

KN antagonist; Castleman's disease; multiple myeloma;

KN cardiac myxoma; cervical cancer; rheumatoid arthritis;

KN autoimmune diabetes; sepsis.

OS Homo sapiens.

PN W09532282-A1.

PD 30-NOV-1995.

PE 17-MAY-1995; 95WO-US06094.

PR 19-MAY-1994; 94US-0246427.

PA (HUMA-) HUMAN GENOME SCI INC.

PI Adams MD, Li H, Ruben S;

DR WPI: 1996-020577/02.

DR N-PSDB; AAT08558.

PT Polynucleotide encoding interleukin 6-splice variant - used for

PT treating auto-immune diseases and inflammation.

PS Claim 1; Page 40; 54pp; English.

CC The human interleukin-6 splice variant (IL-6SV) AAR77649 is encoded

CC by AAT08558 (which is derived from an activated macrophage cDNA

CC library), and may be used in immunotherapeutic and

CC anti-inflammatory compounds, and for the treatment of patients

CC suffering from bone marrow transplant chemotherapy side effects,

CC corneal damage, keratitis and ulcers. Antagonists of IL-6SV may

CC be used to treat diseases caused by the up-regulated prodn. of

CC IL-6 (i.e. Castleman's disease, multiple myeloma, cardiac myxoma,

CC cervical cancer, rheumatoid arthritis and autoimmune diabetes),

CC and sepsis.

CC Sequence 167 AA;

QY 1 l1rsfkeflqsslrqlrqn 19

DB 149 l1rsfkeflqsslrqlrqn 167

RESULT 11

AA077387
ID AAR77387 standard; Protein; 169 AA.

AC AAR77387;

DT 17-APR-1996 (first entry)

DE Human IL-6 mutant IL-6a (amino acids 5-19 deleted).

KN Human interleukin-6; IL-6a mutant; increased stability;

KV recombinant; production; deletion mutant; amino acids 5-19.

OS Homo sapiens.

PN JP07224097-A.

PD 22-AUG-1995.

PE 08-FEB-1994; 94JP-0014461.

PR 08-FEB-1994; 94JP-0014461.

PA (ASAG) ASAMI GLASS CO LTD.

DR WPI; 1995-325556/42.
 DR N-PSDB; AAQ94342.
 XX Interleukin-6 mutant, related DNA and expression vectors - has
 PT higher stability than natural Interleukin-6
 PS Claim 1; Page 10; 18pp; Japanese.
 XX
 CC AAQ94342 encodes AAR77387 the human IL-6 deletion mutant IL-6a, which
 CC lacks the amino acids Gly5-Leu19 of the wild type protein. The
 CC cDNA can be used for the recombinant prodn. of IL-6a, which has
 CC increased stability compared to wild type IL-6.
 CC
 XX Sequence 169 AA:
 SQ
 Query Match 100.0%; Score 88; DB 16; Length 169;
 Best Local Similarity 100.0%; Pred. No. 1.4e-06;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ILRSFKEFIQSSLRALROM 19
 |||||
 DB 151 llrsfkeflqsslraltqgm 169
 RESULT 12
 AAR77389
 ID AAR77389 standard; Protein; 173 AA.
 XX
 AC AAR77389;
 XX
 DT 17-APR-1996 (first entry)
 XX
 DE Human IL-6 mutant IL-6C2 (amino acids 73-83 deleted).
 XX
 KW Human Interleukin-6; IL-6C2 mutant; increased stability;
 KW recombinant; production; deletion mutant; amino acids 73-83.
 XX
 OS Homo sapiens.
 XX
 PH Key Location/Qualifiers
 FT mat_peptide 1..519
 FT /*tag- a
 XX
 XX JP07224097-A.
 XX
 XX
 XX PD 22-AUG-1995.
 XX
 XX PF 08-FEB-1994; 94JP-0014461.
 XX
 XX PR 08-FEB-1994; 94JP-0014461.
 XX
 XX PA (ASAG) ASahi GLASS CO LTD.
 XX
 XX WPI; 1995-325556/42.
 DR N-PSDB; AAQ94344.
 XX
 XX Interleukin-6 mutant, related DNA and expression vectors - has
 PT higher stability than natural Interleukin-6
 PS Claim 1; Page 12; 18pp; Japanese.
 XX
 CC AAQ94344 encodes AAR77389 the human IL-6 deletion mutant IL-6C2,
 CC which lacks the amino acids Cys73-Cys83 of the wild type protein.
 CC The cDNA can be used for the recombinant prodn. of IL-6C2, which
 CC has increased stability compared to wild type IL-6.
 CC
 XX Sequence 173 AA:
 SQ
 Query Match 100.0%; Score 88; DB 16; Length 173;
 Best Local Similarity 100.0%; Pred. No. 1.5e-06;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ILRSFKEFIQSSLRALROM 19
 |||||
 DB 155 llrsfkeflqsslraltqgm 173
 RESULT 13
 AAR77388
 ID AAR77388 standard; Protein; 177 AA.
 XX
 AC AAR77388;
 XX
 DT 17-APR-1996 (first entry)
 XX
 DE Human IL-6 mutant IL-6C1 (amino acids 44-50 deleted).
 XX
 KW Human Interleukin-6; IL-6C1 mutant; increased stability;
 KW recombinant; production; deletion mutant; amino acids 44-50.
 XX
 OS Homo sapiens.
 XX
 XX JP07224097-A.
 XX
 XX PD 22-AUG-1995.
 XX
 XX PF 08-FEB-1994; 94JP-0014461.
 XX
 XX PR 08-FEB-1994; 94JP-0014461.
 XX
 XX PA (ASAG) ASahi GLASS CO LTD.
 XX
 XX WPI; 1995-325556/42.
 DR N-PSDB; AAQ94343.
 XX
 XX Interleukin-6 mutant, related DNA and expression vectors - has
 PT higher stability than natural Interleukin-6
 PS Claim 1; Page 11; 18pp; Japanese.
 XX
 CC AAQ94343 encodes AAR77388 the human IL-6 deletion mutant IL-6C1,
 CC which lacks the amino acids Cys44-Cys50 of the wild type protein.
 CC The cDNA can be used for the recombinant prodn. of IL-6C1, which
 CC has increased stability compared to wild type IL-6.
 CC
 XX Sequence 177 AA:
 SQ
 Query Match 100.0%; Score 88; DB 16; Length 177;
 Best Local Similarity 100.0%; Pred. No. 1.5e-06;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ILRSFKEFIQSSLRALROM 19
 |||||
 DB 159 llrsfkeflqsslraltqgm 177
 RESULT 14
 AAR75334
 ID AAR75334 standard; Protein; 179 AA.
 XX
 AC AAR75334;
 XX
 XX DT 13-DEC-1995 (first entry)
 XX
 DE Human Interleukin-6 (IL-6).
 XX
 KW Cytokine; tumour proliferation; cancer therapy.
 XX
 XX OS Homo sapiens.
 XX
 XX PN WO9513393-A.
 XX
 XX PD 18-MAY-1995.

XX 07-NOV-1994; 94WO-US12873.
 PF
 XX
 PR 08-NOV-1993; 93US-0149101.
 XX
 PA (HUTC-) HUTCHINSON CANCER RES CENTER FRED.
 XX
 PI Leung DM, Rose TM, Todaro GJ;
 XX
 DR WPI: 1995-194111/25.
 XX N-PSDB; AA087153.
 PR New hybrid cytokines with alpha helical sequences from different
 PT sources - also DNA encoding them, vectors and transformed cells,
 PT useful e.g. for treating cancer, remodelling bone etc.
 XX
 PS Disclosure: Page 23-24; 52pp; English.
 XX
 CC The cytokine encoding genes for leukemia inhibitory factor (LIF),
 CC granulocyte-colony stimulating factor (G-CSF), interleukin-6 (IL-6),
 CC interleukin-11 (IL-11), ciliary neurotrophic factor (CNTF) and
 CC oncostatin-M (OSM) have been cloned and reported in the literature.
 CC IL-6, G-CSF, LIF, IL-11, CNTF and OSM each comprise four alpha-
 CC helical sequences. In each cytokine, the four alpha-helical
 CC sequences are linked by non-alpha-helical 'linking' sequences of
 CC about 5-100 AAs, and in some cases the alpha-helices are maintained
 CC in the proper conformation and geometry with respect to each other
 CC through disulfide bridges. The invention provides a group of
 CC therapeutic hybrid cytokines, having a size ranging from about 10
 CC to about 30 kDa. Each hybrid cytokine comprises three or four
 CC alpha-helical sequences and linking sequences, ranging from about
 CC 5-40 AAs in length, selected from the linking sequences of the
 CC above cytokines or other linking sequences.
 XX
 SQ Sequence 179 AA;

Query Match 100.0%; Score 88; DB 16; Length 179;
 Best Local Similarity 100.0%; Pred. No. 1.5e-06;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ILRSFEKFLQSSIRALRQM 19
 DB 161 ILRSFEKFLQSSIRALRQM 179

RESULT 15
 AAR31996
 ID AAR31996 standard; Protein; 181 AA.
 XX
 AC AAR31996;
 XX
 DT 07-JUN-1993 (first entry)
 XX
 DE -4aa IL-6 SSSS muttein.
 XX
 KM Interleukin-6; mutant protein; pBgai/EK/cfil-6.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 41 /note= "Ser replaces wild-type Cys"
 FT Misc-difference 47 /note= "Ser replaces wild-type Cys"
 FT Misc-difference 70 /note= "Ser replaces wild-type Cys"
 FT Misc-difference 80 /note= "Ser replaces wild-type Cys"
 FT Misc-difference 80 /note= "Ser replaces wild-type Cys"
 XX
 PN WO9301212-A.
 XX
 PD 21-JAN-1993.

XX 02-JUL-1992; 92WO-US05612.
 PF
 XX
 PR 02-JUL-1991; 91US-0724698.
 XX
 PA (IMCL-) IMCLONE SYSTEMS INC.
 XX (UYNC-) UNIV NORTH CAROLINA.
 XX
 PI Fowlkes DM, Skelly SM, Snouwaert JN, Tackney CT;
 XX
 DR WPI: 1993-045433/05.
 XX N-PSDB; AA034545.
 PR New cysteine-depleted interleukin-6 muttein - for promoting cell
 PT differentiation (e.g. of B-cells), as antiinflammatory agents and
 PT for treating thrombocytopenia
 XX
 PS Example 1; Fig 2; 118pp; English.
 XX
 CC Plasmid pBgai/EK/cfil-6 contains a DNA sequence which encodes a
 CC fusion protein comprising beta-galactosidase, followed by an
 CC enterokinase cleavage site, which is, in turn, followed by a
 CC synthetic IL-6 peptide sequence. The IL-6 muttein sequence is that
 CC of native IL-6 except that the four cysteine residues, which occur
 CC at positions 45, 51, 74 and 84 of the mature full-length IL-6
 CC molecule are replaced by serine residues. A truncated 0.58kb
 CC Cysteine-free IL-6 sequence lacking the first 4 N-terminal amino
 CC acids can be isolated by EcoRII-HindIII digestion. The fragment was
 CC used in the preparation of various IL-6 muteins, either full-length
 CC or N-terminally truncated. It was found that restoring the last two
 CC Cys residues (at positions 74 and 84) resulted in a muttein which
 CC retained IL-6 activity.
 XX
 SQ Sequence 181 AA;

Query Match 100.0%; Score 88; DB 14; Length 181;
 Best Local Similarity 100.0%; Pred. No. 1.5e-06;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ILRSFEKFLQSSIRALRQM 19
 DB 163 ILRSFEKFLQSSIRALRQM 181

Search completed: December 19, 2001, 16:19:34
 Job time: 359 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: December 19, 2001, 16:22:35 ; Search time 88.82 Seconds
(without alignments)
16.295 Million cell updates/sec

Title: US-09-202-104A-3

Perfect score: 88

Sequence: 1 ILRSFKEFLQSLRALROM 19

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	88	100.0	212	1	IVHUB2
2	59	67.0	212	2	I46621
3	59	67.0	212	2	I46590
4	58	65.9	208	2	T09216
5	52	59.1	208	1	A56610
6	50	56.8	208	1	S29549
7	49	55.7	211	1	ICMS6
8	48	54.5	201	2	A42247
9	45	51.1	1082	2	H81982
10	44	50.0	207	2	I46084
11	44	50.0	211	2	A34247
12	44	50.0	610	2	T08597
13	44	50.0	978	2	T40803
14	43.5	49.4	1159	2	T02866
15	42	47.7	346	2	T19008
16	42	47.7	992	2	T46337
17	41	46.6	249	2	G64415
18	41	46.6	310	2	S35907
19	41	46.6	332	2	D83519
20	41	46.6	427	2	T49122
21	41	46.6	461	2	JN0129
22	41	46.6	487	1	A64472
23	41	46.6	513	2	B70478
24	41	46.6	596	2	T17333
25	41	46.6	831	2	T05265
26	41	46.6	2354	2	T13288
27	40	45.5	251	2	H85781
28	40	45.5	271	2	B64932
29	40	45.5	315	2	T46156

30	40	45.5	532	2	H84123	CTP synthetase ctr
31	40	45.5	1017	2	PC4035	cell-cycle-depende
32	40	45.5	1024	2	F75489	carbamoyl-phosphat
33	40	45.5	1092	2	T33717	carbamoyl-phosphat
34	39	44.3	312	2	H69396	3-hydroxyacyl-CoA
35	39	44.3	371	2	E83807	(5-methylamino)eth
36	39	44.3	398	2	A71482	hypothetical prote
37	39	44.3	437	2	J50237	hypothetical 48k p
38	39	44.3	454	2	C82682	glutamate-cysteine
39	39	44.3	484	1	XVRBSC	glycine hydroxymet
40	39	44.3	566	1	I64243	hypothetical prote
41	39	44.3	641	1	HHEF72	dnak-type molecula
42	39	44.3	649	2	JQ1515	dnak-type molecula
43	39	44.3	825	2	T23612	hypothetical prote
44	39	44.3	1051	2	T43253	carbamoyl-phosphat
45	39	44.3	1161	2	A27069	lethal (2) giant 1

ALIGNMENTS

RESULT 1
IVHUB2
Interleukin-6 precursor [validated] - human
N:Alternate names: B-cell differentiation factor; B-cell hybridoma growth factor; B-c
on factor
C:Species: Homo sapiens (man)
C:date: 28-Dec-1987 #Sequence-Revision 28-Dec-1987 #text-change 08-Dec-2000
C:Accession: A32648; A25692; A25696; A35515; A25801; A25921; I52133; I56003; A27601;
R:Yasukawa, K.; Hirano, T.; Watanabe, Y.; Muratani, K.; Matsuda, T.; Nakai, S.; Kishi
EMBO J. 6, 2939-2945, 1987
A>Title: Structure and expression of human B cell stimulatory factor-2 (BSF-2/IL-6) g
A:Reference number: A32648; MUID:868082664
A:Accession: A32648
A:Molecule type: DNA
A:Residues: 1-212 <YAS>
A:Cross-references: GB:Y00081; NID:929494; PIDN:CAA68278.1; PID:929495
A:Note: The authors translated the codon CAG for residue 130 as Glu
R:Zilberstein, A.; Ruggieri, R.; Korn, J.H.; Revel, M.
EMBO J. 5, 2529-2537, 1986
A>Title: Structure and expression of cDNA and genes for human interferon-beta-2, a di
A:Reference number: A91051; MUID:87053818
A:Accession: A25692
A:Molecule type: mRNA
A:Residues: 1-212 <ZIL>
A:Cross-references: GB:X04430; NID:932673; PIDN:CAA28026.1; PID:932674
R:Hirano, T.; Yasukawa, K.; Harada, H.; Taga, T.; Watanabe, Y.; Matsuda, T.; Kashiwa
I, T.; Kishimoto, T.
Nature 324, 73-76, 1986
A>Title: Complementary DNA for a novel human Interleukin (BSF-2) that induces B lymph
A:Reference number: A93387; MUID:87065033
A:Accession: A25696
A:Molecule type: mRNA
A:Residues: 1-212 <HIR>
A:Cross-references: GB:X04602; NID:933849; PIDN:CAA28268.1; PID:933850
R:Tanouchi, N.; Miwa, K.; Karesuyama, H.; Matsui, H.
Biochem. Biophys. Res. Commun. 163, 1056-1062, 1989
A>Title: Deletion of 3' untranslated region of human BSF-2 mRNA causes stabilization
A:Reference number: A33515; MUID:89391958
A:Accession: A33515
A:Molecule type: mRNA
A:Residues: 1-212 <TRN>
A:Cross-references: GB:M29150; NID:9186349; PIDN:AAA59154.1; PID:9307063
R:Haegeman, G.; Content, J.; Voelckert, G.; Deruyck, R.; Tavernier, J.; Fiers, W.
Eur. J. Biochem. 159, 625-632, 1986
A>Title: Structural analysis of the sequence coding for an inducible 26-kDa protein 1
A:Reference number: A25801; MUID:87004683
A:Accession: A25801
A:Molecule type: DNA: mRNA
A:Residues: 1-212 <HA>
A:Cross-references: GB:X04403
A:Experimental source: fibroblast
R:May, L.T.; Helfgott, D.C.; Sehgal, P.B.

Proc. Natl. Acad. Sci. U.S.A. 83, 8957-8961, 1986
 A:Title: Anti-beta-Interferon antibodies inhibit the increased expression of HLA-B7 mRNA
 A:Reference number: A25921; MUID:87067433
 A:Accession: A25921
 A:Molecule type: mRNA
 A:Residues: 1-212 <MAX>
 A:Cross-references: GB:M14584; NID:g184628; PIDN:AAA52728.1; PID:g306910
 R:Mong, G.G.; Witek-Glancott, J.; Hewick, R.M.; Clark, S.C.; Ogawa, M.
 Behring Inst. Mitt. 83, 40-47, 1988
 A:Title: Interleukin 6: Identification as a hematopoietic colony-stimulating factor.
 A:Reference number: 152193; MUID:89193317
 A:Accession: 152193
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-212 <MON>
 A:Cross-references: GB:M54894; NID:g186351; PIDN:AAC41704.1; PID:g186352
 R:Brakenhoff, J.P.; de Groot, E.R.; Evers, R.F.; Pannekoek, H.; Aarden, L.A.
 J. Immunol. 139, 4116-4121, 1987
 A:Title: Molecular cloning and expression of hybridoma growth factor in Escherichia coli
 A:Reference number: 156003; MUID:88088768
 A:Accession: 156003
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-212 <BBA>
 A:Cross-references: GB:M18403; NID:g184631; PIDN:AAA52729.1; PID:g306911
 R:Van Damme, J.; Van Beeumen, J.; Decock, B.; Van Snick, J.; De Ley, M.; Billiau, A.
 J. Immunol. 140, 1534-1541, 1988
 A:Title: Separation and comparison of two monokines with lymphocyte-activating factor ad
 A:Reference number: A92816; MUID:88154445
 A:Accession: A27601
 A:Molecule type: protein
 A:Residues: 28-51, 'X', 53-57, 'X', 59, 'X', 61 <VANI>
 A:Accession: B27601
 A:Molecule type: protein
 A:Residues: 30-56, 'XX', 59-61, 'X', 63 <VA2>
 R:Yamamoto, R.; Lin, L.S.; Lowe, R.; Warren, M.K.; White, T.J.
 J. Immunol. 144, 1808-1816, 1990
 A:Title: The human lung fibroblast cell line, MRC-5, produces multiple factors involved
 A:Reference number: A60400; MUID:90171574
 A:Accession: A60400
 A:Molecule type: protein
 A:Residues: 30-43 <YAM>
 R:Hitano, T.; Taga, T.; Yasukawa, K.; Nakajima, K.; Nakano, N.; Takatsuki, F.; Shimizu, Proc. Natl. Acad. Sci. U.S.A. 84, 228-231, 1987
 A:Title: Human beta-cell differentiation factor defined by an anti-peptide antibody and
 A:Reference number: A29085; MUID:87092370
 A:Accession: A29085
 A:Molecule type: protein
 A:Residues: 29-42 <HIR2>
 R:Noda, M.; Takeda, K.; Sugimoto, H.; Hosoi, T.; Takechi, K.; Hara, T.; Ishikawa, H.; At Anticancer Res. 11, 961-968, 1991
 A:Title: Purification and characterization of human fibroblast derived differentiation f
 A:Reference number: A61159; MUID:91290785
 A:Accession: A61159
 A:Molecule type: protein
 A:Residues: 30-42 <NOD>
 A:Experimental source: fibroblast
 R:Ming, J.E.; Cerretti, C.; Steinman, R.M.; Graneli-Piperno, A.
 J. Mol. Cell. Immunol. 4, 203-212, 1989
 A:Title: Interleukin 6 is the principal cytolytic T lymphocyte differentiation factor fo
 A:Reference number: A61462; MUID:90121567
 A:Accession: A61462
 A:Molecule type: protein
 A:Residues: 28-48 <MIN>
 A:Experimental source: leukocyte-conditioned medium
 R:May, L.T.; Shaw, J.E.; Khanna, A.K.; Zabriskie, J.B.; Sehgal, P.B.
 Cytokine 3, 204-211, 1991
 A:Title: Marked cell-type-specific differences in glycosylation of human interleukin-6.
 A:Reference number: A48419; MUID:91355644
 A:Accession: A48419
 A:Molecule type: protein
 A:Residues: 30-37, 'X', 39-40 <MAV2>
 A:Experimental source: FS-4 fibroblasts

A:Note: sequence extracted from NCBI backbone
 A:Note: this 28-30k form contained both N-linked and O-linked carbohydrate; a 25k for
 A:Accession: C48419
 A:Molecule type: protein
 A:Residues: 28-40 <MAV3>
 A:Experimental source: FS-4 fibroblasts
 A:Note: sequence extracted from NCBI backbone (NCBI:63787)
 A:Note: this 23-25k form contained O-linked but not N-linked carbohydrate
 R:Orita, T.; Oheya, M.; Hasegawa, M.; Kudonawa, H.; Esaki, K.; Ochi, N.
 J. Biochem. 115, 345-350, 1994
 A:Title: Polypeptide and carbohydrate structure of recombinant human interleukin-6 pr
 A:Reference number: JX0305; MUID:94266765
 A:Contents: annotation; modified sites in recombinant protein from CHO cells
 R:Clagston, C.L.; Boone, T.C.; Crandall, C.; Mendiaz, E.A.; Lu, H.S.
 Arch. Biochem. Biophys. 272, 144-151, 1989
 A:Title: Disulfide structures of human interleukin-6 are similar to those of human gr
 A:Reference number: S04981; MUID:89286115
 A:Contents: annotation; disulfide bonds in recombinant protein
 R:Rock, F.L.; Li, X.; Chong, P.; Ida, N.; Klein, M.
 Biochemistry 33, 5146-5154, 1994
 A:Title: Roles of disulfide bonds in recombinant human interleukin 6 conformation.
 A:Reference number: A54253; MUID:94227044
 A:Contents: annotation; lability and functional significance of each disulfide bond
 C:Comment: Produced by both lymphoid and nonlymphoid tissue in response to growth fac
 C:Comment: This protein plays a regulatory role in various host defense mechanisms an
 C:Genetics:
 A:Gene: GDB:IL6
 A:Cross-references: GDB:120748; OMIM:147620
 A:Map position: 7p21-7p21
 A:Introns: 7/1; 70/3; 108/3; 157/3
 C:Superfamily: Interleukin-6
 C:Keywords: Castleman's disease; cytokine; extracellular protein; glycoprotein; growt
 F:1-27/Domain: signal sequence #status predicted <SIG>
 F:28-212/Product: interleukin-6, long form #status experimental <MNTL>
 F:30-212/Product: interleukin-6, short form #status experimental <MATS>
 F:72-78, 101-111/Disulfide bonds: #status experimental
 F:77/Binding site: carbohydrate (ASN) (covalent) (partial) #status experimental
 F:166/Binding site: carbohydrate (THR) (covalent) (partial) #status experimental
 F:172/Binding site: carbohydrate (ASN) (covalent) #status predicted

Query Match 100.0%; Score 88; DB 1; Length 212;
 Best Local Similarity 100.0%; Pred. No. 5.5e-07;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 ILRSFKFLQSSLRALRQM 19
 |||
 Db 194 ILRSFKFLQSSLRALRQM 212

RESULT 2
 146621
 C:Species: Sus scrofa domestica (domestic pig)
 C:Date: 21-Feb-1997 #sequence, revision 21-Feb-1997 #text, change 16-Jul-1999
 C:Accession: 146621
 R:Richards, C.; Saklatva, J.
 Cytokine 3, 269-276, 1991
 A:Title: Molecular Cloning and Sequence of Porcine Interleukin 6 cDNA and Expression
 A:Reference number: 146621; MUID:91338547
 A:Accession: 146621
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-212 <RIC>
 A:Cross-references: GB:M86722; NID:g164624; PIDN:AAC37333.1; PID:g164625
 C:Genetics:
 A:Gene: IL6
 C:Superfamily: Interleukin-6

Query Match 67.0%; Score 59; DB 2; Length 212;
 Best Local Similarity 66.4%; Pred. No. 0.029;

Matches 13; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 ILRSFKFLOSSLRALROM 19
 |||| ::||| ||||:| |
 Db 194 ILRSLEDFLOFSLRIRIM 212

RESULT 3
 146590
 Interleukin 6 - pig
 C:Species: Sus scrofa domestica (domestic pig)
 C>Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 16-Jul-1999
 C:Accession: I46590
 R:Matlialagan, N.; Bixby, J.; Roberts, M.R.
 Mol. Reprod. Dev. 32, 324-330, 1992
 A:Title: Expression of Interleukin-6 in porcine, ovine, and bovine preimplantation conce
 A:Reference number: I46590; MUID:92360284
 A:Accession: I46590
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-212 <MAT>
 A:Cross-references: GB:M0258; NID:q164514; PIDN:AAC27127.1; PID:q164515
 C:Genetics:
 A:Gene: IL-6
 C:Superfamily: Interleukin-6

Query Match 67.0%; Score 59; DB 2; Length 212;
 Best Local Similarity 68.4%; Pred. No. 0.029;
 Matches 13; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 ILRSFKFLOSSLRALROM 19
 |||| ::||| ||||:| |
 Db 194 ILRSLEDFLOFSLRIRIM 212

RESULT 4
 T09216
 Interleukin-6 precursor - horse
 C:Species: Equus caballus (domestic horse)
 C>Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 23-Jul-1999
 C:Accession: T09216
 R:Swiderski, C.E.; Horohov, D.W.
 submitted to the EMBL Data Library, July 1996
 A:Reference number: Z16613
 A:Accession: T09216
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-208 <SWI>
 A:Cross-references: EMBL:U64794; NID:g2654387; PID:g2654388
 C:Genetics:
 A:Gene: IL-6
 C:Superfamily: Interleukin-6
 C:Keywords: cytokine; growth factor

Query Match 65.9%; Score 58; DB 2; Length 208;
 Best Local Similarity 68.4%; Pred. No. 0.041;
 Matches 13; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 ILRSFKFLOSSLRALROM 19
 |||| ::||| ||||:| |
 Db 190 ILRSLEDFLOFSLRIRIM 208

RESULT 5
 A56610
 Interleukin-6 precursor - bovine
 C:Species: Bos primigenius taurus (cattle)
 C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C:Accession: A56610; S22162
 R:Diogoamans, L.; Cludts, I.; Cleuter, Y.; Kettmann, R.; Bury, A.
 DNA Seq. 2, 411-413, 1992

A:Title: Nucleotide sequence of bovine Interleukin-6 cDNA.
 A:Reference number: A56610; MUID:93076003
 A:Accession: A56610
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-208 <DRO>
 A:Cross-references: EMBL:X57317; NID:q2193; PIDN:CAA40572.1; PID:q2194
 A:Experimental source: BLV induced B cell-Lymphosarcoma
 A>Note: sequence extracted from NCBI backbone (NCBI:118917)
 C:Superfamily: Interleukin-6
 C:Keywords: cytokine

Query Match 59.1%; Score 52; DB 1; Length 208;
 Best Local Similarity 64.7%; Pred. No. 0.39;
 Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 ILRSFKFLOSSLRALR 17
 |||| ::||| ||||:| |
 Db 190 ILRNLENFLOFSLRIR 206

RESULT 6
 S29549
 Interleukin-6 - sheep
 C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
 C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C:Accession: S29549
 R:Ebrahim, B.
 submitted to the EMBL Data Library, October 1992
 A:Reference number: S29549
 A:Accession: S29549
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-208 <EBR>
 A:Cross-references: EMBL:X68723
 C:Superfamily: Interleukin-6

Query Match 56.8%; Score 50; DB 1; Length 208;
 Best Local Similarity 64.7%; Pred. No. 0.82;
 Matches 11; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 ILRSFKFLOSSLRALR 17
 |||| ::||| ||||:| |
 Db 190 ILRSLENFLOFSLRIR 206

RESULT 7
 ICM56
 Interleukin-6 precursor - mouse
 A:Alternate names: B-cell hydridoma growth factor; B-cell stimulating factor 2; hepat
 acytoma growth factor
 C:Species: Mus musculus (house mouse)
 C>Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 22-Jun-1999
 C:Accession: A30531; A27610; A30571; S01323; S12103; E34047; A26662; A40486; A60799;
 R:Ranabe, O.; Akira, S.; Kamya, T.; Wong, G.G.; Hirano, T.; Kishimoto, T.
 J. Immunol. 141, 3875-3881, 1988
 A:Title: Genomic structure of the murine IL-6 gene. High degree conservation of poten
 A:Reference number: A30531; MUID:89035525
 A:Accession: A30531
 A:Molecule type: DNA
 A:Residues: 1-211 <TAN>
 A:Cross-references: GB:M20572; NID:q198369; PIDN:AAA39302.1; PID:q387386
 R:Van Snick, J.; Cayphas, S.; Szikora, J.P.; Renauld, J.C.; Van Roost, E.; Boon, T.;
 Eur. J. Immunol. 18, 193-197, 1988
 A:Title: CDNA cloning of murine interleukin-HP1: homology with human interleukin 6.
 A:Reference number: A27610; MUID:88166883
 A:Accession: A27610
 A:Molecule type: mRNA
 A:Residues: 1-211 <VAN>
 A:Cross-references: GB:X06203; NID:q52701; PIDN:CAA39560.1; PID:q52702
 R:Mock, B.A.; Nordan, R.P.; Justice, M.J.; Kozak, C.; Jenkins, N.A.; Copeland, N.G.;

J. Immunol. 142, 1372-1376, 1989
 A:Title: The murine IL-6 gene maps to the proximal region of chromosome 5.
 A:Reference number: A30571; MUID:89124383
 A:Accession: A30571
 A:Molecule type: mRNA
 A:Residues: 5'211 <MOC>
 A:Cross-references: GB:24221; NID:9341131; PIDN:AAA6814.1; PID:9870699
 R:Simpson, R.J.; Moritz, R.L.; Rubira, M.R.; Van Snick, J.
 Eur. J. Biochem. 176, 187-197, 1988
 A:Title: Murine hybridoma/plasmacytoma growth factor. Complete amino-acid sequence and
 A:Reference number: S01323; MUID:88329059
 A:Accession: S01323
 A:Molecule type: protein
 A:Residues: 25-166, 'X', 168-211 <STM>
 A:Note: the sequence from Fig. 11 is inconsistent with that from Fig. 10 in having 103-A
 R:Grenett, H.E.; Fuentes, N.L.; Fuller, G.M.
 Nucleic Acids Res. 18, 6455, 1990
 A:Title: Cloning and sequence analysis of the cDNA for murine Interleukin-6.
 A:Reference number: S12103; MUID:91057159
 A:Accession: S12103
 A:Molecule type: mRNA
 A:Residues: 1-211 <GRE>
 A:Cross-references: EMBL:X54542; NID:952727; PIDN:CA38411.1; PID:952728
 R:Zhang, W.; Ward, L.D.; Reid, G.E.; Moritz, R.L.; Simpson, R.J.
 Biochem. Biophys. Res. Commun. 166, 139-145, 1990
 A:Title: Internal amino acid sequencing of proteins by in situ cyanogen bromide cleavage
 A:Reference number: A90157; MUID:90147691
 A:Accession: E34047
 A:Molecule type: protein
 A:Residues: 66-69, 'X', 71-75, 78-94, 128-148 <AS>
 R:Van Snick, J.; Cayphas, S.; Vink, A.; Uytendhoeve, C.; Coulle, P.G.; Rubira, M.R.; Simp
 Proc. Natl. Acad. Sci. U.S.A. 83, 9679-9683, 1986
 A:Title: Purification and NH2-terminal amino acid sequence of a T-cell-derived lymphokine
 A:Reference number: A26662; MUID:87092311
 A:Accession: A26662
 A:Molecule type: protein
 A:Residues: 25-39, 'X', 41-42, 'X', 44-45 <VSN>
 R:Chiu, C.P.; Moulds, C.; Coffman, R.L.; Rennick, D.; Lee, F.
 Proc. Natl. Acad. Sci. U.S.A. 85, 7099-7103, 1988
 A:Title: Multiple biological activities are expressed by a mouse Interleukin 6 cDNA clon
 A:Reference number: A40486; MUID:89017145
 A:Accession: A40486
 A:Molecule type: mRNA
 A:Residues: 1-211 <CHI>
 A:Cross-references: GB:003783; NID:9198367; PIDN:AAA39301.1; PID:9309410
 R:Shabo, Y.; Lotem, J.; Rubinstein, M.; Revel, M.; Clark, S.C.; Wolf, S.F.; Kamen, R.; S
 Blood 72, 2070-2073, 1988
 A:Title: The myeloid blood cell differentiation-inducing protein MGI-2A is interleukin-6
 A:Reference number: A60799; MUID:89062753
 A:Accession: A60799
 A:Molecule type: protein
 A:Residues: 77-98 <SHA>
 R:Blankenstein, T.; Qin, Z.; Li, W.; Diamantstein, T.
 J. Exp. Med. 171, 965-970, 1990
 A:Title: DNA rearrangement and constitutive expression of the Interleukin 6 gene in a m
 A:Reference number: S10241; MUID:90171860
 A:Accession: S10241
 A:Molecule type: DNA
 A:Residues: 1-6 <BLA>
 A:Cross-references: EMBL:X51457; NID:949738; PIDN:CA35824.1; PID:9581860
 R:Zhang, J.G.; Reid, G.E.; Moritz, R.L.; Ward, L.D.; Simpson, R.J.
 Eur. J. Biochem. 217, 53-59, 1993
 A:Title: Specific covalent modification of the tryptophan residues in murine interleukin
 A:Reference number: S38254; MUID:94039075
 A:Accession: S38254
 A:Molecule type: protein
 A:Status: preliminary
 A:Residues: 38-60; 75, 'X', 77-79, 176-203 <ZHA>
 C:Genetics:
 A:Gene: IL-6
 A:Map position: 5
 A:Introns: 7/1; 68/3; 106/3; 156/3

C:Superfamily: Interleukin-6
 C:Keywords: Castleman's disease; cytokine; growth factor; Immunoregulation; lymphokine
 F:1.24/Domain: signal sequence #status predicted <Sig>
 F:25-211/Product: Interleukin-6 #status experimental <Mat>
 Query Match 55.78; Score 49; DB 1; Length 211;
 Best Local Similarity 55.68; Pred. No. 1.2;
 Matches 10; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
 QY 1 ILRSFKEFLQSSLRALRQ 18
 |||:||||:||||:|
 Db 193 ILKSLEFLKVTLRSTQ 210
 RESULT 8
 A42247
 myelomonocytic growth factor precursor - chicken
 N:Alternate names: colony-stimulating factor CMGF
 C:Species: Gallus gallus (chicken)
 C:Date: 16-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 16-Jul-1999
 C:Accession: A42247; S03633
 R:Sternneck, E.; Blatner, C.; Graf, T.; Leutz, A.
 Mol. Cell. Biol. 12, 1728-1735, 1992
 A:Title: Structure of the chicken myelomonocytic growth factor gene and specific acti
 A:Reference number: A42247; MUID:92195319
 A:Accession: A42247
 A:Molecule type: DNA
 A:Status: preliminary
 A:Residues: 1-201 <STE>
 A:Note: Sequence extracted from NCBI backbone (NCBIN:89832, NCBIPI:89836)
 R:Leutz, A.; Damm, K.; Sternneck, E.; Kowenz, E.; Ness, S.; Frank, R.; Gausepohl, H.;
 EMBO J. 8, 175-181, 1989
 A:Title: Molecular cloning of the chicken myelomonocytic growth factor (CMGF) reveals
 A:Reference number: S03633; MUID:89231616
 A:Accession: S03633
 A:Molecule type: mRNA
 A:Residues: 1-201 <LEU>
 A:Cross-references: EMBL:X14477; NID:963596; PIDN:CA32639.1; PID:963597
 C:Superfamily: Interleukin-6
 C:Keywords: glycoprotein
 F:1.23/Domain: signal sequence #status predicted <Sig>
 F:24-201/Product: myelomonocytic growth factor #status predicted <Mat>
 F:123,137/Binding site: carbohydrate (Asn) (covalent) #status predicted
 Query Match 54.58; Score 48; DB 2; Length 201;
 Best Local Similarity 47.48; Pred. No. 1.7;
 Matches 9; Conservative 6; Mismatches 4; Indels 0; Gaps 0;
 QY 1 ILRSFKEFLQSSLRALRQ 19
 |||:||||:||||:|
 Db 180 ILANQRFLEAYRALRL 198
 RESULT 9
 H81982
 hypothetical protein NMA0631 [imported] - Neisseria meningitidis (strain 22491 serogr
 C:Species: Neisseria meningitidis
 C:Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
 C:Accession: H81982
 R:Parkhill, J.; Achtman, M.; James, X.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Mo
 R; Holroyd, S.; Jørgensen, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandre
 Nature 404, 502-506, 2000
 A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis 22491
 A:Reference number: A81775; MUID:20222556
 A:Accession: H81982
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-1082 <PAR>
 A:Cross-references: GB:AL162753; GB:AL157959; NID:97379120; PIDN:CA83920.1; PID:9737
 A:Experimental source: serogroup A, strain 22491
 C:Genetics:

A:Gene: MMA0631
C:Superfamily: Neisseria meningitidis hypothetical protein MMA0631

Query Match 51.1%; Score 45; DB 2; Length 1082;
Best Local Similarity 56.2%; Pred. No. 30;
Matches 9; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

OY 4 SFPEFLOSSLRALRQ 19
DB 416 SPDKFVQISLKALRK 431

RESULT 10

Interleukin 6 - cat
C:Species: Felis silvestris catus (domestic cat)
C:Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 16-Jul-1999
C:Accession: I46084
R:Bradley, W.G.; Gibbs, C.; Kraus, L.; Good, R.A.; Day, N.K.
Proc. Soc. Exp. Biol. Med. 204, 301-305, 1993
A:Title: Molecular cloning and characterization of a cDNA encoding feline interleukin-6.
A:Reference number: I46084; MUID:94052249
A:Accession: I46084
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-207

A:Cross-references: GB:I46914; NID:9438519; PIDN:AAA16620.1; PID:9438520
C:Superfamily: Interleukin-6

Query Match 50.0%; Score 44; DB 2; Length 207;
Best Local Similarity 55.6%; Pred. No. 7; 7;
Matches 10; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

OY 2 LRSFKEFIQSSLRALRQ 19
DB 190 LRRLDFQLRLRAVRIM 207

RESULT 11

A34247
Interleukin-6 precursor - rat
N:Alternate names: IL-6
C:Species: Rattus norvegicus (Norway rat)
C:Date: 15-Jun-1990 #sequence_revision 15-Jun-1990 #text_change 16-Jul-1999
C:Accession: A34247
R:Northmann, W.; Braciak, T.A.; Hattori, M.; Lee, F.; Fey, G.H.
J. Biol. Chem. 264, 16072-16082, 1989
A:Title: Structure of the rat interleukin 6 gene and its expression in macrophage-derive
A:Reference number: A34247; MUID:89380206
A:Accession: A34247
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-211 <NR>
A:Cross-references: GB:M26744; NID:9204915; PIDN:AAA77659.1; PID:9204916
C:Superfamily: Interleukin-6
C:Keywords: cytokine; growth factor; immunoregulation; lymphokine; macrophage

Query Match 50.0%; Score 44; DB 2; Length 211;
Best Local Similarity 44.4%; Pred. No. 7; 8;
Matches 8; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

OY 1 IIRSFKEFIQSSLRALRQ 18
DB 193 IIRSFKEFIQSSLRALRQ 210

RESULT 12

T08597
C:Species: Klebsiella oxytoca

C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C:Accession: T08597
R:Mori, K.; Tobimatsu, T.; Hara, T.; Toriya, T.

J. Biol. Chem. 272, 32034-32041, 1997
A:Title: Characterization, sequencing, and expression of the genes encoding a reactiv
A:Reference number: Z16448; MUID:98070363
A:Accession: T08597
A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA
A:Residues: 1-610 <NR>
A:Cross-references: EMBL:AF017781; NID:93115375; PIDN:AA015871.1; PID:93115376
A:Experimental source: strain ATCC 8724
C:Genetics:
A:Gene: ddra

C:Function:
A:Description: probably a reactivating factor for inactivated diol dehydratase
A:Note: large chain
C:Superfamily: Klebsiella oxytoca diol dehydratase-reactivating factor large chain

Query Match 50.0%; Score 44; DB 2; Length 610;
Best Local Similarity 57.1%; Pred. No. 24;
Matches 12; Conservative 4; Mismatches 3; Indels 2; Gaps 1;

OY 1 IIRSFKE--FIQSSLRALRQ 19
DB 520 IIRSAKERVVTNALRALRQV 540

RESULT 13

T40803
probable pre-tRNA nuclear export receptor - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C:Accession: T40803
R:Beck, A.; Reinhardt, R.; Lyne, M.; Rajandream, M.A.; Bartell, B.G.
submitted to the EMBL Data Library, October 1998
A:Reference number: Z21949
A:Accession: T40803
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-978 <BEC>
A:Cross-references: EMBL:AL032684; PIDN:CAA21794.1; GSPDB:GNO0067; SPDB:SPBP8B7.09C
A:Experimental source: strain 97zh-; clone pl p8B7
C:Genetics:
A:Gene: SPDB:SPBP8B7.09C
A:Map position: 2

Query Match 50.0%; Score 44; DB 2; Length 978;
Best Local Similarity 53.3%; Pred. No. 39;
Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

OY 3 RSFKEFIQSSLRALR 17
DB 960 RSFKEFIQSSLRALR 974

RESULT 14

T02866
hypothetical protein CAK2 [imported] - Leishmania major (strain Friedlin)
C:Species: Leishmania major
C:Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 19-May-2000
C:Accession: F81464; T02866
R:Myler, P.J.; Audleman, L.; devos, T.; Hixson, G.; Kiser, P.; Lemley, C.; Magness, C
Proc. Natl. Acad. Sci. U.S.A. 96, 2902-2906, 1999
A:Title: Leishmania major Friedlin chromosome 1 has an unusual distribution of protei
A:Reference number: A81455; MUID:99178987
A:Accession: F81464
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1159 <PVL>
A:Cross-references: GB:AE001274; NID:93264850; PIDN:AAC24689.1; PID:93006218; GSPDB:G

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OM protein - protein search, using sw model

Run on: December 19, 2001, 16:26:13 ; Search time 48.45 Seconds
(without alignments)
14.378 Million cell updates/sec

Title: US-09-202-104A-3
Perfect score: 88
Sequence: 1 ILRSKFELQSLRALRQM 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39:*

Prod. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	88	100.0	212	1 IL6_CERTO	P46650 cercocebus
2	88	100.0	212	1 IL6_HUMAN	P05331 homo sapien
3	88	100.0	212	1 IL6_MACFA	P79341 macaca fasc
4	85	96.6	212	1 IL6_MACMA	P51494 macaca mulia
5	59	67.0	125	1 IL6_MUSVI	P41693 mustela vis
6	59	67.0	212	1 IL6_PIG	P26893 sus scrofa
7	58	65.9	207	1 IL6_CANFA	P41823 canis fami
8	58	65.9	208	1 IL6_HORSE	Q95181 equus cabal
9	58	65.9	209	1 IL6_PHOVI	Q28819 phoca vitul
10	55	62.5	205	1 IL6_ORCOR	Q28747 orcinus orc
11	55	62.5	208	1 IL6_CAPHI	Q28319 capra hircu
12	55	62.5	208	1 IL6_SHEEP	P29455 ovis aries
13	52	59.1	208	1 IL6_BOVIN	P26892 bos taurus
14	51	58.0	207	1 IL6_MARMO	Q35736 marmota mon
15	49	55.7	208	1 IL6_FELCA	P41683 felis silve
16	49	55.7	211	1 IL6_MOUSE	P08505 mus muscula
17	48	54.5	201	1 MGF_CHICK	P13654 gallus gall
18	44	50.0	211	1 IL6_RAT	P20607 rattus norv
19	41	46.6	249	1 Y927_METJA	O58337 methanococc
20	41	46.6	310	1 ADPR_LACLA	Q06715 lactococcus
21	41	46.6	310	1 ADPR_LACLA	P23677 homo sapien
22	40	45.5	271	1 YDIO_ECOLI	P76610 escherichia
23	40	45.5	3210	1 TRMU_HUMAN	P49454 homo sapien
24	39	44.3	371	1 TRMU_HUMAN	O9k4f2 bacillus ha
25	39	44.3	483	1 GLYC_RABIT	P07511 oryctolagus
26	39	44.3	566	1 Y397_MYCGE	P47637 mycoplasma
27	39	44.3	635	1 HS68_DROME	O97125 drosophila
28	39	44.3	638	1 HS70_CERCA	P91302 ceratitlis c
29	39	44.3	640	1 HS71_ANOAL	P41825 anopheles a
30	39	44.3	640	1 HS72_ANOAL	P41826 anopheles a
31	39	44.3	641	1 HS72_DROME	P02824 drosophila
32	39	44.3	642	1 HS70_DROME	P82910 drosophila
33	39	44.3	643	1 HS71_DROME	P02825 drosophila

34	39	44.3	649	1 HS70_CHLRE	P25840 chlamydomon
35	39	44.3	1051	1 CARB_SULSO	Q59969 sulfolobus
36	39	44.3	1161	1 L2GL_DROME	P08111 drosophila
37	39	44.3	1166	1 L2GL_DROPS	Q08470 drosophila
38	39	44.3	3744	1 YHP9_YEAST	P38811 saccharomyc
39	38	43.2	162	1 IL15_MOUSE	P48346 mus musculu
40	38	43.2	329	1 IPNS_STRJU	P18286 streptomyce
41	38	43.2	347	1 YP66_MYCPN	P75194 mycoplasma
42	38	43.2	558	1 FACC_HUMAN	Q00597 homo sapien
43	38	43.2	1967	1 YG50_YEAST	P53327 saccharomyc
44	38	43.2	3038	1 TRIO_HUMAN	O75962 homo sapien
45	37	42.0	119	1 R18E_SULSO	P95990 sulfolobus

ALIGNMENTS

```

RESULT 1
IL6_CERTO
ID IL6_CERTO STANDARD: PRT; 212 AA.
AC P46650;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE INTERLEUKIN-6 PRECURSOR (IL-6).
GN IL6.
OS Cercocebus torquatus atys (Red-crowned mangabey) (Sooty mangabey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Cercocebus.
OX NCBI_TaxID=9531;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FUJ;
RX MEDLINE=96003435; PubMed=7561102;
RA Villinger F.J., Brar S.S., Mayne A.E., Chikkala N., Ansari A.A.;
RT "Comparative sequence analysis of cytokine genes from human and
RT nonhuman primates.";
RL J. Immunol. 155:3946-3954(1995).
CC -I- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
CC FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
CC OF B-CELLS INTO IG-SECRETING CELLS. IT INDUCES MYELOMA AND
CC PLASMACYTOMA GROWTH. IT INDUCES NERVE CELLS DIFFERENTIATION, IN
CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS (BY SIMILARITY).
CC -I- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
CC
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CC
DR EMBL: L26037; AAA99972.1; -
DR HSSP: P05231; IAU.
DR InterPro: IPR003573; IL6_MGF_GCSF.
DR InterPro: IPR003574; Interleukin_6.
DR Pfam: PF00489; IL6; 1.
DR PRINTS: PRO0433; IL6GSEMGF.
DR PRINTS: PRO0434; INTERLEUKIN6.
DR ProDom: PD004356; Interleukin_6; 1.
DR SMART: SM00126; IL6; 1.
DR PROSITE: PS00254; INTERLEUKIN_6; 1.
KW Cytokine; Glycoprotein; Growth factor; Signal.
KW SIGNAL.
FT CHAIN 1 29 BY SIMILARITY.
FT DISULFID 30 212 INTERLEUKIN-6.
FT DISULFID 72 78 POTENTIAL.
FT DISULFID 101 111 POTENTIAL.
FT CARBOHYD 73 73 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 172 172 N-LINKED (GLCNAC...) (POTENTIAL).
SQ
SEQUENCE 212 AA; 2366 MW; C73C035226B44B9F CRC64;

```

Query Match 100.0%; Score 88; DB 1; Length 212;
 Best Local Similarity 100.0%; Pred. No. 2.9e-07;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 ILRSKFELSSLRALRQM 19
 |||||
 Db 194 ILRSKFELSSLRALRQM 212

RESULT 2
 IL6_HUMAN STANDARD; PRT; 212 AA.
 AC POS231;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE INTERLEUKIN-6 PRECURSOR (IL-6) (B-CELL STIMULATORY FACTOR 2) (BSF-2)
 DE (INTERFERON BETA-2) (HBRIDOMA GROWTH FACTOR).
 GN IL6 OR IFNB2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. AND PARTIAL SEQUENCE.
 RX MEDLINE=87065033; PubMed=3491322;
 RA Hirano T., Yasukawa K., Harada H., Taya T., Watanabe Y., Matsuda T.,
 RA Sakiyama S.-I., Nakajima K., Koyama K., Iwamatsu A., Tsunasawa S.,
 RA Sakiyama F., Matsui H., Takahara Y., Taniguchi T., Kishimoto T.,
 RT "Complementary DNA for a novel human interleukin (BSF-2) that induces
 RT B lymphocytes to produce immunoglobulin.";
 RL Nature 324:73-76(1986).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88082664; PubMed=3500852;
 RA Yasukawa K., Hirano T., Watanabe Y., Muratani K., Matsuda T.,
 RA Nakai S., Kishimoto T.,
 RT "Structure and expression of human B cell stimulatory factor-2
 RT (BSF-2/IL-6) gene.";
 RL EMBO J. 6:2939-2945(1987).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87067433; PubMed=3538015;
 RA May L.T., Helfgott D.C., Sehgal P.B.,
 RT "Anti-beta-interferon antibodies inhibit the increased expression of
 RT HLA-B7 mRNA in tumor necrosis factor-treated human fibroblasts:
 RT structural studies of the beta 2 interferon involved.";
 RL Proc. Natl. Acad. Sci. U.S.A. 83:8957-8961(1986).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87053818; PubMed=3023045;
 RA Zilberstein A., Ruggieri R., Korn J.H., Revel M.,
 RT "Structure and expression of cDNA and genes for human
 RT Interferon-beta-2, a distinct species inducible by growth-stimulatory
 RT cytokines.";
 RL EMBO J. 5:2529-2537(1986).
 RN [5]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88088768; PubMed=3320204;
 RA Brakenhoff J.P.J., de Groot E.R., Evers R.F., Pannekoek H.,
 RA Aarden L.A.,
 RT "Molecular cloning and expression of hybridoma growth factor in
 RT Escherichia coli.";
 RL J. Immunol. 139:4116-4121(1987).
 RN [6]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89391958; PubMed=2789513;
 RA Tonouchi N., Miwa K., Karasuyama H., Matsui H.,
 RT "Deletion of 3' untranslated region of human BSF-2 mRNA causes
 RT stabilization of the mRNA and high-level expression in mouse NIH3T3
 RT cells.";
 RL Biochem. Biophys. Res. Commun. 163:1056-1062(1989).

RN [7]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Fibroblast;
 RX MEDLINE=87004683; PubMed=3758081;
 RA Heegeman G., Content J., Volckaert G., Derynck R., Tavernier J.,
 RA Fiers W.,
 RT "Structural analysis of the sequence coding for an inducible 26-kDa
 RT protein in human fibroblasts.";
 RL Eur. J. Biochem. 159:625-632(1986).
 RN [8]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89193317; PubMed=3266463;
 RA Wong G., Witek-Giannotti J., Hewick R., Clark S., Ogawa M.,
 RT "Interleukin 6: Identification as a hematopoietic colony-stimulating
 RT factor.";
 RL Behring Inst. Mitt. 83:40-47(1988).
 RN [9]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93178270; PubMed=1291290;
 RA Chen Q.Y.,
 RT "Stable and efficient expression of human interleukin-6 cDNA in
 RT mammalian cells after gene transfer.";
 RL Chung-Hua Chung Liu Tsa Chih 14:340-344(1992).
 RN [10]
 RP SEQUENCE OF 30-63.
 RX MEDLINE=88154445; PubMed=3279116;
 RA van Damme J., van Beeumen J., Decock B., van Snick J., de Ley M.,
 RA Billiau A.,
 RT "Separation and comparison of two monokines with
 RT lymphocyte-activating factor activity: IL-1 beta and hybridoma growth
 RT factor (NGF). Identification of leukocyte-derived NGF as IL-6.";
 RL J. Immunol. 140:1534-1541(1988).
 RN [11]
 RP SEQUENCE OF 50-212 OF RECOMBINANT FORM LACKING 1ST DISULFIDE BOND.
 RX MEDLINE=95154344; PubMed=7851440;
 RA Breton J., la Faura A., Bertolero F., Orsini G., Valsasina B.,
 RA Ziliocto R., de Filippis V., Polverino de Laureto P., Pontana A.,
 RT "Structure, stability and biological properties of a N-terminally
 RT truncated form of recombinant human interleukin-6 containing a single
 RT disulfide bond.";
 RL Eur. J. Biochem. 227:573-581(1995).
 RN [12]
 RP DISULFIDE BONDS.
 RX MEDLINE=89286115; PubMed=2472117;
 RA Clogston C.L., Boone T.C., Cranall B.C., Mendiaz E.A., Lu H.S.,
 RT "Disulfide structures of human interleukin-6 are similar to those of
 RT human granulocyte colony stimulating factor.";
 RL Arch. Biochem. Biophys. 272:144-151(1989).
 RN [13]
 RP MOTIFGENESIS.
 RX MEDLINE=91243808; PubMed=2037043;
 RA Lietzken C., Krueitgen A., Moeller C., Heinrich P.C., Rose-John S.,
 RT "Evidence for the importance of a positive charge and an
 RT alpha-helical structure of the C-terminus for biological activity of
 RT human IL-6.";
 RL FEBS Lett. 282:265-267(1991).
 RN [14]
 RP STRUCTURE BY NMR.
 RX MEDLINE=96134845; PubMed=8555185;
 RA Nishimura C., Watanabe A., Gode H., Shimada I., Arata Y.,
 RT "Folding topologies of human interleukin-6 and its mutants as studied
 RT by NMR spectroscopy.";
 RL Biochemistry 35:273-281(1996).
 RN [15]
 RP STRUCTURE BY NMR.
 RX MEDLINE=97303053; PubMed=9159484;
 RA Xu G.-Y., Yu H.-A., Hong J., Stahl M., McDonagh T., Kay L.E.,
 RT "Solution structure of recombinant human interleukin-6.";
 RL J. Mol. Biol. 268:468-481(1997).
 RN [16]
 RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
 RX MEDLINE=97224126; PubMed=9118960;

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RA Somers W, Stahl M., Seehra J.S.,
RT "1.9-A crystal structure of interleukin 6: implications for a novel
RT mode of receptor dimerization and signaling.";
RL EMBO J. 16:989-997(1997).
CC
CC -1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
CC FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
CC OF B-CELLS INTO IG-SECRETING CELLS, IT INDUCES MYELOMA AND
CC PLASMACYTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN
CC HEPA2CYTES IT INDUCES ACUTE PHASE REACTANTS.
CC
CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
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CC -----
CC EMBL; X04430; CAA28026.1; -
CC DR EMBL; M14584; AAA52728.1; -
CC DR EMBL; X04602; CAA28268.1; -
CC DR EMBL; Y00081; CAA68278.1; -
CC DR EMBL; M18403; AAA52729.1; -
CC DR EMBL; M29150; AAA59154.1; -
CC DR EMBL; X04402; CAA27990.1; -
CC DR EMBL; X04403; CAA27991.1; -
CC DR EMBL; M54894; AAC41704.1; -
CC DR EMBL; S56892; AAD13886.1; -
CC DR EMBL; A09363; CAA00839.1; -
CC DR PIR; A32648; IVH0B2.
CC DR PIR; A25921; A25921.
CC DR PDB; 1IL6; 04-FEB-98.
CC PDB; 2IL6; 04-FEB-98.
CC PDB; 1ALT; 03-JUN-98.
CC MIM; 147620; -
CC
CC InterPro; IPRO03573; IL6_MGF_GCSF.
CC InterPro; IPRO03574; Interleukin_6.
CC DR Pfam; PF00489; IL6; 1.
CC DR PRINTS; PRO0433; IL6GCSFMGF.
CC DR PRINTS; PRO0434; INTERLEUKIN6.
CC DR PRODOM; PD004356; Interleukin_6; 1.
CC DR SMART; SM00126; IL6; 1.
CC DR PROSITE; PS00254; INTERLEUKIN_6; 1.
CC KW Cytokine; Glycoprotein; Growth factor; Signal; 3D-structure.
CC FT SIGNAL 1 29
CC FT CHAIN 30 212 INTERLEUKIN-6.
CC FT DISULFID 72 78
CC FT DISULFID 101 111
CC FT CARBOHYD 73 73
CC FT MUTAGEN 173 173 A->V; ALMOST NO LOSS OF ACTIVITY.
CC FT MUTAGEN 185 185 W->R; NO LOSS OF ACTIVITY.
CC FT MUTAGEN 204 204 S->P; 13% ACTIVITY.
CC FT MUTAGEN 210 210 R->K,E,Q,T,A,P; LOSS OF ACTIVITY.
CC FT MUTAGEN 212 212 M->I,N,S,R; LOSS OF ACTIVITY.
CC SQ SEQUENCE 212 AA; 23718 MW; 1FED1FEB734079 CRC64;
CC
CC Query Match 100.0%; Score 88; DB 1; Length 212;
CC Best Local Similarity 100.0%; Pred. NO. 2.9e-07;
CC Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC
CC QY 1 ILRSEKFLQSLRALROM 19
CC ||||||||||||||||
CC DB 194 ILRSEKFLQSLRALROM 212
CC
CC RESULT 3
CC IL6_MACFA STANDARD; PRT; 212 AA.
CC AC P79341;
CC DT 15-JUL-1998 (Rel. 36, Created)
CC DT 15-JUL-1998 (Rel. 36, Last sequence update)

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DT 15-JUN-1998 (Rel. 36, last annotation update)
DE INTERLEUKIN-6 PRECURSOR (IL-6).
GN IL6.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecidae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RA Tatsumi M.;
RL submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
CC FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
CC OF B-CELLS INTO IG-SECRETING CELLS, IT INDUCES MYELOID AND
CC PLASMACYTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN
CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
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CC or send an email to license@1sb.ch).
CC -----
DR HSBP; AB000554; BAA19148.1; -.
DR HSSP; P05231; 2IL6
DR InterPro; IPR003573; IL6_MGF_CCSP.
DR InterPro; IPR003574; Interleukin_6.
DR Pfam; PF00489; IL6; 1.
DR PRINTS; PRO0433; IL6GCEFMGF.
DR PRINTS; PRO0434; INTERLEUKIN6.
DR PRODOM; PD004356; Interleukin_6; 1.
DR SMART; SM00126; IL6; 1.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
DR Cytokine; Glycoprotein; Growth factor; Signal.
FT SIGNAL 1 29 BY SIMILARITY.
FT CHAIN 30 212 INTERLEUKIN-6.
FT DISULFD 72 78 POTENTIAL.
FT DISULFD 101 111 POTENTIAL.
FT CARBOHD 73 73 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHD 172 172 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 212 AA; 23654 MW; CFB173FCBF0B0389 CRC64;

Query Match 100.0%; Score 88; DB 1; Length 212;
Best Local Similarity 100.0%; Pred. No. 2,9e-07;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ILRSKFLOSSLRALROM 19
Db 194 ILRSKFLOSSLRALROM 212
|||||

RESULT 4
IL6_MACMU
ID IL6 MACMU STANDARD: PRT: 212 AA.
AC P51494;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, last sequence update)
DT 15-JUN-1998 (Rel. 36, last annotation update)
DE INTERLEUKIN-6 PRECURSOR (IL-6).
GN IL6.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecidae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN-RAC 2;

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RX MEDLINE-96003435; PubMed-7561102;
RA Villinger F.J., Brar S.S., Mayne A.E., Chakkala N., Ansari A.A.;
RT "Comparative sequence analysis of cytokine genes from human and
   nonhuman primates."
RL J. Immunol. 155:3946-3954(1995).
CC -1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
CC FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
CC OF B-CELLS INTO IG-SECRETING CELLS, IT INDUCES MYELOMA AND
CC PLASMACYTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN
CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: L26028; AAA99978.1; -.
DR HSSP: P05231; 1ALU.
DR InterPro: IPR003573; IL6_MGF_GCSF.
DR InterPro: IPR003574; Interleukin_6.
DR Pfam: PF00489; IL6; 1.
DR PRINTS: PR00433; IL6GCSFNGF.
DR PRINTS: PR00434; INTERLEUKIN6.
DR ProDom: PD004356; Interleukin_6; 1.
DR SMART: SM00126; IL6; 1.
DR PROSITE: PS00254; INTERLEUKIN_6; 1.
KW Cytokine; Glycoprotein; Growth factor; Signal.
FT SIGNAL 1 29 BY SIMILARITY.
FT CHAIN 30 212 INTERLEUKIN-6.
FT DISULFID 72 78 POTENTIAL.
FT DISULFID 101 111 POTENTIAL.
FT CARBOHYD 73 73 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 172 172 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 212 AA; 23728 MW; 4130DF0CF0BCAD CRC64;

Query Match 96.64; Score 85; DB 1; Length 212;
Best Local Similarity 94.78; Pred. No. 8.8e-07;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ILRSKFELQSLRALRQM 19
   |||||
DB 194 ILRSKFELQSLRALRQM 212

RESULT 5
IL6_MUSVI STANDARD; PRT; 125 AA.
ID IL6_MUSVI
AC P41693;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE INTERLEUKIN-6 (IL-6) (FRAGMENT).
GN IL6
OS Mustela vison (American mink).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Mustela.
OX NCBI_TaxID=9667;
RN [1]
RP SEQUENCE FROM N.A.
RA Kanno H., Bloom M.E., Perryman S.M., Wolfbarger J.B.;
RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
CC FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
CC OF B-CELLS INTO IG-SECRETING CELLS, IT INDUCES MYELOMA AND
CC PLASMACYTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN
CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS.
CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
CC -----

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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: L34165; AAA96829.1; -.
DR HSSP: P05231; 2IL6.
DR InterPro: IPR003573; IL6_MGF_GCSF.
DR Pfam: PF00489; IL6; 1.
DR SMART: SM00126; IL6; 1.
DR PROSITE: PS00254; INTERLEUKIN_6; 1.
KW Cytokine; Glycoprotein; Growth factor.
FT SIGNAL 1 29 BY SIMILARITY.
FT CHAIN 30 212 INTERLEUKIN-6.
FT DISULFID 72 78 POTENTIAL.
FT DISULFID 101 111 POTENTIAL.
FT CARBOHYD 73 73 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 172 172 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 125 AA; 14604 MW; 8262DD3A989866A CRC64;

Query Match 67.08; Score 59; DB 1; Length 125;
Best Local Similarity 68.44; Pred. No. 0.0078;
Matches 13; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 ILRSKFELQSLRALRQM 19
   |||
DB 107 ILRSKFELQSLRALRQM 125

RESULT 6
IL6_PIG STANDARD; PRT; 212 AA.
ID IL6_PIG
AC P26893;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE INTERLEUKIN-6 PRECURSOR (IL-6).
GN IL6
OS Sus scrofa (pig).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE-91338547; PubMed-1873476;
RA Richards C., Saklatvala J.;
RT "Molecular cloning and sequence of porcine interleukin 6 cDNA and
   expression of mRNA in synovial fibroblasts in vitro."
RL Cytokine 3:269-276(1991).
RN [2]
RP SEQUENCE FROM N.A.
RA MEDLINE-92360284; PubMed-1497880;
RA Mathialagan N., Bixby J.A., Roberts M.R.;
RT "Expression of interleukin-6 in porcine, ovine, and bovine
   preimplantation conceptuses."
RT Mol. Reprod. Dev. 32:324-330(1992).
CC -1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
CC FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
CC OF B-CELLS INTO IG-SECRETING CELLS, IT INDUCES MYELOMA AND
CC PLASMACYTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN
CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS.
CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
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CC -----
DR EMBL: M86722; AAC37333.1; -.
DR EMBL: M80258; AAC27127.1; -.

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DR HSSP; P05231; 1ALU.
 DR InterPro: IPR003573; IL6_MGF_GCSF.
 DR InterPro: IPR003574; Interleukin_6.
 DR Pfam: PF00489; IL6; 1.
 DR PRINTS; PR00433; IL6GCSFMGF.
 DR PRINTS; PR00434; INTERLEUKIN6.
 DR PRODOM; PD004356; Interleukin_6; 1.
 DR SMART; SM00126; IL6; 1.
 DR PROSITE; PS00254; INTERLEUKIN_6; 1.
 DR Cytokine; Glycoprotein; Growth factor; Signal.
 KM SIGNAL 1 29
 FT CHAIN 30 212
 FT DISULFID 72 78
 FT DISULFID 101 111
 FT CONFLICT 30 30
 SQ SEQUENCE 212 AA; 23880 MW; EF100ED030B6FDD0 CRC64;

Query Match 67.0%; Score 59; DB 1; Length 212;
 Best Local Similarity 68.4%; Pred. No. 0.014;
 Matches 13; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 1 IIRSFKEFLQSSLRALROM 19
 |||| :||| |||||
 DB 194 IIRSFLEDFLQSLRAIRIM 212

RESULT 7

IL6_CANFA STANDARD; PRT; 207 AA.

AC P41323;

DT 01-FEB-1995 (Rel. 31, Created)

DT 01-FEB-1995 (Rel. 31, Last sequence update)

DT 15-JUL-1998 (Rel. 36, Last annotation update)

DE INTERLEUKIN-6 PRECURSOR (IL-6).

IL6.

OS Canis familiaris (Dog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Carnivora; Fissipedata; Canidae; Canis.

OX NCBI_TaxID=9615;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=MONGREL;

RX MEDLINE=94303924; PubMed=7913298;

RA Kukeila G.L., Youker K.A., Hawkins H.K., Periard J.L.,

Michael L.H., Ballantyne C.M., Smith C.W., Entman M.L.;

"Regulation of ICAM-1 and IL-6 in myocardial ischemia: effect of

reperfusion.";

RT Ann. N.Y. Acad. Sci. 723:258-270(1994).

RL Ann. N.Y. Acad. Sci. 723:258-270(1994).

-1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL

FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION

OF B-CELLS INTO IG-SECRETING CELLS, IT INDUCES MYELOMA AND

PLASMACYTOMA GROWTH, IT INDUCES ACUTE PHASE REACTANTS, IN

HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS.

-1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.

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DR EMBL; U12234; AAA83030.1; -.

DR HSSP; P05231; 2IL6.

DR InterPro: IPR003573; IL6_MGF_GCSF.

DR InterPro: IPR003574; Interleukin_6.

DR Pfam; PF00489; IL6; 1.

DR PRINTS; PR00433; IL6GCSFMGF.

DR PRINTS; PR00434; INTERLEUKIN6.

DR PRODOM; PD004356; Interleukin_6; 1.

DR SMART; SM00126; IL6; 1.

DR PROSITE; PS00254; INTERLEUKIN_6; 1.
 KM Cytokine; Glycoprotein; Growth factor; Signal.
 FT SIGNAL 1 2
 FT CHAIN 2 207
 FT DISULFID 67 73
 FT DISULFID 96 106
 SQ SEQUENCE 207 AA; 22945 MW; 45540154E9C0F50 CRC64;

Query Match 65.9%; Score 58; DB 1; Length 207;
 Best Local Similarity 68.4%; Pred. No. 0.02;
 Matches 13; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 1 IIRSFKEFLQSSLRALROM 19
 |||| :||| |||||
 DB 189 IIRSFLEDFLQSLRAIRIM 207

RESULT 8

IL6_HORSE STANDARD; PRT; 208 AA.

AC Q95181; O19007; 046568;

DT 01-NOV-1997 (Rel. 35, Created)

DT 15-JUL-1999 (Rel. 38, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE INTERLEUKIN-6 PRECURSOR (IL-6).

IL6.

OS Equus caballus (Horse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.

OX NCBI_TaxID=9796;

RN [1]

RP SEQUENCE FROM N.A.

RA Swiderski C.E., Horohov D.W.;

Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RA Leutenegger C.M., Huder J.B., von Rechenberg B., Akens M., Auer J.;

Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.

RN [3]

RP SEQUENCE FROM N.A.

RA Lai A.C.K.;

"Cloning and expression of equine interleukin-6.";

Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.

-1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL

FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION

OF B-CELLS INTO IG-SECRETING CELLS, IT INDUCES MYELOMA AND

PLASMACYTOMA GROWTH, IT INDUCES ACUTE PHASE REACTANTS, IN

HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS (BY SIMILARITY).

-1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.

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DR EMBL; U64794; AAB87703.1; -.

DR EMBL; AF005227; AAB62246.1; -.

DR EMBL; AF041975; AAC04574.1; -.

DR HSSP; P05231; 1ALU.

DR InterPro: IPR003573; IL6_MGF_GCSF.

DR InterPro: IPR003574; Interleukin_6.

DR Pfam; PF00489; IL6; 1.

DR PRINTS; PR00433; IL6GCSFMGF.

DR PRINTS; PR00434; INTERLEUKIN6.

DR PRODOM; PD004356; Interleukin_6; 1.

DR SMART; SM00126; IL6; 1.

DR PROSITE; PS00254; INTERLEUKIN_6; 1.

DR Cytokine; Glycoprotein; Growth factor; Signal.

FT SIGNAL 1 27

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FT CHAIN 26 208 INTERLEUKIN-6.
FT DISULFID 69 73 BY SIMILARITY.
FT DISULFID 98 108 BY SIMILARITY.
FT CARBOHYD 71 71 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 184 184 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 4 5 LS -> FF (IN REF. 1).
FT CONFLICT 8 8 T -> A (IN REF. 3).
FT CONFLICT 137 137 I -> V (IN REF. 2).
FT CONFLICT 205 205 V -> I (IN REF. 3).
SO SEQUENCE 208 AA: 23325 MW: A62F4C234056BF66 CRC64;

Query Match 65.9%; Score 58; DB 1; Length 208;
Best Local Similarity 68.4%; Pred. No. 0.02;
Matches 13; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 1 ILRSKFELQSLRALRQ 19
    ||| :||| |||:|
DB 190 ILRSLEDFLOSLRAVRIM 208

RESULT 9
ID IL6_PROVI STANDARD; PRT; 209 AA.
AC Q28819;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE INTERLEUKIN-6 PRECURSOR (IL-6) (FRAGMENT).
GN IL6.
OS Phoca vitulina (Harbor seal).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Plinipedia; Phocidae; Phoca.
OX NCBI_TaxID=9720;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96163018; Pubmed=8575817;
RA King D.P., Schrenzel M.D., McKnight M.L., Reidarson T.H., Hanni K.D.,
RA Stott J.L., Ferrick D.A.;
RT "Molecular cloning and sequencing of interleukin 6 cDNA fragments from
RT the harbor seal (Phoca vitulina), killer whale (Orcinus orca), and
RT Southern sea otter (Enhydra lutris nereis).";
RN Immunogenetics 43:190-195(1996).
CC -1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
CC FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
CC OF B-CELLS INTO Ig-SECRETING CELLS, IT INDUCES MYELOMA AND
CC PLASMACYTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN
CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: SECRETED.
CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
CC
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CC
CC EMBL: I46802; AAB01430.1; -
DR HSSP: P05231; 2IL6.
DR InterPro: IPR003573; IL6_MGF_GCSF.
DR InterPro: IPR003574; Interleukin_6.
DR Pfam: PF00489; IL6; 1.
DR SMART: SM00126; IL6; 1.
DR PROSITE: PS00254; INTERLEUKIN_6; 1.
KW Cytokine; Glycoprotein; Growth factor; Signal.
FT SIGNAL <1 26 BY SIMILARITY.
FT CHAIN 27 209 INTERLEUKIN-6.
FT DISULFID 69 75 BY SIMILARITY.
FT DISULFID 98 108 BY SIMILARITY.
SO SEQUENCE 209 AA: 23483 MW: 75144922E43B48E9 CRC64;
```

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Query Match 65.9%; Score 58; DB 1; Length 209;
Best Local Similarity 68.4%; Pred. No. 0.02;
Matches 13; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 1 ILRSKFELQSLRALRQ 19
    ||| :||| |||:|
DB 191 ILRSLEDFLOSLRAVRIM 209

RESULT 10
ID IL6_ORCOR STANDARD; PRT; 205 AA.
AC Q28747;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE INTERLEUKIN-6 PRECURSOR (IL-6) (FRAGMENT).
GN IL6.
OS Orcinus orca (killer whale).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti; Delphinidae;
OC Orcinus.
OX NCBI_TaxID=9733;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96163018; Pubmed=8575817;
RA King D.P., Schrenzel M.D., McKnight M.L., Reidarson T.H., Hanni K.D.,
RA Stott J.L., Ferrick D.A.;
RT "Molecular cloning and sequencing of interleukin 6 cDNA fragments from
RT the harbor seal (Phoca vitulina), killer whale (Orcinus orca), and
RT Southern sea otter (Enhydra lutris nereis).";
RN Immunogenetics 43:190-195(1996).
CC -1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
CC FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
CC OF B-CELLS INTO Ig-SECRETING CELLS, IT INDUCES MYELOMA AND
CC PLASMACYTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN
CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: SECRETED.
CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: I46803; AAB01429.1; -
DR HSSP: P05231; 1ALU.
DR InterPro: IPR003573; IL6_MGF_GCSF.
DR InterPro: IPR003574; Interleukin_6.
DR Pfam: PF00489; IL6; 1.
DR SMART: SM00126; IL6; 1.
DR PROSITE: PS00254; INTERLEUKIN_6; 1.
KW Cytokine; Glycoprotein; Growth factor; Signal.
FT SIGNAL 1 21 BY SIMILARITY.
FT CHAIN 22 205 INTERLEUKIN-6.
FT DISULFID 64 70 BY SIMILARITY.
FT DISULFID 93 103 BY SIMILARITY.
FT CARBOHYD 164 164 N-LINKED (GLCNAC. . .) (POTENTIAL).
SO SEQUENCE 205 AA: 23266 MW: 6308F3A457960832 CRC64;

Query Match 62.5%; Score 55; DB 1; Length 205;
Best Local Similarity 70.6%; Pred. No. 0.059;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 ILRSKFELQSLRALR 17
    ||| :||| |||:|
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Db 187 ILRSLNLFQSLRAIR 203

RESULT 11

ID IL6_CAPRI STANDARD; PRT; 208 AA.

AC Q28319;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 15-JUL-1998 (Rel. 36, Last annotation update)

DE INTERLEUKIN-6 PRECURSOR (IL-6).

GN IL6.

OS Capra hircus (Goat).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Caprinae; Capra.

OC NCBI_TaxID=9925;

OX [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=97392354; PubMed=9250586;

RA Takakura H., Mori Y., Tatsumi M.;

RT Molecular cloning of caprine IL-6 cDNA and its expression in insect cells.

RL Int. Arch. Allergy Immunol. 113:409-416(1997).

CC -1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION OF B-CELLS INTO IG-SECRETING CELLS, IT INDUCES MYELOMA AND HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS.

CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.

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CC -----

DR EMBL: D86589; BAA13118.1; -.

DR HSSP: P05231; 2IL6.

DR InterPro: IPR003573; IL6_MGF_GCSF.

DR InterPro: IPR003574; Interleukin_6.

DR Pfam: PF00489; IL6; 1.

DR PRINTS: PR00433; IL6GCSFNGF.

DR PRINTS: PR00434; INTERLEUKIN6.

DR ProDom: PD004356; Interleukin_6; 1.

DR SMART: SM00126; IL6; 1.

DR PROSITE: PS00254; INTERLEUKIN_6; 1.

DR Cytokine; Glycoprotein; Growth factor; Signal.

KW SIGNAL

FT CHAIN 1 29 BY SIMILARITY.

FT CHAIN 30 208 INTERLEUKIN-6.

FT DISULFID 72 78 BY SIMILARITY.

FT DISULFID 101 111 BY SIMILARITY.

FT CARBOHYD 38 38 N-LINKED (GLCNAC...) (POTENTIAL).

FT CARBOHYD 38 38 N-LINKED (GLCNAC...) (POTENTIAL).

FT CONFLICT 171 171 S -> R (IN REF. 2).

FT CONFLICT 201 201 S -> R (IN REF. 2).

SO SEQUENCE 208 AA; 23423 MW; E92E08BF3E3230A0 CRC64;

Query Match 62.5%; Score 55; DB 1; Length 208;

Best Local Similarity 70.6%; Pred. No. 0.06;

Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 ILRSFKFLQSLRAIR 17

DB 190 ILRSLNLFQSLRAIR 206

RESULT 12

ID IL6_SHEEP STANDARD; PRT; 208 AA.

AC P29455;

DT 01-APR-1993 (Rel. 25, Created)

DT 01-JUN-1994 (Rel. 29, Last sequence update)

DT 15-JUL-1998 (Rel. 36, Last annotation update)

DE INTERLEUKIN-6 PRECURSOR (IL-6).

GN IL6.

OS Ovis aries (Sheep).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Caprinae; Ovis.

OC NCBI_TaxID=9940;

OX [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=94041419; PubMed=8225400;

RA Andrews A.E., Batcham G.J., Ashman K., Meusen E.N.T., Brandon M.R., Nash A.D.;

RT Molecular cloning and characterization of a ruminant interleukin-6 cDNA.

RL Immunol. Cell Biol. 71:341-348(1993).

RL [2]

RP SEQUENCE FROM N.A.

RX Ebrahim B.;

RT Submitted (OCT-1992) to the EMBL/Genbank/DBI databases.

CC -1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION OF B-CELLS INTO IG-SECRETING CELLS, IT INDUCES MYELOMA AND PLASMACYTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS.

CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.

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CC -----

DR EMBL: X62501; CAA44363.1; -.

DR EMBL: X68723; CAA48662.1; -.

DR EMBL: A19159; CAA01443.1; -.

DR PIR: S29549; S29549.

DR HSSP: P05231; 2IL6.

DR InterPro: IPR003573; IL6_MGF_GCSF.

DR InterPro: IPR003574; Interleukin_6.

DR Pfam: PF00489; IL6; 1.

DR PRINTS: PR00433; IL6GCSFNGF.

DR PRINTS: PR00434; INTERLEUKIN6.

DR ProDom: PD004356; Interleukin_6; 1.

DR SMART: SM00126; IL6; 1.

DR PROSITE: PS00254; INTERLEUKIN_6; 1.

DR Cytokine; Glycoprotein; Growth factor; Signal.

KW SIGNAL

FT CHAIN 1 29 BY SIMILARITY.

FT CHAIN 30 208 INTERLEUKIN-6.

FT DISULFID 72 78 BY SIMILARITY.

FT DISULFID 101 111 BY SIMILARITY.

FT CARBOHYD 38 38 N-LINKED (GLCNAC...) (POTENTIAL).

FT CONFLICT 4 4 L -> R (IN REF. 2).

FT CONFLICT 110 110 I -> V (IN REF. 2).

FT CONFLICT 171 171 M -> L (IN REF. 2).

FT CONFLICT 201 201 S -> R (IN REF. 2).

SO SEQUENCE 208 AA; 23446 MW; EEC996C13E3230A0 CRC64;

Query Match 62.5%; Score 55; DB 1; Length 208;

Best Local Similarity 70.6%; Pred. No. 0.06;

Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 ILRSFKFLQSLRAIR 17

DB 190 ILRSLNLFQSLRAIR 206

RESULT 13

ID IL6_BOVIN STANDARD; PRT; 208 AA.

```

AC P26892;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE INTERLEUKIN-6 PRECURSOR (IL-6).
GN IL6.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HOLSTEIN;
RX MEDLINE=93076003; PubMed=1446077;
RA Drocman L., Cluets I., Kleuter Y., Kettmann R., Burny A.;
RT "Nucleotide sequence of bovine Interleukin-6 cDNA."
RL DNA Seq. 2:411-413(1992)
CC -1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
CC FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
CC OF B-CELLS INTO IG-SECRETING CELLS, IT INDUCES MYELOMA AND
CC PLASMACYTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN
CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS.
CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
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CC or send an email to license@isb-sib.ch).
-----
DR EMBL: X57317; CAA40572.1;
DR PIR: S2162; S22162;
DR HSP: P05231; 21L6.
DR InterPro: IPR003573; IL6_MGF_GCSF.
DR InterPro: IPR003574; Interleukin_6.
DR Pfam: PF00489; IL6; 1.
DR PRINTS: PRO0433; IL6GCSFMGF.
DR PRINTS: PRO0434; INTERLEUKIN6.
DR ProDom: PD004356; Interleukin_6; 1.
DR SMART: SM00126; IL6; 1.
DR PROSITE: PS00234; INTERLEUKIN_6; 1.
DR CytoKine: Glycoprotein; Growth factor; Signal.
FT SIGNAL 1 29 BY SIMILARITY.
FT CHAIN 30 208 INTERLEUKIN-6.
FT DISULFID 72 78 BY SIMILARITY.
FT DISULFID 101 111 BY SIMILARITY.
FT CARBOHYD 38 38 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 208 AA; 23758 MW; ADF000B9BA2EC341 CRC64;

Query Match 59.1%; Score 52; DB 1; Length 208;
Best Local Similarity 64.7%; Pred. No. 0.18;
Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 ILRSFKEFLQSSLRALRQ 17
   |||: ||| ||||: |
Db 190 ILRNLENFLQFSLRAIR 206

RESULT 14
ID IL6_MARMO STANDARD; PRT; 207 AA.
AC 035736;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE INTERLEUKIN-6 PRECURSOR (IL-6).
GN IL6.
OS Marmota monax (Woodchuck).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;

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OC Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;
OC Marmota.
NCBI_TaxID=9995;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Periphera blood;
RX MEDLINE=98139533; PubMed=9472070;
RA Lohrenge B., Lu M., Kogendort M.;
RT "Molecular cloning of the woodchuck cytokines: TNF-alpha, IFN-gamma,
RT and IL-6."
RL Immunogenetics 47:332-335(1998).
CC -1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
CC FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
CC OF B-CELLS INTO IG-SECRETING CELLS, IT INDUCES MYELOMA AND
CC PLASMACYTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN
CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
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-----
DR EMBL: Y14139; CAA74571.1;
DR InterPro: IPR003573; IL6_MGF_GCSF.
DR InterPro: IPR003574; Interleukin_6.
DR Pfam: PF00489; IL6; 1.
DR PRINTS: PRO0433; IL6GCSFMGF.
DR PRINTS: PRO0434; INTERLEUKIN6.
DR ProDom: PD004356; Interleukin_6; 1.
DR SMART: SM00126; IL6; 1.
DR PROSITE: PS00254; INTERLEUKIN_6; 1.
DR CytoKine: Glycoprotein; Growth factor; Signal.
FT SIGNAL 1 18 POTENTIAL.
FT CHAIN 19 207 INTERLEUKIN-6.
FT DISULFID 65 71 POTENTIAL.
FT DISULFID 94 104 POTENTIAL.
SQ SEQUENCE 207 AA; 23770 MW; F30D19F86AD6A600 CRC64;

Query Match 58.0%; Score 51; DB 1; Length 207;
Best Local Similarity 55.6%; Pred. No. 0.26;
Matches 10; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 1 ILRSFKEFLQSSLRALRQ 18
   ||: ||| ||||: |
Db 189 ILSNFEDFLQFTLRVVRK 206

RESULT 15
ID IL6_FELCA STANDARD; PRT; 208 AA.
AC P41683;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE INTERLEUKIN-6 PRECURSOR (IL-6).
GN IL6.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94162386; PubMed=8117820;
RA Hasegawa A.;
RA Ohashi T., Matsumoto Y., Watarai T., Goitsuka R., Tsujimoto H.,
RT "Molecular cloning of feline interleukin-6 cDNA."
RL J. Vet. Med. Sci. 55:941-944(1993).
RN [2]

```

RP SEQUENCE FROM N.A.
RC TISSUE=Lymphocytes;
RX MEDLINE=94052249; PubMed=8234373;
RA Bradley W.G., Gibbs C., Kraus L., Good R.A., Day N.K.;
RT "Molecular cloning and characterization of a cDNA encoding feline
interleukin-6.";
RL Proc. Soc. Exp. Biol. Med. 204:301-305(1993).
CC -I- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
CC FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
CC OF B-CELLS INTO IG-SECRETING CELLS. IT INDUCES MYELOMA AND
CC PLASMACYTOMA GROWTH. IT INDUCES NERVE CELLS DIFFERENTIATION, IN
CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS.
CC -I- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
CC -----
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CC -----
DR EMBL: L16914; AAA16620.1; -;
DR EMBL: D13227; BAA02507.1; -;
DR HSSP: P05231; 2IL6.
DR InterPro: IPR003573; IL6_MGF_GCSF.
DR InterPro: IPR003574; Interleukin_6.
DR Pfam: PF00489; IL6; 1. GCSF.
DR PRINTS: PR00433; IL6GCSFMGF.
DR PRINTS: PR00434; INTERLEUKIN6.
DR ProDom: PD004356; Interleukin_6; 1.
DR SMART: SM00126; IL6; 1.
DR PROSITE: PS00254; INTERLEUKIN_6; 1.
DR Cytokine; Glycoprotein; Growth factor; Signal.
KW SIGNAL
FT 1 27
FT CHAIN 28 208
FT DISULFID 68 74
FT DISULFID 97 107
FT CONFLICT 2 2
FT CONFLICT 45 45
FT CONFLICT 133 133
FT CONFLICT 173 187
FT CONFLICT 200 201
FT CONFLICT 23401 MM; 93B4456B2989CA4C CRC64;
SQ SEQUENCE 208 AA; 23401 MM; 93B4456B2989CA4C CRC64;

Query Match 55.7%; Score 49; DB 1; Length 208;
Best Local Similarity 61.1%; Pred. No. 0.56;
Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
QY 2 LRSFKEFLQSLRALRQW 19
11 ::||| ||||| |
DB 191 LRLLEDLFQSLRAVRIM 208

Search completed: December 19, 2001, 16:26:14
Job time: 369 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: December 19, 2001, 16:25:19 ; Search time 157.32 Seconds
(without alignments)
17.666 Million cell updates/sec

Title: US-09-202-104A-3
Perfect score: 88
Sequence: 1 ILRSKFQSSLRALROM 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: SPREMBL_17.*
2: sp.archaea.*
3: sp.bacteria.*
4: sp.fungi.*
5: sp.human.*
6: sp.invertebrate.*
7: sp.mammal.*
8: sp.mhc.*
9: sp.organelle.*
10: sp.phage.*
11: sp.plant.*
12: sp.yeast.*
13: sp.virus.*
14: sp.unclassified.*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	73	83.0	209	6	097540
2	73	83.0	209	6	097540
3	58	65.9	207	6	09MYZ7
4	54	61.4	207	6	028403
5	54	61.4	208	6	09XT80
6	51	58.0	207	11	09JH3
7	49	55.7	94	6	062775
8	47	53.4	118	6	09MZ80
9	47	53.4	118	6	09MZ08
10	47	53.4	118	6	09MZ08
11	47	53.4	118	6	09MZ08
12	45	51.1	210	11	09WV08
13	45	51.1	344	2	050219
14	45	51.1	427	12	09PYT0
15	45	51.1	588	5	016111
16	45	51.1	1082	2	09JYX9
17	44	50.0	108	6	09BDL5
18	44	50.0	610	2	068195
19	44	50.0	610	2	031043

20	44	50.0	772	3	09HGH0	Q9hgh0 clavispura
21	44	50.0	978	3	094258	Q94258 schizosacch
22	43.5	49.4	1159	5	060981	Q60981 leishmania
23	42	47.7	236	5	09YLM0	Q9YLM0 drosophila
24	42	47.7	346	5	062030	Q62030 caenorhabdi
25	42	47.7	539	10	09ASS8	Q9ASS8 arabidopsis
26	42	47.7	643	5	09GSU2	Q9GSU2 drosophila
27	42	47.7	963	10	09LTS0	Q9LTS0 arabidopsis
28	42	47.7	992	4	09MTH6	Q9MTH6 homo sapien
29	42	47.7	1455	4	09UPV0	Q9UPV0 homo sapien
30	41.5	47.2	446	10	09LVA0	Q9LVA0 arabidopsis
31	41	46.6	332	2	0914X0	Q914X0 pseudomonas
32	41	46.6	427	10	09LX06	Q9LX06 arabidopsis
33	41	46.6	482	1	058773	Q58773 methanococc
34	41	46.6	513	2	067854	Q67854 aquifex aeo
35	41	46.6	596	4	09UF06	Q9UF06 homo sapien
36	41	46.6	831	10	065673	Q65673 arabidopsis
37	41	46.6	889	5	09VVG4	Q9VVG4 drosophila
38	41	46.6	991	5	095024	Q95024 dictyosteli
39	41	46.6	1491	10	09LYO2	Q9LYO2 arabidopsis
40	41	46.6	2354	5	024135	Q24135 drosophila
41	41	46.6	2354	5	09VXG8	Q9VXG8 drosophila
42	41	46.6	126	5	09VMH8	Q9VMH8 drosophila
43	40	45.5	154	5	001674	Q01674 acanthocheil
44	40	45.5	175	4	09GHT7	Q9GHT7 homo sapien
45	40	45.5	315	10	09SCQ1	Q9SCQ1 arabidopsis

ALIGNMENTS

RESULT 1
ID 097540 PRELIMINARY; PRT; 209 AA.
AC 097540;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE INTERLEUKIN-6 (FRAGMENT).
GN IL-6.
OS Aotus nancymae (Owl monkey).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotidae; Aotus.
OX NCBI_TaxID=37293;
RN [1]
RP SEQUENCE FROM N.A.
RA Echeverry S.J., Hernandez E., Moreno A., Patarioto M.E., Murillo L.A.;
RT "Identification, cloning and sequencing of different interleukin genes
in 4 Aotus species.";
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF014510; FAD01536.1; -.
DR HSSP: P05231; 1AU.
DR InterPro: IPR003573; IL6_MGF_GCSF.
DR Pfam: PF00489; IL6_1.
DR PRINTS: PR00433; IL6GCSFGF.
DR SMART: SM00126; IL6_1.
DR PROSITE: PS00254; INTERLEUKIN_6; 1.
FT NON_TER 1
FT NON_TER 209
SQ SEQUENCE 209 AA; 23406 MW; E84F085DB84002DD CRC64;

Query Match 83.0%; Score 73; DB 6; Length 209;
Best Local Similarity 100.0%; Pred. No. 0.00056;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ILRSKFQSSLRAL 16
Db 194 ILRSKFQSSLRAL 209
RESULT 2
097TH3

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ID Q9TTH3 PRELIMINARY; PRT; 209 AA.
AC Q9TTH3;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE INTERLEUKIN-6 (FRAGMENT).
GN IL-6.
OS Aotus lemurinus (Northern gray-necked night monkey).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.
OX NCBI_TaxID=43147;
RN [1]
RP SEQUENCE FROM N.A.
RA Morillo L.A., Hernandez E., Echeverry S.J., Mendez J.A.,
RA Patarroyo M.E.;
RT "Aotus lemurinus gene for IL-6."
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF097323; AAF21298.1; -.
DR HSSP: P05231; 1ALU.
DR InterPro: IPR003573; IL6_MGF_GCSF.
DR Pfam: PF00489; IL6; 1.
DR PRINTS: PR00433; IL6GCSFMGF.
DR SMART: SM00126; IL6; 1.
DR PROSITE: PS00254; INTERLEUKIN_6; 1.
FT NON_TER 1
FT NON_TER 209
SQ SEQUENCE 209 AA; 23115 MW; A0A3DFAA4BF560CC CRC64;

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Query Match 83.0%; Score 73; DB 6; Length 209;
Best Local Similarity 100.0%; Pred. No. 0.00056;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ILRSKFELQSLRAL 16
Db 194 ILRSKFELQSLRAL 209

```

```

RESULT 3
ID Q9MYZ7 PRELIMINARY; PRT; 207 AA.
AC Q9MYZ7;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE INTERLEUKIN-6.
GN IL-6.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RA Youn H.-Y., Shin I.-S.;
RT "Canine IL-6 mRNA."
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF275796; AAF86275.1; -.
DR InterPro: IPR003573; IL6_MGF_GCSF.
DR Pfam: PF00489; IL6; 1.
DR PRINTS: PR00433; IL6GCSFMGF.
DR SMART: SM00126; IL6; 1.
DR PROSITE: PS00254; INTERLEUKIN_6; 1.
SQ SEQUENCE 207 AA; 23042 MW; 45541AE011C80F50 CRC64;

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```

Query Match 65.9%; Score 58; DB 6; Length 207;
Best Local Similarity 68.4%; Pred. No. 0.13;
Matches 13; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 1 ILRSKFELQSLRAL 19
Db 189 ILRSLEDFLQSLRAVRIM 207

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RESULT 4
ID Q28403 PRELIMINARY; PRT; 207 AA.
AC Q28403;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE INTERLEUKIN 6 (FRAGMENT).
GN IL-6.
OS Euhydra lutris (Sea otter).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Euhydra.
OX NCBI_TaxID=34882;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=96163018; Pubmed=8575817;
RA King D.P., Schrenzel M.D., McKnight M.L., Reidarson T.H., Hanni K.D.,
RA Stott J.L., Ferrick D.A.;
RT "Molecular cloning and sequencing of interleukin 6 cDNA fragments from
RT the harbor seal (Phoca vitulina), killer whale (Orcinus orca), and
RT Southern sea otter (Euhydra lutris nevels).";
RL Immunogenetics 43:190-195(1996).
DR EMBL: I46804; AAB01428.1; -.
DR HSSP: P05231; 1IL6.
DR InterPro: IPR003573; IL6_MGF_GCSF.
DR Pfam: PF00489; IL6; 1.
DR PRINTS: PR00433; IL6GCSFMGF.
DR SMART: SM00126; IL6; 1.
DR PROSITE: PS00254; INTERLEUKIN_6; 1.
FT NON_TER 1
FT NON_TER 207
SQ SEQUENCE 207 AA; 23527 MW; 729EE0CD91136D8B CRC64;

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Query Match 61.4%; Score 54; DB 6; Length 207;
Best Local Similarity 63.2%; Pred. No. 0.58;
Matches 12; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

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QY 1 ILRSKFELQSLRAL 19
Db 189 ILRLLEDLQSLRAVRIM 207

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RESULT 5
ID Q9XT80 PRELIMINARY; PRT; 208 AA.
AC Q9XT80;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE INTERLEUKIN 6 PRECURSOR.
OS Delphinapterus leucas (Beluga whale).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti;
OC Monodontidae; Delphinapterus.
OX NCBI_TaxID=9749;
RN [1]
RP SEQUENCE FROM N.A.
RA St-Laurent G., De Guise S., Fournier M., Archambault D.;
RT "Molecular cloning and phylogenetic analysis of beluga whale
RT (Delphinapterus leucas) Interleukin 6."
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF076643; AAD42929.1; -.
DR HSSP: P05231; 1ALU.
DR InterPro: IPR003573; IL6_MGF_GCSF.
DR Pfam: PF00489; IL6; 1.
DR PRINTS: PR00433; IL6GCSFMGF.
DR SMART: SM00126; IL6; 1.
DR PROSITE: PS00254; INTERLEUKIN_6; 1.
SQ SEQUENCE 208 AA; 23456 MW; 81CC85C6E80389C4 CRC64;

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```

Query Match 61.4%; Score 54; DB 6; Length 208;

```

Best Local Similarity 70.6%; Pred. No. 0.58;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 IIRSFKEFLQSSLRALR 17
1111 : 111 1111 : 1
DB 190 IIRSFKEFLQSSLRALR 206

RESULT 6

Q9JHH3 PRELIMINARY; PRT; 207 AA.

AC Q9JHH3;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE INTERLEUKIN-6.

GN IL-6.

OS Marmota monax (Woodchuck).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;

OC Marmota.

NCBI_TaxID=9995;

RP (1)

RP SEQUENCE FROM N.A.

RC TISSUE-PERIPHERAL BLOOD;

RA Li D.H., Cullen J.M.;

RT Submitted (JUL-1997) to the EMBL/Genbank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RA Li D.H., Cullen J.M.;

RT Submitted (JAN-1999) to the EMBL/Genbank/DBJ databases.

DR EMBL; AF122908; AAF34861.1; -

DR EMBL; AF122896; AAF28873.1; -

DR InterPro; IPR003573; IL6_MGF_GCSF.

DR Pfam; PF00489; IL6; 1.

DR PRINTS; PR00433; IL6GCSFMGF.

DR SMART; SM00126; IL6; 1.

DR PROSITE; PS00254; INTERLEUKIN_6; 1.

DR PROSITE; PS00254; AD2F46E450E13470 CRC64;

SEQ SEQUENCE 207 AA; 23645 MW; AD2F46E450E13470 CRC64;

Query Match 58.0%; Score 51; DB 11; Length 207;
Best Local Similarity 55.6%; Pred. No. 1.7;
Matches 10; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 1 IIRSFKEFLQSSLRALR 18
11 : 11 : 11 : 11 : 1
DB 189 IIRSFKEFLQSSLRALR 206

RESULT 7

Q62775 PRELIMINARY; PRT; 94 AA.

AC Q62775;
DT 01-AUG-1998 (TREMBLrel. 07, Created)

DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)

DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)

DE INTERLEUKIN 6 (FRAGMENT).

OS Fells silvestris catus (Cat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.

NCBI_TaxID=9685;

RP (1)

RP SEQUENCE FROM N.A.

RA Harley R., Helms C.R., Gruffydd-Jones T.J., Day M.J., Harbour D.A.;

RL Submitted (MAR-1998) to the EMBL/Genbank/DBJ databases.

DR EMBL; AF034603; AAC15976.1; -

DR HSSP; P05231; IALU.

DR InterPro; IPR003573; IL6_MGF_GCSF.

DR Pfam; PF00489; IL6; 1.

DR SMART; SM00126; IL6; 1.

FT NON_TER 1 1
SQ SEQUENCE 94 AA; 11099 MW; 12B473B69ED94861 CRC64;

Query Match 55.7%; Score 49; DB 6; Length 94;
Best Local Similarity 61.1%; Pred. No. 1.6;
Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 IIRSFKEFLQSSLRALR 19
11 : 11 : 11 : 11 : 1
DB 77 IIRSFKEFLQSSLRALR 94

RESULT 8

Q9MZRO PRELIMINARY; PRT; 118 AA.

AC Q9MZRO;
DT 01-OCT-2000 (TREMBLrel. 15, Created)

DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)

DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)

DE INTERLEUKIN 6 (FRAGMENT).

GN IL-6.

OS Sylvilagus auduboni (desert cottontail).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Lagomorpha; Leporidae; Sylvilagus.

NCBI_TaxID=30581;

RP (1)

RP SEQUENCE FROM N.A.

RC TISSUE-Ovary;

RX MEDLINE-20304414; PubMed-10843729;

RA Perkins H.D., van Leeuwen B.H., Hardy C.M., Kerr P.J.;

RT "The complete cDNA sequences of IL-2, IL-4, IL-6 and IL-10 from the

European rabbit (Oryctolagus cuniculus).";

RL Cytokine 12:555-565(2000).

DR EMBL; AF169177; AAF86661.1; -

DR InterPro; IPR003573; IL6_MGF_GCSF.

DR Pfam; PF00489; IL6; 1.

DR PRINTS; PR00433; IL6GCSFMGF.

DR SMART; SM00126; IL6; 1.

DR PROSITE; PS00254; INTERLEUKIN_6; UNKNOWN_1.

DR PROSITE; PS00254; INTERLEUKIN_6; UNKNOWN_1.

FT NON_TER 1 1

SEQ SEQUENCE 118 AA; 13763 MW; 9DDDB8C812ED31049 CRC64;

Query Match 53.4%; Score 47; DB 6; Length 118;
Best Local Similarity 52.6%; Pred. No. 4.3;
Matches 10; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 IIRSFKEFLQSSLRALR 19
11 : 11 : 11 : 11 : 1
DB 100 IIRSFKEFLQSSLRALR 118

RESULT 9

Q9MZ09 PRELIMINARY; PRT; 118 AA.

AC Q9MZ09;
DT 01-OCT-2000 (TREMBLrel. 15, Created)

DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)

DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)

DE INTERLEUKIN 6 (FRAGMENT).

GN IL-6.

OS Sylvilagus nuttalli (mountain cottontail).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Lagomorpha; Leporidae; Sylvilagus.

NCBI_TaxID=50378;

RP (1)

RP SEQUENCE FROM N.A.

RC TISSUE-Ovary;

RX MEDLINE-20304414; PubMed-10843729;

RA Perkins H.D., van Leeuwen B.H., Hardy C.M., Kerr P.J.;

RT "The complete cDNA sequences of IL-2, IL-4, IL-6 and IL-10 from the

European rabbit (Oryctolagus cuniculus).";

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RL Cytokine 12:555-565(2000).
DR EMBL: AF169178; AAF86662.1; -.
DR InterPro: IPR003573; IL6_MGF_GCSF.
DR Pfam: PF00489; IL6; 1.
DR PRINTS: PR00433; IL6GCSFMGF.
DR SMART: SM00126; IL6; 1.
DR PROSITE: PS00254; INTERLEUKIN_6; UNKNOWN_1.
FT NON_TER 1
SQ SEQUENCE 118 AA; 13834 MW; 62E97FD3BDDEABEC CRC64;

Query Match 53.4%; Score 47; DB 6; Length 118;
Best Local Similarity 52.6%; Pred. No. 4.3;
Matches 10; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

OY 1 ILRSKFELQSSLRALROM 19
DB 100 ILRGLTDFLQFLRAVGIM 118

RESULT 10
O9MZ08 PRELIMINARY; PRT; 118 AA.
AC O9MZ08;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE INTERLEUKIN 6 (FRAGMENT).
GN IL-6.
OS Lepus californicus (Black-tailed jackrabbit).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Lagomorpha; Leporidae; Lepus.
OX NCBI_TaxID=48087;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=OVARY;
RX MEDLINE=20304414; PubMed=10843729;
RA Perkins H.D., van Leeuwen B.H., Hardy C.M., Kerr P.J.;
RT "The complete cDNA sequences of IL-2, IL-4, IL-6 and IL-10 from the
RT European rabbit (Oryctolagus cuniculus).";
RL Cytokine 12:555-565(2000).
DR EMBL: AF169179; AAF86663.1; -.
DR InterPro: IPR003573; IL6_MGF_GCSF.
DR Pfam: PF00489; IL6; 1.
DR PRINTS: PR00433; IL6GCSFMGF.
DR SMART: SM00126; IL6; 1.
DR PROSITE: PS00254; INTERLEUKIN_6; 1.
FT NON_TER 1
SQ SEQUENCE 118 AA; 13712 MW; 3EFF24AF8D70A219 CRC64;

Query Match 53.4%; Score 47; DB 6; Length 118;
Best Local Similarity 57.9%; Pred. No. 4.3;
Matches 11; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

OY 1 ILRSKFELQSSLRALROM 19
DB 100 ILRMLTDFLQFLRAVGIM 118

RESULT 11
O9MZ07 PRELIMINARY; PRT; 118 AA.
AC O9MZ07;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE INTERLEUKIN 6 (FRAGMENT).
GN IL-6.
OS Lepus townsendii (white-tailed jackrabbit).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Lagomorpha; Leporidae; Lepus.
OX NCBI_TaxID=63225;

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RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=OVARY;
RX MEDLINE=20304414; PubMed=10843729;
RA Perkins H.D., van Leeuwen B.H., Hardy C.M., Kerr P.J.;
RT "The complete cDNA sequences of IL-2, IL-4, IL-6 and IL-10 from the
RT European rabbit (Oryctolagus cuniculus).";
RL Cytokine 12:555-565(2000).
DR EMBL: AF169180; AAF86664.1; -.
DR InterPro: IPR003573; IL6_MGF_GCSF.
DR Pfam: PF00489; IL6; 1.
DR PRINTS: PR00433; IL6GCSFMGF.
DR SMART: SM00126; IL6; 1.
DR PROSITE: PS00254; INTERLEUKIN_6; 1.
FT NON_TER 1
SQ SEQUENCE 118 AA; 13712 MW; 3EFF24AF8D70A219 CRC64;

Query Match 53.4%; Score 47; DB 6; Length 118;
Best Local Similarity 57.9%; Pred. No. 4.3;
Matches 11; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

OY 1 ILRSKFELQSSLRALROM 19
DB 100 ILRMLTDFLQFLRAVGIM 118

RESULT 12
O9WY08 PRELIMINARY; PRT; 210 AA.
AC O9WY08;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE IL-6 (FRAGMENT).
OS Mesocricetus auratus (Golden hamster).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Cricetinae;
OX NCBI_TaxID=10036;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=APA; TISSUE=KIDNEY;
RA Nishida E.;
RT "APA hamsters IL-6 partial cDNA.";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB028635; BAA78766.1; -.
DR HSP: P05231; IALU
DR InterPro: IPR003573; IL6_MGF_GCSF.
DR Pfam: PF00489; IL6; 1.
DR PRINTS: PR00433; IL6GCSFMGF.
DR SMART: SM00126; IL6; 1.
DR PROSITE: PS00254; INTERLEUKIN_6; 1.
FT NON_TER 1
SQ SEQUENCE 210 AA; 24060 MW; HD9319AFBB913AB3 CRC64;

Query Match 51.1%; Score 45; DB 11; Length 210;
Best Local Similarity 44.4%; Pred. No. 16;
Matches 8; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

OY 1 ILRSKFELQSSLRALRO 18
DB 192 ILKALEFLQVTRSTRQ 209

RESULT 13
O50219 PRELIMINARY; PRT; 344 AA.
AC O50219;
DT 01-JUN-1998 (TREMBlrel. 06, Created)
DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)

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DE HYPOTHETICAL 38.5 KDA PROTEIN.
 OS Pseudomonas aeruginosa.
 OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
 OC Pseudomonas 287;
 OX NCBI_TaxID=287;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-UCBPP-PAL4;
 RA Rahme L.G., Tan M.-W., Le L., Wong S., Tompkins R.G., Calderwood S.B.,
 RA Ausubel F.M.,
 RA Proc. Natl. Acad. Sci. U.S.A. 94:0-0(1997).
 CC -1- SIMILARITY: TO THE LYSR FAMILY OF TRANSCRIPTIONAL REGULATORS.
 DR EMBL: AF031571; AAB84447.1; -
 DR InterPro: IPR000847; HTH_LysR.
 DR Pfam: PF00126; HTH_1; 1.
 DR DNA-binding; Hypothetical protein; Transcription regulation.
 SK SEQUENCE 344 AA: 38528 MW: 04228A3F06C8D2F6 CRC64;

Query Match 51.1%; Score 45; DB 2; Length 344;
 Best Local Similarity 47.1%; Pred. No. 26;
 Matches 8; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

OY 3 RSFKFLOSSLRALROM 19
 DB 279 RSFRRLSASRQLREL 295
 |||:||||:||||:
 |||:||||:||||:

RESULT 14
 O9PYT0 PRELIMINARY; PRT; 427 AA.

ID O9PYT0
 AC O9PYT0
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE ORF114.
 GN ORF114.
 OS Xestia c-nigrum granulosis virus (Xngv) (Xestia c-nigrum
 OS granulovirus).
 OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae; Granulovirus.
 OX NCBI_TaxID=51677;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99434230; PubMed=10502508;
 RA Hayakawa T., Ko R., Okano K., Seong S.I., Goto C., Maeda S.;
 RT "Sequence analysis of the Xestia c-nigrum granulovirus genome."
 RL Virology 262:277-297(1999).
 DR EMBL: AF162221; AAF05228.1; -
 SQ SEQUENCE 427 AA: 49747 MW: DA3412C416207AC CRC64;

Query Match 51.1%; Score 45; DB 12; Length 427;
 Best Local Similarity 50.0%; Pred. No. 32;
 Matches 9; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

OY 1 LRSFKFLOSSLRALROM 18
 DB 206 LRAFKQITSEFERQLKQ 223
 |||:||||:||||:
 |||:||||:||||:

RESULT 15
 O16111 PRELIMINARY; PRT; 588 AA.

ID O16111
 AC O16111
 DT 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE TEL (FRAGMENT).
 GN TEL.
 OS Drosophila vitilis (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidae; Drosophilidae; Drosophila.

OX NCBI_TaxID=7244;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TRANSPOSON-TELEMAC;
 RA Vieira J., Vieira C.P., Hartl D.L., Iozovskaya E.R.;
 RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF009439; AAB66824.1; -
 DR Flybase: FBgn0044144; DvirTel\Tel1.
 DR InterPro: IPR001878; Znf_CCHC.
 DR SMART; SM00343; Znf_C2HC; 2.
 FT NON_TER 588
 SQ SEQUENCE 588 AA: 64680 MW: 469108D1F44F6673 CRC64;

Query Match 51.1%; Score 45; DB 5; Length 588;
 Best Local Similarity 55.6%; Pred. No. 45;
 Matches 10; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

OY 2 LRSFKFLOSSLRALROM 19
 DB 249 LRFSKXLSHRLAKSM 266
 |||:||||:||||:
 |||:||||:||||:

Search completed: December 19, 2001, 16:25:20
 Job time: 545 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: December 19, 2001, 16:20:58 ; Search time 78.52 Seconds
(without alignments)
5.445 Million cell updates/sec

Title: US-09-202-104A-3

Perfect score: 88
Sequence: 1 ILRSFKFELQSLRALROM 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/PTOS.COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	88	100.0	162	2	US-08-716-317-10
2	88	100.0	163	2	US-08-716-317-15
3	88	100.0	164	1	US-08-318-193-60
4	88	100.0	167	1	US-08-246-427A-2
5	88	100.0	167	2	US-08-766-620-2
6	88	100.0	167	5	PCT-US95-06094-2
7	88	100.0	181	1	US-08-209-182C-4
8	88	100.0	181	5	PCT-US92-05612-4
9	88	100.0	183	1	US-08-009-973-1
10	88	100.0	184	1	US-08-567-047-2
11	88	100.0	184	2	US-08-693-182-2
12	88	100.0	184	2	US-08-567-048-2
13	88	100.0	184	2	US-09-008-482-2
14	88	100.0	184	2	US-08-945-529-8
15	88	100.0	184	2	US-08-945-529-9
16	88	100.0	184	2	US-08-945-529-10
17	88	100.0	184	2	US-08-945-529-11
18	88	100.0	184	4	US-08-149-101A-23
19	88	100.0	184	5	PCT-US94-12873-23
20	88	100.0	184	6	PCT-US94-12873-23
21	88	100.0	185	1	US-07-632-070B-1
22	88	100.0	185	1	US-07-918-181A-2
23	88	100.0	185	1	US-08-231-575-2
24	88	100.0	185	1	US-08-246-427A-5
25	88	100.0	185	2	US-08-716-317-7
26	88	100.0	185	2	US-08-766-620-5
27	88	100.0	185	5	PCT-US92-05612-2

28	88	100.0	185	5	PCT-US93-06928-2	Sequence 2, Appl1
29	88	100.0	185	6	US186931-2	Patent No. 5186931
30	88	100.0	186	1	US-07-632-070B-2	Sequence 2, Appl1
31	88	100.0	186	1	US-07-745-382-20	Sequence 20, Appl1
32	88	100.0	186	1	US-07-921-848-20	Sequence 20, Appl1
33	88	100.0	186	1	US-08-209-182C-2	Sequence 2, Appl1
34	88	100.0	186	1	US-08-165-301A-20	Sequence 2, Appl1
35	88	100.0	186	3	US-08-469-318-163	Sequence 163, Appl
36	88	100.0	186	3	US-08-468-609A-163	Sequence 163, Appl
37	88	100.0	186	4	US-08-810-436-20	Sequence 20, Appl
38	88	100.0	186	5	PCT-US94-14179-20	Sequence 20, Appl
39	88	100.0	186	5	PCT-US95-01185-163	Sequence 163, Appl
40	88	100.0	187	1	US-07-632-070B-3	Sequence 3, Appl1
41	88	100.0	188	3	US-09-122-443-12	Sequence 12, Appl
42	88	100.0	192	4	US-08-149-101A-19	Sequence 19, Appl
43	88	100.0	192	5	PCT-US94-12873-19	Sequence 19, Appl
44	88	100.0	194	4	US-08-149-101A-18	Sequence 18, Appl
45	88	100.0	194	5	PCT-US94-12873-18	Sequence 18, Appl

ALIGNMENTS

RESULT 1
US-08-716-317-10
; Sequence 10, Application US/08716317
; Patent No. 5919654
; GENERAL INFORMATION:
; APPLICANT: HAMA, YUKO
; APPLICANT: TOHDA, HIDEKI
; APPLICANT: TSUKAMOTO, HIROKO
; APPLICANT: NIKAIKO, KIYOKAZU
; APPLICANT: KURAGAI, HIROMICHI
; TITLE OF INVENTION: SECRETION SIGNAL GENE AND EXPRESSION
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MATIER & NEUSTADT,
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/716,317
; FILING DATE: 02-OCT-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP96/00198
; FILING DATE: 01-FEB-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 17167/1995
; FILING DATE: 03-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 59-924-0 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 162 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-716-317-10

Query Match 100.0%; Score 88; DB 2; Length 162;
Best Local Similarity 100.0%; Pred. No. 5.5e-07;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ILRSKFLOSSLRALROM 19
|||||
Db 144 ILRSKFLOSSLRALROM 162

RESULT 2

US-08-716-317-15
; Sequence 15, Application US/08716317
; Patent No. 5919654

; GENERAL INFORMATION:

; APPLICANT: HAMA, YUKO

; APPLICANT: TOMIDA, HIDEKI

; APPLICANT: TSUKAMOTO, HIROKO

; APPLICANT: NIKAIIDO, KIYOKAZU

; APPLICANT: KUNAGAI, HIROMICHI

; TITLE OF INVENTION: SECRETION SIGNAL GENE AND EXPRESSION

; TITLE OF INVENTION: VECTOR CONTAINING IT

; NUMBER OF SEQUENCES: 35

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,

; ADDRESSEE: P.C.

; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400

; CITY: ARLINGTON

; STATE: VA

; COUNTRY: USA

; ZIP: 22202

; COMPUTER READABLE FORM:

; MEDIUM TYPE: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/716.317

; FILING DATE: 02-OCT-1996

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/JP96/00198

; FILING DATE: 01-FEB-1996

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: JP 17167/1995

; FILING DATE: 03-FEB-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: OBLON, NORMAN F.

; REGISTRATION NUMBER: 24,618

; REFERENCE/DOCKET NUMBER: 59-924-0 PCT

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 703-413-3000

; TELEFAX: 703-413-2220

; INFORMATION FOR SEQ ID NO: 15:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 163 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; US-08-716-317-15

Query Match 100.0%; Score 88; DB 2; Length 163;
Best Local Similarity 100.0%; Pred. No. 5.5e-07;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ILRSKFLOSSLRALROM 19
|||||
Db 145 ILRSKFLOSSLRALROM 163

RESULT 3

US-08-318-193-60
; Sequence 60, Application US/08318193
; Patent No. 5641663

; GENERAL INFORMATION:

; APPLICANT: GARVIN, Robert F.

; APPLICANT: MALEK, Lawrence T.

; TITLE OF INVENTION: AN EXPRESSION SYSTEM FOR THE SECRETION

; TITLE OF INVENTION: OF BIOACTIVE HUMAN GRANULOCYTE MACROPHAGE COLONY

; TITLE OF INVENTION: STIMULATING FACTOR (GM-CSF) AND OTHER HETEROLOGOUS

; TITLE OF INVENTION: PROTEINS FROM STREPTOMYCES

; NUMBER OF SEQUENCES: 91

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Foley & Lardner

; STREET: 1800 Diagonal Road, Suite 500

; CITY: Alexandria

; STATE: Virginia

; COUNTRY: USA

; ZIP: 22313-0299

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/318.193

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/07/935.314

; FILING DATE:

; APPLICATION NUMBER: US 07/224.568

; ATTORNEY/AGENT INFORMATION:

; NAME: BENT, Stephen A.

; REGISTRATION NUMBER: 29,768

; REFERENCE/DOCKET NUMBER: 18740/116 CACO

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (703)836-9300

; TELEFAX: (703)683-4109

; INFORMATION FOR SEQ ID NO: 60:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 164 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-08-318-193-60

Query Match 100.0%; Score 88; DB 1; Length 164;
Best Local Similarity 100.0%; Pred. No. 5.6e-07;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ILRSKFLOSSLRALROM 19
|||||
Db 146 ILRSKFLOSSLRALROM 164

RESULT 4

US-08-246-427A-2
; Sequence 2, Application US/08246427A
; Patent No. 5641657

; GENERAL INFORMATION:

; APPLICANT: RUBEN, ET AL.

; TITLE OF INVENTION: Interleukin-6 Splice Variant

; NUMBER OF SEQUENCES: 5

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: CARELLA, BYRNE, BAIN, GIFFILLAN,

; STREET: 6 BECKER FARM ROAD

; CITY: ROSELAND

; STATE: NEW JERSEY

COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/246,427A
FILING DATE: Submitted herewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/246,427
FILING DATE: MAY 19, 1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: FERRARO, GREGORY D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 167 AMINO ACIDS
TYPE: AMINO ACID
STRANDEDNESS:
TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN
US-08-246-427A-2

Query Match 100.0%; Score 88; DB 1; Length 167;
Best Local Similarity 100.0%; Pred. No. 5.7e-07;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ILSRKEFLQSSLRALROM 19
DB 149 ILSRKEFLQSSLRALROM 167

RESULT 5
US-08-766-620-2
Sequence 2, Application us/08766620
Patent No. 5958400
GENERAL INFORMATION:
APPLICANT: RUBEN, ET AL.
TITLE OF INVENTION: Interleukin-6 Splice Variant
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
ADDRESSEE: CECCHI, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/766,620
FILING DATE: December 12, 1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/246,427
FILING DATE: MAY 19, 1994
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: MULLINS, J.G.
REGISTRATION NUMBER: 33,073

REFERENCE/DOCKET NUMBER: 325800-593 (PFI20)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 167 AMINO ACIDS
TYPE: AMINO ACID
STRANDEDNESS:
TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN
US-08-766-620-2

Query Match 100.0%; Score 88; DB 2; Length 167;
Best Local Similarity 100.0%; Pred. No. 5.7e-07;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ILSRKEFLQSSLRALROM 19
DB 149 ILSRKEFLQSSLRALROM 167

RESULT 6
PCT-US95-06094-2
Sequence 2, Application PC/TUS9506094
GENERAL INFORMATION:
APPLICANT: RUBEN, ET AL.
TITLE OF INVENTION: Interleukin-6 Splice Variant
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
ADDRESSEE: CECCHI, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/06094
FILING DATE: Submitted herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/246,427
FILING DATE: MAY 19, 1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: FERRARO, GREGORY D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 167 AMINO ACIDS
TYPE: AMINO ACID
STRANDEDNESS:
TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN
PCT-US95-06094-2

Query Match 100.0%; Score 88; DB 5; Length 167;
Best Local Similarity 100.0%; Pred. No. 5.7e-07;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ILSRKEFLQSSLRALROM 19

Db 149 ILRSKFLOSSLRALROM 167

RESULT 7
US-08-209-182C-4
Sequence 4, Application US/08209182C
Patent No. 5545537

GENERAL INFORMATION:
APPLICANT: Skelly, Susan M.
APPLICANT: Tackney, Charles T.
APPLICANT: Snouwaert, John N.
APPLICANT: Fowlkes, Dana M.
TITLE OF INVENTION: Cysteine Depleted IL-6 Mutelins
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Imclone Systems Incorporated
STREET: 180 Varick Street
CITY: New York
STATE: New York
COUNTRY: United States
ZIP: 10014

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/209,182C
FILING DATE: 10-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/724,698
FILING DATE: 02-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: Felt, Irving N.
REGISTRATION NUMBER: 28,601
REFERENCE/DOCKET NUMBER: SKE-1-PD
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-645-1405
TELEFAX: 212-645-2054

INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 181 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-209-182C-4

Query Match 100.0%; Score 88; DB 1; Length 181;
Best Local Similarity 100.0%; Pred. No. 6.1e-07;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ILRSKFLOSSLRALROM 19
Db 163 ILRSKFLOSSLRALROM 181

RESULT 8
PCT-US92-05612-4
Sequence 4, Application PC/TUS9205612
GENERAL INFORMATION:
APPLICANT: Skelly, Susan M.
APPLICANT: Tackney, Charles T.
APPLICANT: Snouwaert, John N.
APPLICANT: Fowlkes, Dana M.
TITLE OF INVENTION: Cysteine Depleted IL-6 Mutelins
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Imclone Systems Incorporated
STREET: 180 Varick Street
CITY: New York
STATE: New York

COUNTRY: United States
ZIP: 10014
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05612
FILING DATE: 19920702
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Felt, Irving N.
REGISTRATION NUMBER: 28,601
REFERENCE/DOCKET NUMBER: SKE-1-PT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-645-1405
TELEFAX: 212-645-2054
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 181 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US92-05612-4

Query Match 100.0%; Score 88; DB 5; Length 181;
Best Local Similarity 100.0%; Pred. No. 6.1e-07;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ILRSKFLOSSLRALROM 19
Db 163 ILRSKFLOSSLRALROM 181

RESULT 9
US-08-009-973-1
Sequence 1, Application US/08009973
Patent No. 5338834
GENERAL INFORMATION:
APPLICANT: WILLIAMS, Ashley M.
TITLE OF INVENTION: Ultrapure Human Interleukin-6
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington, D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/009,973
FILING DATE: 19930126
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 16777/199 ALLE
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEFAX: 904136
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 183 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
US-08-009-973-1

Query Match 100.0%; Score 88; DB 1; Length 184;
Best Local Similarity 100.0%; Pred. No. 6.3e-07;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ILRSKFLOSSLRALRM 19
|||||

Db 166 ILRSKFLOSSLRALRM 184

RESULT 10
US-08-567-047-2
; Sequence 2, Application US/08567047
; Patent No. 5789552 5789555
; GENERAL INFORMATION:
; APPLICANT: SAVINO, Rocco
; APPLICANT: LAHM, Armin
; TITLE OF INVENTION: METHOD FOR SELECTING SUPERAGONISTS,
; TITLE OF INVENTION: ANTAGONISTS AND SUPERANTAGONISTS FOR HORMONES HAVING
; TITLE OF INVENTION: GP 130 AS PART OF THEIR RECEPTOR COMPLEX
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/567,047
; FILING DATE: 04-DEC-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/387,924
; FILING DATE: 23-FEB-1995
; APPLICATION NUMBER: IT RM93A000409
; FILING DATE: 23-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: SAVINO-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 184 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-567-047-2

Query Match 100.0%; Score 88; DB 1; Length 184;
Best Local Similarity 100.0%; Pred. No. 6.3e-07;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ILRSKFLOSSLRALRM 19
|||||

Db 166 ILRSKFLOSSLRALRM 184

RESULT 11
US-08-693-182-2

; Sequence 2, Application US/08693182
; Patent No. 5849283
; GENERAL INFORMATION:
; APPLICANT: CILIBERTO, Gennaro
; APPLICANT: SAVINO, Rocco
; APPLICANT: LAHM, Armin
; APPLICANT: TONLATI, Carlo
; TITLE OF INVENTION: A METHODOLOGY FOR SELECTING
; TITLE OF INVENTION: SUPERAGONISTS, ANTAGONISTS AND SUPERANTAGONISTS OF HUMAN
; TITLE OF INVENTION: INTERLEUKIN-6 BASED ON RECEPTOR COMPLEX THREE DIMENSIONAL
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Browdy and Neimark, P.L.L.C.
; STREET: 419 Seventh Street N.W., Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: United States of America
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/693,182
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/IT95/00216
; FILING DATE: 13-DEC-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IT RM 94A000805
; FILING DATE: 14-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: CILIBERTO-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 184 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-693-182-2

Query Match 100.0%; Score 88; DB 2; Length 184;
Best Local Similarity 100.0%; Pred. No. 6.3e-07;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ILRSKFLOSSLRALRM 19
|||||

Db 166 ILRSKFLOSSLRALRM 184

RESULT 12
US-08-567-048-2
; Sequence 2, Application US/08567048
; Patent No. 5891998
; GENERAL INFORMATION:
; APPLICANT: SAVINO, Rocco
; APPLICANT: LAHM, Armin
; APPLICANT: CILIBERTO, Gennaro
; TITLE OF INVENTION: METHOD FOR SELECTING SUPERAGONISTS,
; TITLE OF INVENTION: ANTAGONISTS AND SUPERANTAGONISTS FOR HORMONES HAVING
; TITLE OF INVENTION: GP 130 AS PART OF THEIR RECEPTOR COMPLEX
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK

STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/567,048
FILING DATE: 04-DEC-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/387,924
FILING DATE: 23-FEB-1995
APPLICATION NUMBER: IT RM93A000409
FILING DATE: 23-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: SAVINO-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 184 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-567-048-2

Query Match 100.0%; Score 88; DB 2; Length 184;
Best Local Similarity 100.0%; Pred. No. 6.3e-07;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ILRSKFLOSSLRALROM 19
DB 166 ILRSKFLOSSLRALROM 184

RESULT 13
US-09-008-482-2
Sequence 2, Application US/09008482
Patent No. 5914106
GENERAL INFORMATION:
APPLICANT: CILIBERTO, Gennaro
APPLICANT: SAVINO, Rocco
APPLICANT: LAHM, Armin
APPLICANT: TONATILI, Carlo
TITLE OF INVENTION: A METHODOLOGY FOR SELECTING
SUPERAGONISTS, ANTAGONISTS AND SUPERANTAGONISTS OF HUMAN
INTERLEUKIN-6 BASED ON RECEPTOR COMPLEX THREE DIMENSIONAL
MODELING
TITLE OF INVENTION: INTERLEUKIN-6 BASED ON RECEPTOR COMPLEX THREE DIMENSIONAL
MODELING
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Browdy and Neimark, P.L.L.C.
STREET: 419 Seventh Street N.W., Ste. 300
CITY: Washington
STATE: D.C.
COUNTRY: United States of America
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/008,482

FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/693,182
FILING DATE: 14-AUG-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/IT95/00216
FILING DATE: 13-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IT RM 94A000805
FILING DATE: 14-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: YUN, Allen C.
REGISTRATION NUMBER: 37,971
REFERENCE/DOCKET NUMBER: CILIBERTO-2A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 184 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-008-482-2

Query Match 100.0%; Score 88; DB 2; Length 184;
Best Local Similarity 100.0%; Pred. No. 6.3e-07;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ILRSKFLOSSLRALROM 19
DB 166 ILRSKFLOSSLRALROM 184

RESULT 14
US-08-945-529-8
Sequence 8, Application US/08945529
Patent No. 5972902
GENERAL INFORMATION:
APPLICANT: CILIBERTO, Gennaro
APPLICANT: SAVINO, Rocco
APPLICANT: PIONESSA, Giacomo
TITLE OF INVENTION: ANTAGONISTS OF HUMAN INTERLEUKIN-6 THAT
ARE TOTALLY INCAPABLE OF BINDING GP 130, AND THEIR USE IN
THE PREPARATION OF PHARMACEUTICAL COMPOUNDS
TITLE OF INVENTION: THE PREPARATION OF PHARMACEUTICAL COMPOUNDS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
STREET: 419 Seventh Street N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/945,529
FILING DATE: 28-OCT-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IT RM95A000273
FILING DATE: 28-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/IT96/00084
FILING DATE: 26-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: YUN, Allen C.
REGISTRATION NUMBER: 37,971
REFERENCE/DOCKET NUMBER: CILIBERTO-3

TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 184 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-945-529-8

Query Match 100.0%; Score 88; DB 2; Length 184;
Best Local Similarity 100.0%; Pred. No. 6.3e-07;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IIRSFKEFLQSSIRALROM 19
|||||
DB 166 IIRSFKEFLQSSIRALROM 184

RESULT 15
US-08-945-529-9
Sequence 9, Application US/08945529
Patent No. 5972902
GENERAL INFORMATION:
APPLICANT: CLIBERTO, Gennaro
APPLICANT: SAVINO, Rocco
APPLICANT: PAVNESSA, Giacomo
TITLE OF INVENTION: ANTAGONISTS OF HUMAN INTERLEUKIN-6 THAT
TITLE OF INVENTION: ARE TOTALLY INCAPABLE OF BINDING GP 130, AND THEIR USE IN
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
STREET: 419 Seventh Street N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/945,529
FILING DATE: 28-OCT-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IT RM95A000273
FILING DATE: 28-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/IT96/00084
FILING DATE: 26-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: YUN, Allen C
REGISTRATION NUMBER: 37,971
REFERENCE/DOCKET NUMBER: CLIBERTO-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 184 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-945-529-9

Query Match 100.0%; Score 88; DB 2; Length 184;
Best Local Similarity 100.0%; Pred. No. 6.3e-07;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IIRSFKEFLQSSIRALROM 19
|||||
DB 166 IIRSFKEFLQSSIRALROM 184

Search completed: December 19, 2001, 16:20:59
Job time: 404 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: December 19, 2001, 16:19:34 ; Search time 170.68 seconds
(without alignments)
6.510 Million cell updates/sec

Title: US-09-202-104a-4
Perfect score: 80
Sequence: 1 OLSCFRRKPLSNVVC 15

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues
Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
A.Geneseq.1101.*
1: /SIDS8/gcgdata/geneseq/geneseq/AA1980.DAT:*
2: /SIDS8/gcgdata/geneseq/geneseq/AA1981.DAT:*
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14: /SIDS8/gcgdata/geneseq/geneseq/AA1993.DAT:*
15: /SIDS8/gcgdata/geneseq/geneseq/AA1994.DAT:*
16: /SIDS8/gcgdata/geneseq/geneseq/AA1995.DAT:*
17: /SIDS8/gcgdata/geneseq/geneseq/AA1996.DAT:*
18: /SIDS8/gcgdata/geneseq/geneseq/AA1997.DAT:*
19: /SIDS8/gcgdata/geneseq/geneseq/AA1998.DAT:*
20: /SIDS8/gcgdata/geneseq/geneseq/AA1999.DAT:*
21: /SIDS8/gcgdata/geneseq/geneseq/AA2000.DAT:*
22: /SIDS8/gcgdata/geneseq/geneseq/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	80	100.0	15	AAW52204	Interleukin-6 anta
2	80	100.0	315	AAW70805	Amino acid sequenc
3	80	100.0	315	AAV92200	Soluble human IL-6
4	80	100.0	323	AAV90527	B cell stimulating
5	80	100.0	325	AAV15389	Human interleukin
6	80	100.0	325	AAV15390	Human interleukin
7	80	100.0	344	AAV90528	B cell stimulating
8	80	100.0	345	AAV55071	SR345 protein sequ
9	80	100.0	360	AAW70804	Amino acid sequenc
10	80	100.0	360	AAV92199	Soluble human IL-6
11	80	100.0	386	AAV90526	B cell stimulating

ALIGNMENTS

RESULT ID	AAW52204	standard; peptide; 15 AA.	AAW52204	standard; peptide; 15 AA.	Human IL-6 recepto
12	80	100.0	419	20	Human IL-6 recepto
13	80	100.0	468	10	B cell stimulating
14	80	100.0	468	10	Sequence of a rece
15	80	100.0	468	10	IL-6 receptor. Sy
16	80	100.0	468	17	Interleukin-6 rece
17	80	100.0	468	19	Human interleukin-
18	80	100.0	468	21	Human IL-6R-alpha
19	80	100.0	468	22	Human IL-6 recepto
20	80	100.0	477	21	Human IL-6R-alpha
21	80	100.0	500	21	Human fusion polyp
22	80	100.0	515	21	IL-6R/IL-6 fusion
23	80	100.0	525	18	Human fusion polyp
24	80	100.0	543	20	Chimeric sIL-6R/IL
25	80	100.0	592	20	Human interleukin-
26	80	100.0	592	21	Human IL-6R-alpha
27	80	100.0	690	21	Human IL-6R-alpha
28	80	100.0	1042	16	IL8-R type 1-GBP 1
29	80	100.0	1158	21	Fusion polypeptide
30	80	100.0	1168	21	Interleukin-6 anta
31	71	88.8	182	17	Interleukin-6 anta
32	67	83.8	12	17	IL-6 receptor. Mu
33	62	77.5	460	12	IL-6R for soluble
34	62	77.5	460	13	Mouse IL-6 recepto
35	62	77.5	460	13	Mouse IL-6 recepto
36	62	77.5	460	13	Salimiri boliviensi
37	43	53.8	215	22	Salimiri sciureus o
38	43	53.8	215	22	Interleukin-6 rece
39	42	52.5	11	18	Human olfactory re
40	42	52.5	328	22	Mouse CD100 antige
41	42	52.5	861	19	Mouse semaphorin.
42	42	52.5	861	19	Mouse CD100 antige
43	42	52.5	861	22	Mouse CD100 antige
44	42	52.5	861	22	Mouse CD100 antige
45	41	51.2	216	22	Callithrix jacchus

RESULT 1
ID AAW52204 standard; peptide; 15 AA.
AC AAW52204;
DT 09-JUN-1998 (first entry)
DE Interleukin-6 antagonist peptide.
KW Interleukin-6; IL-6; antagonist; IL-6 related disease; multiple myeloma;
KW acquired immune deficiency syndrome-related lymphoma; immune response;
KW rheumatoid arthritis; psoriasis; sepsis; osteoporosis; therapy;
KW Alzheimer's disease.
OS Synthetic.
OS Homo sapiens.
PN WO9748728-A1.
PD 24-DEC-1997.
PF 19-JUN-1997; 97WO-NL00345.
PR 20-JUN-1996; 96EP-0201720.
PA (KOSTER) KOSTER H W.
PI Hoebe KHN, Van Leengoed LAMG;
XX WPI; 1998-063080/06.
XX New peptide(s) with interleukin-6 agonist or antagonist activity -
XX useful for treatment, prevention and diagnosis of IL-6 associated

PT diseases
XX
PS Claim 6; Page 17; 28pp; English.
XX
CC This sequence represents a Interleukin-6 (IL-6) antagonist peptide. This
CC sequence is a peptide of the invention, which are of 5-30 amino acids
CC and have antagonistic activity against: (a) IL-6; (b) the alpha chain
CC and/or beta chain of the IL-6 receptor (IL-6R); or (c) IL-6 activity. The
CC antagonists are used to treat or prevent IL-6 related diseases (typical
CC of many exemplified are multiple myeloma, acquired immune deficiency
CC syndrome-related lymphoma, rheumatoid arthritis, psoriasis, sepsis,
CC osteoporosis, Alzheimer's disease etc.), also to remove IL-6 or IL-6R
CC from extracellular blood. They may also be used diagnostically for such
CC diseases and IL-6 agonists are additives for cell cultures. Antibodies
CC specific for the antagonists may be administered to subjects previously
CC treated with the antagonists to counter their effects, also in
CC extracorporeal dialysis and diagnosis. The antagonists are too small to
CC induce an immune response and have minimal side effects (they are not
CC lytic for erythrocytes nor toxic for polymorphonuclear cells or
CC hepatocytes); contrast no human anti-IL-6 antibodies. The mixtures, or
CC multimers, have greater activity (acting on both IL-6 and its receptor)
CC and the peptides can be engineered to increase half-life or to target
CC organs by incorporating unnatural aa or altering the
CC hydrophilic/lipophilic balance.
XX
SQ Sequence 15 AA:

Query Match 100.0%; Score 80; DB 19; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.3e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QLSCEKSPSLSNVC 15
Db 1 qlscfkrkspslsnvc 15
|||||
1 qlscfkrkspslsnvc 15

RESULT 2
AAW70805
ID AAW70805 standard; protein: 315 AA.
XX
AC AAW70805;
XX
DT 03-FEB-1999 (first entry)
XX
DE Amino acid sequence of the interleukin (IL)-6R-alpha-313 domain.
XX
KW gp130: cytokine antagonist; interleukin; gamma-interferon;
KW granulocyte macrophage colony-stimulating factor; J peptide;
KW transforming growth factor-beta.
XX
OS Synthetic.
XX
FH Key
FT Protein 1..313
FT /note= "truncated Interleukin (IL)-6R-alpha domain"
XX
PN US5844099-A.
XX
PD 01-DEC-1998.
XX
PF 27-NOV-1995; 95US-0563105.
XX
PR 27-NOV-1995; 95US-0563105.
PR 20-OCT-1993; 93US-0140222.
XX
PA (REG-) REGENERON PHARM INC.
PI Economides A, Stahl N, Yancopoulos GD;
PT WPI: 1999-044669/04.
XX
DR Cytokine antagonists - comprising extracellular domains of

PT specificity-determining and signal-transducing components of
PT cytokine receptor
XX
PS Example 4; Fig 16; 46pp; English.
XX
CC The present sequence represents the amino acid sequence of Interleukin
CC (IL)-6R-alpha-313 domain. The protein is used in the course of the
CC invention. The specification describes cytokine antagonists comprising
CC only the extracellular domain of the specificity-determining component of
CC the cytokine receptor and the extracellular domain of a
CC signal-transducing component of the cytokine receptor. The cytokine
CC is an interleukin (IL-1, IL-2, IL-3, IL-4, IL-5 or IL-15),
CC granulocyte macrophage colony-stimulating factor (GM-CSF),
CC gamma-interferon or transforming growth factor-beta (TGF-beta). The
CC antagonist is capable of binding the cytokine to form a nonfunctional
CC complex. The compounds have therapeutic activity as cytokine antagonists
CC and can also be used in assays for identifying novel agonists and
CC antagonists of cytokines.
XX
SQ Sequence 315 AA:

Query Match 100.0%; Score 80; DB 20; Length 315;
Best Local Similarity 100.0%; Pred. No. 3.6e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QLSCEKSPSLSNVC 15
Db 118 qlscfkrkspslsnvc 132
|||||
1 qlscfkrkspslsnvc 132

RESULT 3
AAW92200
ID AAW92200 standard; protein: 315 AA.
XX
AC AAW92200;
XX
DT 01-AUG-2000 (first entry)
XX
DE Soluble human IL-6-R-alpha-313.
XX
KW Soluble IL-6-R-alpha-313; cytokine; antagonist; CNTF; receptor;
KW fusion protein; cytosolic; immunomodulator; osteopathic.
XX
OS Homo sapiens.
XX
FH Key
FT Protein 1..313
FT /label= "truncated_IL-6-R-alpha
FT Peptide 314..315
FT /note= "Thr-Gly bridge"
XX
PN WO200018932-A2.
XX
PD 06-APR-2000.
XX
PF 22-SEP-1999; 99WO-US22045.
XX
PR 25-SEP-1998; 98US-0101858.
PR 19-MAY-1999; 99US-0313942.
XX
PA (REG-) REGENERON PHARM INC.
PI Stahl N, Yancopoulos GD;
PT WPI: 2000-293165/25.
XX
DR Isolated nucleic acid molecule for treating cytokine-related diseases
PT or disorders encodes a fusion polypeptide capable of binding a cytokine
PT to form a nonfunctional complex
XX
PS Example 4; Fig 16; 152pp; English.
XX

CC The invention concerns production of antagonists to any cytokine that
 CC utilizes an alpha specificity determining component, which when combined
 CC with the cytokine, binds to a first beta signal transducing component to
 CC form a non-functional intermediate which then binds to a second beta
 CC signal transducing component causing beta-receptor dimerization, the
 CC soluble alpha specificity determining component of the receptor
 CC (SR-alpha) and the extracellular domain of the first beta signal
 CC transducing component of the cytokine receptor (beta-1) are combined to
 CC form heterodimers (SR-alpha:beta-1) that act as antagonist to the
 CC cytokine by binding the cytokine to form a non-functional complex. The
 CC receptor components are shared by cytokines such as the CNTF (ciliary
 CC neurotrophic factor) family of cytokines. The invention provides the
 CC basis for the development of IL-6 antagonists, as they show that if, in
 CC the presence of a ligand, a non-functional intermediate complex,
 CC consisting of the ligand, its alpha receptor and its beta-1 receptor
 CC component, can be formed, it will effectively block the action of the
 CC ligand. Effective antagonists of IL-6 or CNTF consist of heterodimers
 CC of the extracellular domains of the alpha and beta-1 receptor
 CC components of their receptors and the extracellular domain of gp130.
 CC The resultant heterodimers, function as high-affinity traps, rendering
 CC the cytokine inaccessible to form a signal transducing complex with the
 CC native membrane-bound forms of their receptor. The nucleic acids and
 CC polypeptides are useful for treating cytokine-related diseases or
 CC disorders such as osteoporosis and primary and secondary effects of
 CC cancer including multiple myeloma or cachexia.

SO Sequence 315 AA:

Query Match 100.0%; Score 80; DB 21; Length 315;
 Best Local Similarity 100.0%; Pred. No. 3.6e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QLSCFRKSPLSNVC 15
 ||||||||||||
 DB 118 qlscfrkspisnvc 132

RESULT 4
 AAP90527
 ID AAP90527 standard; protein; 323 AA.
 XX
 AC AAP90527;
 XX
 DT 25-JAN-1990 (first entry)
 XX
 DE B cell stimulating factor-2 receptor.
 XX
 KW B cell stimulating factor-2 receptor; monocytic U937 cell line.
 XX
 OS Homo sapiens.
 XX
 PN A08928720-A.
 XX
 PD 27-JUL-1989.
 XX
 PF 23-JAN-1989; 89AU-0028720.
 XX
 PR 22-JAN-1988; 88JP-0012387.
 XX
 PR 25-JAN-1988; 88JP-0012599.
 XX
 PR 04-AUG-1988; 88JP-0194885.
 XX
 PR 14-JAN-1989; 89JP-0007461.
 XX
 PA (KISH) TADAMITSU KISHIMOTO.
 XX
 PI Kishimoto T;
 XX
 DR WPI: 1989-264012/37.
 DR N-PSDB: AAP90525.
 XX
 PT Receptor protein for human B cell stimulating factor-2 - used for
 PT developing prophylactic, therapeutic and diagnostic agents for
 PT associated disorders.

XX
 PS Claim 6; page 39; 76pp; english.
 XX
 CC The BSF2 receptor has amino acids at the C-terminal deleted. The receptor
 CC is derived from a monocytic U937 cell line. It can be used to develop
 CC prophylactic and therapeutic pharmaceuticals, as agents to relate
 CC diseases and disorders to abnormal BSF-2 prodn. It can also be used to
 CC study an immune mechanism with which BSF-2 or the receptor is concerned.
 XX

SO Sequence 323 AA:

Query Match 100.0%; Score 80; DB 10; Length 323;
 Best Local Similarity 100.0%; Pred. No. 3.7e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QLSCFRKSPLSNVC 15
 ||||||||||||
 DB 118 qlscfrkspisnvc 132

RESULT 5
 AAB15389
 ID AAB15389 standard; protein; 325 AA.
 XX
 AC AAB15389;
 XX
 DT 11-DEC-2000 (first entry)
 XX
 DE Human Interleukin 6 receptor protein.
 XX
 KW Human: Interleukin-6 receptor; fungus; Pichia pastoris; PCR primer;
 XX expression vector; immunoglobulin-like region; cytokine receptor region.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 57 /note="encoded by GGC"
 FT Misc-difference 281 /note="encoded by CAA"
 FT
 PN JP2000157280-A.
 XX
 PD 13-JUN-2000.
 XX
 PF 26-NOV-1998; 98JP-0335464.
 XX
 PR 26-NOV-1998; 98JP-0335464.
 XX
 PA (TOYJ) TOSOH CORP.
 XX
 DR WPI: 2000-468203/41.
 DR N-PSDB: AAA70701.
 XX
 PT Yeasts transformed with IL-6 receptor gene -
 XX
 PS Example 1; Page 6-8; 10pp; Japanese.
 XX
 CC The invention relates to the production of human interleukin-6 receptor
 CC (IL-6R) protein in the fungus Pichia pastoris. The fungus was
 CC transformed with an expression vector (pPIC9-A20UL) containing a gene
 CC encoding an IL-6R protein having an immunoglobulin-like region and
 CC cytokine receptor region and spanning amino acids from Leu20-A1a323. The
 CC human IL-6R region was PCR amplified using the primers AAA70702-A70703.
 CC This sequence represents the recombinant IL-6R protein of the invention.
 XX

SO Sequence 325 AA:

Query Match 100.0%; Score 80; DB 21; Length 325;
 Best Local Similarity 100.0%; Pred. No. 3.7e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QLSCKRKSPLSNVVC 15
| | | | | | | | | | | | | | |
Db 99 qlscfkrksplsnvvc 113

RESULT 6
AA015390
ID AAB15390 standard; Protein: 325 AA.
XX
AC AAB15390;
XX
DT 15-DEC-2000 (first entry)
XX
DE Bovine interleukin-12 p35 subunit protein.
XX
KW Antifective; bovine; interleukin 12; IL12; heterodimer; infection.
XX
OS Bos taurus.
XX
PN JP2000157274-A.
XX
PD 13-JUN-2000.
XX
PF 20-NOV-1998; 98JP-0331052.
XX
PR 20-NOV-1998; 98JP-0331052.
XX
PA (DAUC) DALICHI PHARM CO LTD.
XX
XX WPI: 2000-468201/41.
DR N-PSDB; AAA70708.
XX
XX Preparation of bovine interleukin 12 comprising using a vector
PT containing the gene encoding it, useful for the prevention and
PT treatment of chronic and opportunistic infections -
XX
XX Example 1; Page 8; 11pp; Japanese.
XX
XX The invention relates to a method for the preparation of bovine
CC interleukin 12 (BoIL12). BoIL12 consists of a heterodimer of p35
CC and p40 subunits. BoIL12 is produced by introducing into a host cell,
CC recombinant vectors containing genes encoding the p35 and p40 subunits.
CC This sequence represents the bovine IL12 p35 subunit. Interleukin 12
CC is used for the prevention and treatment of chronic infections and
CC opportunistic infections.
XX
SQ Sequence 325 AA;

Query Match 100.0%; Score 80; DB 21; Length 325;
Best Local Similarity 100.0%; Pred. No. 3.7e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QLSCKRKSPLSNVVC 15
| | | | | | | | | | | | | | |
Db 99 qlscfkrksplsnvvc 113

RESULT 7
AAP90528
ID AAP90528 standard; Protein: 344 AA.
XX
AC AAP90528;
XX
DT 25-JAN-1990 (first entry)
XX
DE B cell stimulating factor-2 receptor.
XX
KW B cell stimulating factor-2 receptor; monocyte U937 cell line.
XX
OS Homo sapiens.
XX

PN AUB928720-A.
XX
XX 27-JUL-1989.
PD
XX
XX 23-JAN-1989; 89AU-0028720.
PF
XX
XX 22-JAN-1988; 88JP-0012387.
PR 25-JAN-1988; 88JP-0012589.
PR 04-AUG-1988; 88JP-0194885.
PR 14-JAN-1989; 89JP-0007461.
XX
XX (KISH) TADAMITSU KISHIMOTO.
PA
XX
XX Kishimoto T;
XX
XX WPI: 1989-264012/37.
DR N-PSDB; AAP90525.
XX
XX Receptor protein for human B cell stimulating factor-2 - used for
PT developing prophylactic, therapeutic and diagnostic agents for
PT associated disorders.
XX
XX Claim 7; page 40; 76pp; English.
XX
XX The Bsf2 receptor has amino acids at the C-terminal deleted. The receptor
CC is derived from a monocyte U937 cell line. It can be used to develop
CC prophylactic and therapeutic pharmaceuticals, as agents to relate
CC diseases and disorders to abnormal Bsf-2 prodn. It can also be used to
CC study an immune mechanism with which Bsf-2 or the receptor is concerned.
XX
XX Sequence 344 AA;
SQ

Query Match 100.0%; Score 80; DB 10; Length 344;
Best Local Similarity 100.0%; Pred. No. 3.9e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QLSCKRKSPLSNVVC 15
| | | | | | | | | | | | | | |
Db 118 qlscfkrksplsnvvc 132

RESULT 8
AA055071
ID AAY55071 standard; Protein: 345 AA.
XX
AC AAY55071;
XX
DT 25-FEB-2000 (first entry)
XX
XX SR345 protein sequence.
DE
XX Gene isolation; membrane-bound protein; fusion protein; drug production;
KW antigen-binding cell; secretible; functional protein; antigenic protein;
KW protein isolation; diagnosis; SR345 protein.
XX
XX Homo sapiens.
OS
XX W09960113-A1.
PN
XX 25-NOV-1999.
PD
XX 30-APR-1999; 99WO-JP02341.
PF
XX 20-MAY-1998; 98JP-0138652.
PR 01-OCT-1998; 98JP-0279876.
PR
XX (CHUS) CHUGAI SEIYAKU KK.
PA
XX Tsuchiya M, Saito M, Ohtomo T;
PI
XX WPI: 2000-039382/03.
DR N-PSDB; AA240288.

cytokine by binding the cytokien to form a non-functional complex. The receptor components are shared by cytokines such as the CNTF (ciliary neurotrophic factor) family of cytokines. The invention provides the basis for the development of IL-6 antagonists, as they show that if, in the presence of a ligand, a non-functional intermediate complex, consisting of the ligand, its alpha receptor and its beta-1 receptor component, can be formed, it will effectively block the action of the ligand. Effective antagonists of IL-6 or CNTF consist of heterodimers of the extracellular domains of the alpha specificity determining components of their receptors and the extracellular domain of gp130. The resultant heterodimers, function as high-affinity traps, rendering the cytokine inaccessible to form a signal transducing complex with the native membrane-bound forms of their receptor. The nucleic acids and polypeptides are useful for treating cytokine-related diseases or disorders such as osteoporosis and primary and secondary effects of cancer including multiple myeloma or cachexia.

Sequence 360 AA;

Query Match 100.0%; Score 80; DB 21; Length 360;

Best Local Similarity 100.0%; Pred. No. 4.1e-06; Mismatches 0; Indels 0; Gaps 0;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QLSCFRKSPLSNVVC 15

Db 118 qlscfrksplsnvvc 132

RESULT 11

AAP90526 standard; protein: 386 AA.

XX AAP90526;

DT 25-JAN-1990 (first entry)

DE B cell stimulating factor-2 receptor.

KW B cell stimulating factor-2 receptor; monocyte U937 cell line.

OS Homo sapiens.

PN A08928720-A.

PD 27-JUL-1989.

PF 23-JAN-1989; 89AU-0028720.

PR 22-JAN-1988; 88JP-0012387.

PR 25-JAN-1988; 88JP-0012599.

PR 04-AUG-1988; 88JP-0194885.

PR 14-JAN-1989; 89JP-0007461.

PA (KISH) TADAMITSU KISHIMOTO.

PI Kishimoto T;

DR WPI; 1989-264012/37.

DR N-PSDB; AAP90525.

PT Receptor protein for human B cell stimulating factor-2 - used for developing prophylactic, therapeutic and diagnostic agents for associated disorders.

PS Claim 4; page 37-8; 76pp; english.

CC The BSF2 receptor has residues near the N-terminal deleted. The receptor is derived from a monocytic U937 cell line. It can be used to develop prophylactic and therapeutic pharmaceuticals as agents to relate diseases and disorders to abnormal BSF-2 prodn. It can also be used to study an immune mechanism with which BSF-2 or the receptor is concerned.

XX

SO Sequence 386 AA;

Query Match

Best Local Similarity 100.0%; Score 80; DB 10; Length 386; Mismatches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QLSCFRKSPLSNVVC 15

Db 36 qlscfrksplsnvvc 50

RESULT 12

AAY30938 standard; protein: 419 AA.

XX AAY30938;

DT 19-OCT-1999 (first entry)

DE Human IL-6 receptor/IL-6 fusion protein.

KW IL-6; interleukin-6; receptor; human; fusion protein; bone marrow; stem cell; platelet; reduced antigenicity.

OS Homo sapiens.

PN Synthetic.

FT Key Location/Qualifiers

FT Protein 1.420 /note= "No start codon given"

PN JP1196867-A.

PD 27-JUL-1999.

PF 09-JAN-1998; 98JP-0002921.

PR 09-JAN-1998; 98JP-0002921.

PA (TOYU) TOSOH CORP.

DR WPI; 1998-486648/42.

DR N-PSDB; AA209202.

PT New interleukin-6 receptor-interleukin-6 fused protein and gene - used for growth of bone marrow stem cells and platelets

PS Example 1; Page 5-8; 8pp; Japanese.

CC This invention describes a novel gene which encodes a fusion protein of interleukin-6 (IL-6) receptor and bound with a gene sequence encoding

CC for IL-6 at the downstream of IL-6 receptor gene. The gene and its encoding protein has applications for the growth of bone marrow stem

CC cells and platelets. Transmission of a signal of IL-6 to target cells for stimulation with reduced antigenicity is possible. This sequence

CC represents the IL-6 receptor/IL-6 fusion protein described in the

CC invention.

XX Sequence 419 AA;

Query Match 100.0%; Score 80; DB 20; Length 419;

Best Local Similarity 100.0%; Pred. No. 4.8e-06; Mismatches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QLSCFRKSPLSNVVC 15

Db 3 qlscfrksplsnvvc 17

RESULT 13

AAP90525


```

ID AAP90525 standard; protein: 468 AA.
XX
AC AAP90525;
XX
DT 23-JAN-1990 (first entry)
XX
DE B cell stimulating factor-2 receptor.
XX
KW B cell stimulating factor-2 receptor; monocytic U937 cell line.
XX
OS Homo sapiens.
XX
PN AU8928720-A.
XX
PD 27-JUL-1989.
XX
PF 23-JAN-1989; 89AU-0028720.
XX
PR 22-JAN-1988; 88JP-0012387.
PR 25-JAN-1988; 88JP-0012599.
PR 04-AUG-1988; 88JP-0194885.
PR 14-JAN-1989; 89JP-0007461.
XX
PA (KISH ) TADAMITSU KISHIMOTO.
XX
PI Kishimoto T;
XX
DR WPI: 1989-264012/37.
DR N-PSDB: AAP90525.
XX
PT Receptor protein for human B cell stimulating factor-2 - used for
PT developing prophylactic, therapeutic and diagnostic agents for
PT associated disorders.
XX
PS Claim 2; page 36; 76pp; english.
XX
CC The BSF2 receptor is derived from a monocytic U937 cell line. It can be
CC used to develop prophylactic and therapeutic pharmaceuticals, as agents to
CC relate diseases and disorders to abnormal BSF-2 prodn. It can also be
CC used to study an immune mechanism with which BSF-2 or the receptor is
CC concerned.
XX
SQ Sequence 468 AA;

Query Match 100.0%; Score 80; DB 10; Length 468;
Best Local Similarity 100.0%; Pred. No. 5.5e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QUSCFRKSPLSNVVC 15
   |||||
DB 118 qlscfrksplsnvvc 132

RESULT 14
ID AAP90284 standard; protein: 468 AA.
XX
AC AAP90284;
XX
DT 31-MAR-1992 (first entry)
XX
DE Sequence of a receptor protein for human B cell stimulating
DE factor-2 (BSF2 receptor).
XX
KW B cell; immune disorder; therapy; diagnosis; prophylaxis.
XX
OS Homo sapiens.
XX
PI Key
XX
FH Location/Qualifiers
FT 2..22
FT /label= hydrophobic region
FT Region 362..386

```

```

FT EP325474-A.
XX
PN 26-JUL-1989.
XX
PD 20-JAN-1989; 89EP-0300536.
XX
PF 14-JAN-1988; 89JP-0017461.
PR 22-JAN-1988; 88JP-0012387.
PR 25-JAN-1988; 88JP-0012599.
PR 04-AUG-1988; 88JP-0194885.
PR 20-JAN-1989; 89JP-0009774.
XX
PA (KISH/) KISHIMOTO T.
XX
PI Kishimoto T;
XX
DR WPI: 1989-214667/30.
DR N-PSDB: AAN90340.
XX
PT Receptor protein for human B cell stimulating factor-2 - obt'd. by
PT recombinant DNA techniques and used as diagnostic, prophylactic or
PT therapeutic agent
XX
PS Claim 2; Page 19-21; 63pp; English.
XX
CC The cDNA in AAN90340 was derived from monocytic cell line U937.
CC Isolated BSF2 receptor and DNA encoding it are claimed, as are
CC (b) expression vectors; (c) host organisms; (d) antibodies; and
CC (e) hybridomas.
XX
SQ Sequence 468 AA;

Query Match 100.0%; Score 80; DB 10; Length 468;
Best Local Similarity 100.0%; Pred. No. 5.5e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QUSCFRKSPLSNVVC 15
   |||||
DB 118 qlscfrksplsnvvc 132

RESULT 15
ID AAR37215 standard; protein: 468 AA.
XX
AC AAR37215;
XX
DT 13-SEP-1993 (first entry)
XX
DE IL-6 receptor.
XX
KW Interleukin-6; IL-6; receptor; immunoglobulin-like; domain; truncated;
KW transmembrane; multiple myeloma; binding; ability; signal transfer;
KW disease; intracellular.
XX
OS Synthetic.
XX
PN JP05091892-A.
XX
PD 16-APR-1993.
XX
PF 02-OCT-1991; 91JP-0255521.
PR 02-OCT-1991; 91JP-0255521.
XX
PA (CHUS ) CHUGAI PHARM CO LTD.
PA (KISH/) KISHIMOTO C.
PA (TOYJ ) TOSOH CORP.
XX
DR WPI: 1993-161739/20.

```


GenCore version 4.5
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OM protein - protein search, using sw model

Run on: December 19, 2001, 16:22:36 ; Search time 88.82 seconds
(without alignments)
12.864 Million cell updates/sec

Title: US-09-202-104A-4

Perfect score: 80

Sequence: 1 QLSCFRKSPLSNVVC 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	80	100.0	468	1 A41242	interleukin-6 rece
2	62	77.5	440	2 JI0144	interleukin-6 rece
3	62	77.5	460	2 JI0145	interleukin-6 rece
4	58	72.5	462	1 A37986	interleukin-6 rece
5	43	53.8	205	2 T15044	heat shock protein
6	43	53.8	1436	2 B61704	conserved hypotet
7	42	52.5	264	2 PC4369	olfactory receptor
8	41	51.2	807	2 T40821	probable ubiquitin
9	40	50.0	171	2 D70830	hypothetical prote
10	40	50.0	356	2 T22478	hypothetical prote
11	40	50.0	379	2 T10971	Pv42 protein - kid
12	40	50.0	383	2 S73420	methionine adenosy
13	39	48.8	359	2 T47208	manipoline biosynth
14	39	48.8	930	2 T13927	hypothetical prote
15	39	48.8	977	2 T16232	HD protein - mouse
16	39	48.8	3119	2 T49729	Huntington disease
17	39	48.8	3144	2 A46068	hypothetical prote
18	39	48.8	1787	2 T00798	hypothetical prote
19	38.5	48.1	787	2 T00798	hypothetical prote
20	38	47.5	161	2 S40711	lysine-tRNA ligase
21	38	47.5	170	2 C55349	4-hydroxyphenylace
22	38	47.5	395	2 S65800	methionine adenosy
23	38	47.5	533	2 T46975	lysine-tRNA ligase
24	38	47.5	557	2 T27752	hypothetical prote
25	38	47.5	630	2 J00271	voltage-sensitive
26	38	47.5	968	2 T01733	hypothetical prote
27	38	47.5	4859	2 S74173	ryanodine receptor
28	38	47.5	4868	2 B54161	ryanodine-binding
29	38	47.5	4869	2 S65572	ryanodine receptor
					ryanodine receptor

30	38	47.5	4967	2 S72269	ryanodine receptor
31	38	47.5	4969	2 A37113	ryanodine receptor
32	38	47.5	5032	1 A35041	ryanodine receptor
33	38	47.5	5035	1 T46646	ryanodine receptor
34	38	47.5	5037	1 A54161	ryanodine-binding
35	38	47.5	5037	1 B35041	ryanodine receptor
36	37.5	46.9	161	2 C85605	unknown in ISEC8
37	37.5	46.9	161	2 D85656	unknown in ISEC8
38	37	46.2	113	2 E83338	hypothetical prote
39	37	46.2	157	2 D84987	smg protein [impor
40	37	46.2	208	1 BVECIB	incB protein - pha
41	37	46.2	228	2 T46477	hypothetical prote
42	37	46.2	334	2 S44299	hypothetical prote
43	37	46.2	364	2 T18972	hypothetical prote
44	37	46.2	401	2 T32167	hypothetical prote
45	37	46.2	418	2 S62483	hypothetical prote

ALIGNMENTS

RESULT 1
A41242
Interleukin-6 receptor precursor - human
N:Contains: interleukin-6 receptor, soluble form
C:Species: Homo sapiens (man)
C>Date: 27-Mar-1992 #sequence_revision 02-Dec-1994 #text_change 21-Jul-2000
C:Accession: A41242; J00080; S17468; A61459; S14621
R:Yamasaki, K.; Taga, T.; Hirata, Y.; Yawata, H.; Kawashishi, Y.; Seed, B.; Taniguchi, Science 241, 825-828, 1988
A>Title: Cloning and expression of the human interleukin-6 (BSF-2/IFNbeta 2) receptor
A:Reference number: A41242; MUID:8830547
A:Accession: A41242
A:Molecule type: mRNA
A:Residues: 1-468 <YAA>
A:Cross-references: GB:M20566; NID:933845; PIDN:CAA31312.1; PID:933846
R:Yamasaki, K.; Taga, T.; Hirata, Y.; Yawata, H.; Kawashishi, Y.; Seed, B.; Taniguchi, Proc. Jpn. Acad. 64, 209-211, 1988
A>Title: Molecular structure of Interleukin 6 receptor.
A:Reference number: J00080
A:Accession: J00080
A:Molecule type: mRNA
A:Residues: 1-468 <YAA>
R:Schmidt, H.; Stoyan, T.; Lenz, D.; Schmitz, H.; Hirano, T.; Kishimoto, T.; Heinrich, Biochem. J. 277, 659-664, 1991
A>Title: Structural and functional studies on the human hepatic interleukin-6 recepto
A:Reference number: S17468; MUID:91336983
A:Accession: S17468
A:Molecule type: mRNA
A:Residues: 1-468 <SCH>
A:Cross-references: EMBL:X58298; NID:932580; PIDN:CAA41231.1; PID:932581
A:Experimental source: hepatoma cell line HepG2
R:Novick, D.; Engelmann, H.; Wallach, D.; Rubinstein, M. J. Exp. Med. 170, 1409-1414, 1989
A>Title: Soluble cytokine receptors are present in normal human urine.
A:Reference number: A61459; MUID:90010793
A:Accession: A61459
A:Molecule type: protein
A:Residues: 20-49 <NOV>
C:Comment: Through this receptor, interleukin-6 induces proliferation, activation, an
C:Comment: This growth factor receptor does not have a tyrosine kinase domain.
C:Genetics:
A:Gene: GDB:IL6R
A:Cross-references: GDB:127966; OMIM:147880
A:Map position: 1q21-1q21
C:Superfamily: ciliary neurotrophic factor receptor; cytokine receptor homology; immu
C:Keywords: acute phase; cytokine receptor; glycoprotein; transmembrane protein
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-468/Product: interleukin-6 receptor #status predicted <MAT>
F:20-363/Domain: extracellular #status predicted <EXT>
F:40-98/Domain: immunoglobulin homology <IMM2>
F:121-309/Domain: cytokine receptor homology <CRS>
F:364-386/Domain: transmembrane #status predicted <TM>

A>Note: Intron positions not resolved (incomplete sequence)
 C:Superfamily: alpha-crystallin
 C:Keywords: chloroplast; heat shock; stress-induced protein

Query Match 53.8%; Score 43; DB 2; Length 205;
 Best Local Similarity 69.2%; Pred. No. 4.6;
 Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 LSCFRKSPLSNV 14
 DB 1 LTCSAASPLSNV 13

RESULT 6
 B81704
 Conserved hypothetical protein TC0424 [imported] - Chlamydia muridarum (strain Nigg)
 C:Species: Chlamydia muridarum, Chlamydia trachomatis MOpn
 C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 11-May-2000
 C:Accession: B81704
 R:Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey,
 C.; Dodson, R.; Gwin, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg,
 Nucleic Acids Res. 28, 1397-1406, 2000
 A:Title: Genome sequences of Chlamydia trachomatis MOpn and Chlamydia pneumoniae AR39.
 A:Reference number: A81500; MUID:20150255
 A:Accession: B81704
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-1436 <TE>
 A:Cross-references: GB:AE002309; GB:AE002160; NID:g7190464; PIDN:AAF39280.1; PID:g719046
 A:Experimental source: strain Nigg (MOpn)
 C:Genetics:
 A:Gene: TC0424

Query Match 53.8%; Score 43; DB 2; Length 1436;
 Best Local Similarity 46.7%; Pred. No. 26;
 Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 QUSCFRKSPLSNVC 15
 DB 771 ELSSSRKDEIDNLTLC 785

RESULT 7
 PC4369
 olfactory receptor, HT2 - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 15-Oct-1997 #sequence_revision 07-Nov-1997 #text_change 20-Jun-2000
 C:Accession: PC4369
 R:Vanderhaeghen, P.; Schumann, S.; Vassart, G.; Parmentier, M.
 Biochem. Biophys. Res. Commun. 237, 283-287, 1997
 A:Title: Molecular cloning and chromosomal mapping of olfactory receptor genes expressed
 A:Reference number: J05624; MUID:97415789
 A:Contents: Testis
 A:Accession: PC4369
 A:Molecule type: mRNA
 A:Residues: 1-264 <YAN>
 A:Cross-references: GB:Y10529; NID:g2792015; PIDN:CAA71557.1; PID:g2792016
 C:Comment: This receptor is involved in the control of sperm physiology.
 C:Genetics:
 A:Map position: 19p13.12-13.3
 C:Superfamily: olfactory receptor OR14
 C:Keywords: G protein-coupled receptor

Query Match 52.5%; Score 42; DB 2; Length 264;
 Best Local Similarity 46.7%; Pred. No. 8.5;
 Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 QUSCFRKSPLSNVC 15
 DB 108 QLTGCFKDVDSNFC 122

RESULT 8
 T40821
 probable ubiquitin-protein ligase - fission yeast (Schizosaccharomyces pombe)

C:Species: Schizosaccharomyces pombe
 C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 04-Mar-2000
 C:Accession: T40821
 R:Beck, A.; Reinhardt, R.; Lyne, M.; Rajandream, M.A.; Barrell, B.G.
 submitted to the EMBL Data Library, October 1998
 A:Reference number: Z21949
 A:Accession: T40821
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-807 <BEC>
 A:Cross-references: EMBL:AL032684; PIDN:CAA21812.1; GSPDB:GN00067; SPDB:SPBP8B7.27
 A:Experimental source: strain 972h; clone p1 p8B7
 C:Genetics:
 A:Gene: SPDB:SPBP8B7.27
 A:Map position: 2
 A:Introns: 78/3
 C:Superfamily: ubiquitin--protein ligase homology
 F:458-802/Domain: ubiquitin--protein ligase homology <DBI>

Query Match 51.2%; Score 41; DB 2; Length 807;
 Best Local Similarity 54.5%; Pred. No. 35;
 Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 LSCFRKSPLSN 12
 DB 288 ISCFRKPYPNN 298

RESULT 9
 D70830
 hypothetical protein RV0443 - Mycobacterium tuberculosis (strain H37RV)
 C:Species: Mycobacterium tuberculosis
 C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 08-Sep-2000
 C:Accession: D70830
 R:Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon
 Connor, R.; Davies, R.; Devlin, K.; Felkwell, T.; Gentles, S.; Hamlin, N.; Holroyd,
 Rajandream, M.A.; Rogers, J.; Ruter, S.; Seeger, K.; Skelton, S.; Squares, S.
 Nature 393, 537-544, 1998
 A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
 A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete geno
 A:Reference number: A70500; MUID:98295987
 A:Accession: D70830
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-171 <COL>
 A:Cross-references: GB:AL021932; GB:AL123456; NID:g3261527; PIDN:CAA17400.1; PID:g290
 A:Experimental source: strain H37RV
 C:Genetics:
 A:Gene: RV0443
 C:Superfamily: Streptomyces coelicolor hypothetical protein SC5H1.23

Query Match 50.0%; Score 40; DB 2; Length 171;
 Best Local Similarity 42.9%; Pred. No. 13;
 Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 QUSCFRKSPLSNV 14
 DB 33 QIACRYRTPSANSI 46

RESULT 10
 T22478
 hypothetical protein F52A8.2 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 31-Jan-2000
 C:Accession: T22478

R.Wilkinson, J.
Submitted to the EMBL Data Library, April 1996
A:Reference number: Z19568
A:Accession: T22478
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-356 <WIL>
A:Cross-references: EMBL:Z19568.1; PIDN:CAA95824.1; GSPDB:GN00019; CESP:F52A8.2
A:Experimental source: clone F52A8
C:Genetics:
A:Gene: CESP:F52A8.2
A:Map position: 1
A:Introns: 13/2; 43/1; 88/3; 128/2; 192/3; 265/3; 298/1
C:Superfamily: GTP-binding regulatory protein beta chain; WD repeat homology

Query Match 50.0%; Score 40; DB 2; Length 356;
Best Local Similarity 46.7%; Pred. No. 25;
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

OY 1 QLSCKRSPLSNVYC 15
:::| | | | |
Db 330 RISCLRTSPDGTAVC 344

RESULT 11
T10971
Pv42 protein - kidney bean
C:Species: Phaseolus vulgaris (kidney bean)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C:Accession: T10971
R:Ade, H.
Submitted to the EMBL Data Library, November 1995
A:Reference number: Z17236
A:Accession: T10971
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-379 <ABE>
A:Cross-references: EMBL:U040713; NID:g1113940; PID:g1113941

Query Match 50.0%; Score 40; DB 2; Length 379;
Best Local Similarity 46.2%; Pred. No. 26;
Matches 6; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

OY 2 LSCFRKSPLSNVYC 14
:::| | | | |
Db 323 VTCYAESPLSEVI 335

RESULT 12
S73420
methionine adenosyltransferase (EC 2.5.1.6) 2 - Mycoplasma pneumoniae (strain ATCC 29342
N:Alternate names: hypochetrical protein D09_crf383; S-adenosylmethionine synthetase 2
C:Species: Mycoplasma pneumoniae
A:Variety: ATCC 29342
C:Date: 26-Feb-1997 #sequence_revision 25-Apr-1997 #text_change 05-May-2000
C:Accession: S73420
R:Himmelreich, R.; Hilbert, H.; Plagens, H.; Pflkl, E.; Li, B.C.; Herrmann, R.
Nucleic Acids Res. 24, 4420-4449, 1996
A:Title: Complete sequence analysis of the genome of the bacterium Mycoplasma pneumoniae
A:Reference number: S73327; MUID:91105885
A:Accession: S73420
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-383 <HIM>
A:Cross-references: EMBL:AE000011; GB:U00089; NID:g1673740; PIDN:AA895742.1; PID:g167374
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1996
C:Genetics:
A:Gene: metX
A:Genetic code: GCC
C:Superfamily: methionine adenosyltransferase
C:Keywords: S-adenosylmethionine; transferase

Query Match 50.0%; Score 40; DB 2; Length 383;
Best Local Similarity 50.0%; Pred. No. 26;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 4 CFRKSPLSNVYC 15
| : | | | | |
Db 38 CIKOSPTSHVAC 49

RESULT 13
T47208
methionine adenosyltransferase (EC 2.5.1.6) [imported] - Neurospora crassa (fragment)
C:Species: Neurospora crassa
C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 02-Sep-2000
C:Accession: T47208
R:Barra, J.L.; Martino, M.R.; Rosa, A.L.
Submitted to the EMBL Data Library, September 1995
A:Description: Eth-1r, a mutant allele of Neurospora crassa S-adenosylmethionine synt
A:Reference number: Z24392
A:Accession: T47208
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-359 <BAR>
A:Cross-references: EMBL:U36761; PIDN:AAA83756.1
C:Genetics:
A:Gene: eth-1r
A>Note: Intron positions not resolved (incomplete sequence)
C:Superfamily: methionine adenosyltransferase
C:Keywords: S-adenosylmethionine; transferase

Query Match 48.8%; Score 39; DB 2; Length 359;
Best Local Similarity 46.2%; Pred. No. 37;
Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 3 SCFRKSPLSNVYC 15
: | : | | | | |
Db 14 ACLAENPLSKVAC 26

RESULT 14
I39727
manopine biosynthesis protein masI' - Agrobacterium rhizogenes plasmid pR18196
C:Species: Agrobacterium rhizogenes
C:Date: 09-Mar-1996 #sequence_revision 09-Mar-1996 #text_change 08-Oct-1999
C:Accession: I39727
R:Hansen, G.; Larribe, M.; Vaubert, F.; Tempe, J.; Biermann, B.J.; Montoya, A.L.; Chi
Proc. Natl. Acad. Sci. U.S.A. 88, 7763-7767, 1991
A:Title: Agrobacterium rhizogenes pR18196 T-DNA: Mapping and DNA sequence of function
A:Reference number: I39720; MUID:91352070
A:Accession: I39727
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-430 <RES>
A:Cross-references: GB:M60490; NID:g142245; PIDN:AAA22101.1; PID:g142253
C:Genetics:
A:Gene: masI'
A:Genome: plasmid
A>Note: encoded within the T-DNA (transferred DNA) segment of the plasmid; this segme
t disease
C:Superfamily: short-chain alcohol dehydrogenase homology
F:200-377/Domain: short-chain alcohol dehydrogenase homology <SADH>

Query Match 48.8%; Score 39; DB 2; Length 430;
Best Local Similarity 70.0%; Pred. No. 44;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 6 RKSPLSNVYC 15
| | | | | | |
Db 70 RKLPISSVYC 79

RESULT 15

T16232

Hypothetical protein F32A5.2 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999

C:Accession: T16232

R:Pauley, A.

Submitted to the EMBL Data Library, July 1995

A:Description: The sequence of C. elegans cosmid F32A5.

A:Reference number: 218482

A:Accession: T16232

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-977 <PAU>

A:Cross-references: EMBL:U20864; NID:g669026; PID:g669033; PIDN:AAC4666.1; CESP:F32A5.2

A:Experimental source: strain Bristol N2

C:Genetics:

A:Gene: CESP:F32A5.2

A:Introns: 23/1; 58/3; 102/3; 136/2; 277/2; 380/2; 422/1; 502/1; 580/2; 648/1; 935/2

Query Match

48.8%; Score 39; DB 2; Length 977;

Best Local Similarity 53.3%; Pred. No. 91;

Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 QLSCFRKSPLSNVVC 15

11 111 11 : :1

DB 948 OLVEIRKSSLSRRIIC 962

Search completed: December 19, 2001, 16:22:37
Job time: 457 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: December 19, 2001, 16:26:14 ; Search time 48.45 Seconds

(without alignments)
11.351 Million cell updates/sec

Title: US-09-202-104A-4

Perfect score: 80

Sequence: 1 QLSCFRKSPLSNVVC 15

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	80	100.0	468	1 IL6A_HUMAN	P08887 homo sapien
2	73	91.2	467	1 IL6A_PIG	O18796 sus scrofa
3	62	71.5	460	1 IL6A_MOUSE	P22272 mus musculu
4	58	72.5	462	1 IL6A_RAT	P22273 rattus norv
5	42	52.5	861	1 SMAD_MOUSE	O09126 mus musculu
6	42	52.5	863	1 YS97_CAEL	O09866 caenorhabd
7	41	51.2	1818	1 Z294_HUMAN	O94822 homo sapien
8	40	50.0	356	1 GBB5_CAEL	O20636 caenorhabd
9	40	50.0	383	1 MERT_MYCPN	P78603 mycoplasma
10	39	48.8	430	1 MS12_AGRH	P50201 agrobacteri
11	39	48.8	805	1 CC48_CAPAN	O96372 capsicum an
12	39	48.8	3110	1 HD_RAT	P51111 rattus norv
13	39	48.8	3119	1 HD_HUMAN	P42859 mus musculu
14	39	48.8	3144	1 HD_MOUSE	P42858 homo sapien
15	38	47.5	161	1 YKT9_CAEL	P34320 caenorhabd
16	38	47.5	393	1 MERT_ASCIM	P50304 ascobolus i
17	38	47.5	395	1 MERT_NEUCR	P48866 neurospora
18	38	47.5	533	1 STK_MERMP	O30322 methanococ
19	38	47.5	722	1 MFP1_TOBAC	O9m14 nicotiana t
20	38	47.5	754	1 PURL_MYCLE	O50023 mycobacteri
21	38	47.5	4969	1 RYNC_RABIT	P30597 oryctolagus
22	38	47.5	5032	1 RYNR_HUMAN	P21817 homo sapien
23	38	47.5	5035	1 RYNR_HUMAN	P16960 sus scrofa
24	38	47.5	5037	1 RYNR_PIG	P11716 oryctolagus
25	37	46.2	157	1 SMG_BUCAI	P57562 buchnera ap
26	37	46.2	183	1 MGR1_MOUSE	P97772 mus musculu
27	37	46.2	208	1 INCB_ECOLI	P05831 escherichia
28	37	46.2	364	1 YP91_CAEL	P48858 caenorhabd
29	37	46.2	418	1 YAD6_SCHPO	O09932 schizosach
30	37	46.2	690	1 E75_CHOFO	O01339 christionon
31	37	46.2	699	1 E75_MANSE	O08893 manduca sex
32	37	46.2	711	1 E75_GALME	P50239 gallieria me
33	37	46.2	874	1 SYLM_SCHPO	O09828 schizosach

34	37	46.2	2820	1 NF1_RAT	P97526 rattus norv
35	37	46.2	2839	1 NF1_HUMAN	P21339 homo sapien
36	37	46.2	2841	1 NF1_MOUSE	O04690 mus musculu
37	36	45.0	118	1 PAZH_LATCO	P10117 latitanda c
38	36	45.0	202	1 Y740_ARCFU	O29518 archaeglob
39	36	45.0	261	1 ASPX_MOUSE	P50289 mus musculu
40	36	45.0	393	1 ACKA_MYCGE	P47599 mycoplasma
41	36	45.0	743	1 PURL_BACHD	O9k157 bacillus ha
42	36	45.0	794	1 SYG_LUPRU	P52780 lupinus lut
43	36	45.0	962	1 YBX7_SCHPO	O10201 schizosach
44	36	45.0	1141	1 SYL_CAEL	O21926 caenorhabd
45	36	45.0	3097	1 CADN_DROME	O15943 drosophilla

ALIGNMENTS

RESULT 1
ID IL6A_HUMAN STANDARD: PRT: 468 AA.
AC P08887; 016202;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE INTERLEUKIN-6 RECEPTOR ALPHA CHAIN PRECURSOR (IL-6R-ALPHA) (IL-6R 1)
DE (CD126 ANTIGEN).
GN IL6R
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A. (LONG ISOFORM).
RX MEDLINE=88305347; PubMed=3136546;
RA Yamasaki K., Taga T., Hirata Y., Yawata H., Kawanishi Y., Seed B.,
RA Taniguchi T., Hirano T., Kishimoto T.;
RT "Cloning and expression of the human interleukin-6 (BSF-2/IFN beta 2)
RT receptor.";
RT Science 241:825-828(1988).
RN [2]
RP SEQUENCE FROM N.A. (LONG ISOFORM).
RA Yamasaki K., Taga T., Hirata Y., Yawata H., Kawanishi Y., Seed B.,
RA Taniguchi T., Hirano T., Kishimoto T.;
RT "Molecular structure of interleukin 6 receptor.";
RT Proc. Jpn. Acad., B, Phys. Biol. Sci. 64:209-211(1988).
RN [3]
RP SEQUENCE FROM N.A. (LONG ISOFORM).
RX MEDLINE=91336983; PubMed=1872801;
RA Schollink H., Stoyan T., Lenz D., Schmitz H., Hirano T.,
RA Kishimoto T., Heinrich P.C., Rose-John S.;
RT "Structural and functional studies on the human hepatic interleukin-6
RT receptor. Molecular cloning and overexpression in HepG2 cells.";
RT Biochem. J. 277:659-664(1991).
RN [4]
RP SEQUENCE OF 313-365 FROM N.A. (SHORT ISOFORM).
RX MEDLINE=94334499; PubMed=8056053;
RA Horuchi S., Koyanagi Y., Zhou Y., Miyamoto H., Tanaka Y., Waki M.,
RA Matsumoto A., Yamamoto M., Yamamoto N.;
RT "Soluble interleukin-6 receptors released from T cell or
RT granulocyte/macrophage cell lines and human peripheral blood
RT mononuclear cells are generated through an alternative splicing
RT mechanism.";
RT Eur. J. Immunol. 24:1945-1948(1994).
RN [5]
RP PARTIAL SEQUENCE, CARBOHYDRATE-LINKAGE SITES, AND DISULFIDE BONDS.
RX MEDLINE=99167486; PubMed=10066782;
RA Cole A.R., Hall N.E., Treutlein H.R., Eddes J.S., Reid G.E.,
RA Moritz R.L., Simpson R.J.;
RT "Disulfide bond structure and N-glycosylation sites of the
RT extracellular domain of the human interleukin-6 receptor.";
RT J. Biol. Chem. 274:7207-7215(1999).
RN [6]
RP MUTAGENESIS.

RA MEDLINE-9323711; PubMed-8467812;
 RA Yawata H., Yasukawa K., Natsuka S., Murakami M., Yamasaki K., Hibi M.,
 RA Taga T., Kishimoto T.;
 RT "Structure-function analysis of human IL-6 receptor: dissociation of
 RT amino acid residues required for IL-6-binding and for IL-6 signal
 RT transduction through gp130.";
 RL EMBO J. 12:1705-1712(1993).
 CC -1- FUNCTION: PART OF THE RECEPTOR FOR INTERLEUKIN 6. BINDS TO IL-6
 CC WITH LOW AFFINITY, BUT DOES NOT TRANSDUCE A SIGNAL. SIGNAL
 CC ACTIVATION NECESSITATE AN ASSOCIATION WITH IL6ST. ACTIVATION MAY
 CC LEAD TO THE REGULATION OF THE IMMUNE RESPONSE, ACUTE-PHASE
 CC REACTIONS AND HEMATOPOIESIS.
 CC -1- FUNCTION: LOW CONCENTRATION OF A SOLUBLE FORM OF INTERLEUKIN-6
 CC RECEPTOR ACTS AS AN AGONIST OF IL-6 ACTIVITY.
 CC -1- SUBUNIT: HEXAMER OF 2 IL6, 2 IL6R-ALPHA AND 2 IL6ST.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (LONG FORM) AND
 CC SECRETED (SHORT FORM).
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: A LONG FORM (SHOWN HERE) AND A
 CC SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: THE SHORT FORM IS EXPRESSED IN PERIPHERAL
 CC BLOOD MONONUCLEAR CELLS AND WEARLY FOUND IN URINE AND SERUM.
 CC -1- DOMAIN: THE TWO FIBROECTIN TYPE III-LIKE DOMAINS CONTAINED IN THE
 CC N-TERMINAL PART FORM TOGETHER A CYTOKINE-BINDING DOMAIN.
 CC -1- PTM: A SHORT SOLUBLE FORM MAY ALSO BE RELEASED FROM THE MEMBRANE
 CC BY PROTEOLYSIS.
 CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
 CC -1- SIMILARITY: CONTAINS 3 FIBROECTIN TYPE III-LIKE DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 CC -1- DATABASE: NAME-PROV: NOTE-CD guide CD126 entry;
 CC WWW-http://www.ncbi.nlm.nih.gov/prov/cd/cd126.htm".
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 DR EMBL: X12830; CAA31312.1; -;
 DR EMBL: X58298; CAA41231.1; -;
 DR EMBL: S72848; AAC60635.1; -;
 DR PIR: A41242; A41242.
 DR PIR: J00080; J00080.
 DR PIR: S14621; S14621.
 DR PIR: S17468; S17468.
 DR MIM: 147880; -;
 DR InterPro: IPR002996; CRIA.
 DR InterPro: IPR001777; FN_III.
 DR InterPro: IPR003530; Hematopo_receptor_L_F3.
 DR InterPro: IPR003506; Ig_MHC.
 DR InterPro: IPR003598; Ig_C2.
 DR Pfam: PF00041; fn3; 1.
 DR Pfam: PF00047; Ig; 1.
 DR SMART: SM00060; FN3; 1.
 DR SMART: SM00408; IgC2; 1.
 DR PROSITE: PS01354; HEMATOPO_REC_L_F3; 1.
 DR Receptor; Transmembrane; Glycoprotein; Immunoglobulin domain; Repeat;
 KM Alternative splicing; Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 468 INTERLEUKIN-6 RECEPTOR ALPHA CHAIN.
 FT DOMAIN 20 365 EXTRACELLULAR (POTENTIAL).
 FT TRANSEM 366 386 POTENTIAL.
 FT DOMAIN 387 468 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 40 103 IG-LIKE C2-TYPE DOMAIN.
 FT DISULFID 25 193
 FT DISULFID 47 96
 FT DISULFID 121 132
 FT DISULFID 165 176
 FT CARBOHYD 55 55
 FT CARBOHYD 93 93
 FT CARBOHYD 221 221 N-LINKED (GLCNAC. . .).
 FT VARSPPLIC 356 365 VOSSSVPLP -> GSRRRSGCL (IN SHORT

FT VARSPPLIC 366 468 ISOFORM).
 FT MUTAGEN 121 121 MISSING (IN SHORT ISOFORM).
 FT MUTAGEN 122 122 C->S: COMPLETE LOSS OF LIGAND-BINDING.
 FT MUTAGEN 132 132 F->A: NO CHANGE OF LIGAND-BINDING AND IL6
 FT MUTAGEN 133 133 SIGNALING.
 FT MUTAGEN 134 134 C->A: COMPLETE LOSS OF LIGAND-BINDING.
 FT MUTAGEN 140 140 W->L: COMPLETE LOSS OF LIGAND-BINDING.
 FT MUTAGEN 140 140 P->G: NO CHANGE OF LIGAND-BINDING AND IL6
 FT MUTAGEN 153 153 SIGNALING.
 FT MUTAGEN 153 153 F->L: NO CHANGE OF LIGAND-BINDING AND IL6
 FT MUTAGEN 165 165 SIGNALING.
 FT MUTAGEN 174 174 C->L: COMPLETE LOSS OF LIGAND-BINDING.
 FT MUTAGEN 174 174 F->L: NO CHANGE OF LIGAND-BINDING AND IL6
 FT MUTAGEN 176 176 SIGNALING.
 FT MUTAGEN 184 184 C->A: COMPLETE LOSS OF LIGAND-BINDING.
 FT MUTAGEN 190 190 D->T: 30% DECREASE OF LIGAND-BINDING AND
 FT MUTAGEN 190 190 IL6 SIGNALING.
 FT MUTAGEN 193 193 V->G: 80% DECREASE OF LIGAND-BINDING AND
 FT MUTAGEN 193 193 NO IL6 SIGNALING.
 FT MUTAGEN 211 211 C->D: COMPLETE LOSS OF LIGAND-BINDING.
 FT MUTAGEN 217 217 C->A: NO CHANGE OF LIGAND-BINDING AND IL6
 FT MUTAGEN 232 232 SIGNALING.
 FT MUTAGEN 233 233 D->V: COMPLETE LOSS OF LIGAND-BINDING.
 FT MUTAGEN 233 233 R->S: 30% DECREASE OF LIGAND-BINDING AND
 FT MUTAGEN 254 254 IL6 SIGNALING.
 FT MUTAGEN 277 277 W->O: 30% DECREASE OF LIGAND-BINDING AND
 FT MUTAGEN 278 278 INCREASE OF IL6 SIGNALING.
 FT MUTAGEN 279 279 E->A: 50% DECREASE OF LIGAND-BINDING AND
 FT MUTAGEN 280 280 IL6 SIGNALING.
 FT MUTAGEN 281 281 C->D: 30% INCREASE OF LIGAND-BINDING AND
 FT MUTAGEN 285 285 100% INCREASE IN IL6 SIGNALING.
 FT MUTAGEN 291 291 V->N: 50% DECREASE OF LIGAND-BINDING AND
 FT MUTAGEN 293 293 50% INCREASE IN IL6 SIGNALING.
 FT MUTAGEN 293 293 I->D: COMPLETE LOSS OF LIGAND-BINDING.
 FT MUTAGEN 281 281 H->I: NO CHANGE OF LIGAND-BINDING AND NO
 FT MUTAGEN 281 281 IL6 SIGNALING.
 FT MUTAGEN 285 285 D->G: 70% DECREASE OF LIGAND-BINDING AND
 FT MUTAGEN 285 285 NO IL6 SIGNALING.
 FT MUTAGEN 291 291 G->D: 80% DECREASE OF LIGAND-BINDING AND
 FT MUTAGEN 293 293 NO IL6 SIGNALING.
 FT MUTAGEN 293 293 Q->K: COMPLETE LOSS OF LIGAND-BINDING.
 FT MUTAGEN 293 293 R->G: COMPLETE LOSS OF LIGAND-BINDING.
 FT SEQUENCE 468 AA; 51547 MW; 67AA239FA14F1BB8 CRC64;
 SO
 QY 1 QLSCFRKSPLSNVVC 15
 Db 118 QLSCFRKSPLSNVVC 132
 Db 118 QLSCFRKSPLSNVVC 132
 RESULT 2
 IL6A_PIG STANDARD; PRT; 467 AA.
 ID IL6A_PIG
 AC 018796;
 DT 20-AUG-2001 (Rel. 40, Created)
 DT 20-AUG-2001 (Rel. 40, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE INTERLEUKIN-6 RECEPTOR ALPHA CHAIN PRECURSOR (IL-6R-ALPHA) (IL-6R 1).
 GN IL6R.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.
 OC NCBI_TaxID=9823;
 OX [1]
 RN SEQUENCE FROM N.A.
 RP Morris K.R., Strom A.D.G.;
 RA "Cloning and expression of biologically active porcine IL-6 receptor
 RT alpha chain.";
 RT Submitted (May-1999) to the EMBL/GenBank/DBJ databases.

[2]
 RN SEQUENCE OF 123-186 FROM N.A.
 RP TISSUE-LIVER;
 RC Klier J.J., Matteri R.L.;
 RT "Patented cDNA sequence of porcine interleukin 6 receptor";
 RL Submitted (JUL-1997) to the EMBL/Genbank/DBJ databases.
 CC -1- FUNCTION: PART OF THE RECEPTOR FOR INTERLEUKIN 6. BINDS TO IL-6
 CC WITH LOW AFFINITY, BUT DOES NOT TRANSDUCE A SIGNAL. SIGNAL
 CC ACTIVATION NECESSITATE AN ASSOCIATION WITH IL6ST. ACTIVATION MAY
 CC LEAD TO THE REGULATION OF THE IMMUNE RESPONSE, ACUTE-PHASE
 CC REACTIONS AND HEMATOPOIESIS.
 CC -1- SUBUNIT: HEXAMER OF 2 IL6, 2 IL6R-ALPHA AND 2 IL6ST (BY
 CC SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN LIVER.
 CC -1- DOMAIN: THE TWO FIBRONECTIN TYPE III-LIKE DOMAINS CONTAINED IN THE
 CC C-TERMINAL PART FORM TOGETHER A CYTOKINE-BINDING DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
 CC -1- SIMILARITY: CONTAINS 3 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
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 CC DR HSSP: P16471; 1BP3.
 CC DR InterPro: IPR002996; CR1A.
 CC DR InterPro: IPR001777; FN_III.
 CC DR InterPro: IPR003530; Hematopo_rceptor_L_F3.
 CC DR InterPro: IPR003006; IG_MHC.
 CC DR InterPro: IPR003598; IG_C2.
 CC DR Pfam: PF00041; fn3; 1.
 CC DR Pfam: PF00047; Ig; 1.
 CC DR SMART: SM00060; FN3; 1.
 CC DR SMART: SM00408; IGC2; 1.
 CC DR PROSITE: PS00340; RECEPTOR_CYTOKINES_2; 1.
 CC KW Receptor; Transmembrane; Glycoprotein; Immunoglobulin domain; Repeat;
 CC KW Signal.
 CC FT SIGNAL 1 19 BY SIMILARITY.
 CC FT CHAIN 20 467 INTERLEUKIN-6 RECEPTOR ALPHA CHAIN.
 CC FT DOMAIN 20 365 EXTRACELLULAR (POTENTIAL).
 CC FT TRANSMEM 366 386 POTENTIAL.
 CC FT DOMAIN 387 467 CYTOPLASMIC (POTENTIAL).
 CC FT DOMAIN 40 103 IG-LIKE C2-TYPE DOMAIN.
 CC FT DISULFID 25 193 BY SIMILARITY.
 CC FT DISULFID 47 96 BY SIMILARITY.
 CC FT DISULFID 121 132 BY SIMILARITY.
 CC FT DISULFID 165 176 BY SIMILARITY.
 CC FT CAROXYD 55 55 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CAROXYD 93 93 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CAROXYD 221 221 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CAROXYD 350 350 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT SEQUENCE 467 AA; 51066 MW; A2B0B84BE21C502 CRC64;

AC P22272;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE INTERLEUKIN-6 RECEPTOR ALPHA CHAIN PRECURSOR (IL-6R-ALPHA) (IL-6R 1).
 GN IL6RA OR IL6R.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_Taxid=10090;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN-BALB/C; TISSUE-Spleen;
 RX MEDLINE=90278354; PubMed=2112585;
 RA Sugita T., Totsuka T., Saio M., Yamasaki K., Taga T., Hirano T.,
 RA Kishimoto T.;
 RT "Functional murine interleukin 6 receptor with the intracellular A
 RT particle gene product at its cytoplasmic domain. Its possible role in
 RT plasmacytomagenesis";
 RL J. Exp. Med. 171:2001-2009(1990).
 RN (2)
 RP SEQUENCE FROM N.A.
 RC STRAIN-C3H; TISSUE-Liver;
 RA Florillo M.T., Cliberto G., Dente L.;
 RL Submitted (JUL-1990) to the EMBL/Genbank/DBJ databases.
 CC -1- FUNCTION: PART OF THE RECEPTOR FOR INTERLEUKIN 6. BINDS TO IL-6
 CC WITH LOW AFFINITY, BUT DOES NOT TRANSDUCE A SIGNAL. SIGNAL
 CC ACTIVATION NECESSITATE AN ASSOCIATION WITH IL6ST. ACTIVATION MAY
 CC LEAD TO THE REGULATION OF THE IMMUNE RESPONSE, ACUTE-PHASE
 CC REACTIONS AND HEMATOPOIESIS.
 CC -1- SUBUNIT: HEXAMER OF 2 IL6, 2 IL6R-ALPHA AND 2 IL6ST (BY
 CC SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- DOMAIN: THE TWO FIBRONECTIN TYPE III-LIKE DOMAINS CONTAINED IN THE
 CC C-TERMINAL PART FORM TOGETHER A CYTOKINE-BINDING DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
 CC -1- SIMILARITY: CONTAINS 3 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 CC -----
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 CC -----
 CC EMBL: X51975; CAA36237.1; -;
 CC DR EMBL: X53802; CAA37810.1; -;
 CC DR PIR: J10144; J10144.
 CC DR PIR: J10145; J10145.
 CC DR PIR: S14543; S14543.
 CC DR HSSP: P16471; 1BP3.
 CC DR MGD: MG1:105304; IL6ra.
 CC DR InterPro: IPR002996; CR1A.
 CC DR InterPro: IPR001777; FN_III.
 CC DR InterPro: IPR003530; Hematopo_rceptor_L_F3.
 CC DR InterPro: IPR003006; IG_MHC.
 CC DR InterPro: IPR003598; IG_C2.
 CC DR Pfam: PF00041; fn3; 1.
 CC DR Pfam: PF00047; Ig; 1.
 CC DR SMART: SM00060; FN3; 1.
 CC DR SMART: SM00408; IGC2; 1.
 CC DR PROSITE: PS01354; HEMATOPO_REC_L_F3; 1.
 CC KW Receptor; Transmembrane; Glycoprotein; Immunoglobulin domain; Repeat;
 CC KW Signal.
 CC FT SIGNAL 1 19
 CC FT CHAIN 20 460 INTERLEUKIN-6 RECEPTOR ALPHA CHAIN.
 CC FT DOMAIN 20 364 EXTRACELLULAR (POTENTIAL).
 CC FT TRANSMEM 365 385 POTENTIAL.
 CC FT DOMAIN 386 460 CYTOPLASMIC (POTENTIAL).
 CC FT DOMAIN 40 99 IG-LIKE C2-TYPE DOMAIN.
 CC FT DISULFID 25 190 BY SIMILARITY.

Query Match 91.2%; Score 73; DB 1; Length 467;
 Best Local Similarity 93.3%; Pred. No. 8.9e-06;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QLSCEKSPLSNVVC 15
 DB 118 QLSCEKSPLSNVGC 132

RESULT 3
 IL6A_MOUSE STANDARD; PRT; 460 AA.

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FT DISULFID 47 92 BY SIMILARITY.
FT DISULFID 117 128 BY SIMILARITY.
FT DISULFID 162 173 BY SIMILARITY.
FT CARBOHYD 32 32 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 35 35 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 150 150 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 374 374 A -> R (IN REF. 2).
SO SEQUENCE 460 AA; 50454 MW; F85C5906D08525C4 CRC64;

Query Match 77.5%; Score 62; DB 1; Length 460;
Best Local Similarity 66.7%; Pred. No. 0.00086;
Matches 10; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 QLSGFRKPSLSNVYC 15
DB 114 KLSGFRKPNPLVNAIC 128

RESULT 4
ID IL6A_RAT STANDARD; PRT; 462 AA.
AC P22273;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE INTERLEUKIN-6 RECEPTOR ALPHA CHAIN PRECURSOR (IL-6R-ALPHA) (IL-6R 1).
GN IL6R.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_Taxid=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FISCHER 344; TISSUE=Liver;
RX MEDLINE=91060602; Pubmed=2174054;
RA Baumann M., Baumann H., Fey G.H.;
RT "Molecular cloning, characterization and functional expression of the
RT rat liver Interleukin 6 receptor.";
RT J. Biol. Chem. 265:19853-19862(1990).
RN [2]
RP IDENTIFICATION OF PROBABLE FRAMESHIFT IN 227-261.
RA Gibson T.;
RL Unpublished observations (Feb-1995).
CC -1- FUNCTION: PART OF THE RECEPTOR FOR INTERLEUKIN 6. BINDS TO IL-6
CC WITH LOW AFFINITY, BUT DOES NOT TRANSDUCE A SIGNAL. SIGNAL
CC ACTIVATION NECESSITATE AN ASSOCIATION WITH IL6ST. ACTIVATION MAY
CC LEAD TO THE REGULATION OF THE IMMUNE RESPONSE. ACUTE-PHASE
CC REACTIONS AND HEMATOPOIESIS.
CC -1- SUBUNIT: HEXAMER OF 2 IL6, 2 IL6R-ALPHA AND 2 IL6ST (BY
CC SIMILARITY).
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- DOMAIN: THE TWO FIBROBLAST TYPE III-LIKE DOMAINS CONTAINED IN THE
CC C-TERMINAL PART FORM TOGETHER A CYTOKINE-BINDING DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC -1- SIMILARITY: CONTAINS 3 FIBROBLAST TYPE III-LIKE DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC
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CC
CC EMBL; M58587; AAA41431.1; -.
CC PIR; A37986; A37986.
CC HSP; P16471; 1BP3.
CC InterPro; IPR002996; CRIA.
CC InterPro; IPR001777; FN_III.
CC InterPro; IPR003530; Hematopo_receptor_L_F3.
CC InterPro; IPR003006; Ig_MHC.

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DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF00041; fn3; 1.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00060; FN3; 1.
DR SMART; SM00408; ICG2; 1.
DR PROSITE; PS01354; HEMATOPO_RBC_L_F3; 1.
DR Receptor; Transmembrane; Glycoprotein; Immunoglobulin domain; Repeat;
KW Signal.
FT SIGNAL 1 19
FT CHAIN 20 462 INTERLEUKIN-6 RECEPTOR ALPHA CHAIN.
FT DOMAIN 20 364 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 365 385 POTENTIAL.
FT DOMAIN 386 462 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 40 99 IG-LIKE C2-TYPE DOMAIN.
FT DISULFID 25 190 BY SIMILARITY.
FT DISULFID 47 92 BY SIMILARITY.
FT DISULFID 117 128 BY SIMILARITY.
FT DISULFID 162 173 BY SIMILARITY.
FT CARBOHYD 32 32 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 35 35 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 85 85 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 150 150 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 227 261 XPRILVSMQDPSPSPSYLLQFLRYRWSEKX ->
FT SLVGSKSVGRTLSFGIVTTCSSPDTLXGQRT
FT (IN REF. 1).
SO SEQUENCE 462 AA; 50398 MW; A4D6064CEDC0537D CRC64;

Query Match 72.5%; Score 58; DB 1; Length 462;
Best Local Similarity 66.7%; Pred. No. 0.0046;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 QLSGFRKPSLSNVYC 15
DB 114 KLSGFRKPNPLVNAIC 128

RESULT 5
ID SM4D_MOUSE STANDARD; PRT; 861 AA.
AC O09126;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE SEMAPHORIN 4D PRECURSOR (SEMAPHORIN J) (SEMA J) (SEMAPHORIN C-LIKE 2)
DE (SEMA G).
GN SEMA4D OR SEMA J OR SEMA C L2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE=9715976; Pubmed=8969198;
RA Furuyama T., Inagaki S., Kosugi A., Noda S., Satoh S.-I., Ogata M.,
RA Iwahashi Y., Miyazaki N., Hamada T., Tohyama M.;
RT "Identification of a novel transmembrane semaphorin expressed on
RT lymphocytes.";
RT J. Biol. Chem. 271:33376-33381(1996).
RN [2]
RP IDENTIFICATION OF A FUNCTIONAL ROLE IN THE IMMUNE SYSTEM, AS WELL
CC AS IN THE NERVOUS SYSTEM.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: STRONGLY EXPRESSED IN LYMPHOID TISSUES.
CC -1- TISSUE SPECIFICITY: STRONGLY EXPRESSED IN THE NERVOUS TISSUES.
CC -1- SIMILARITY: BELONGS TO THE SEMAPHORIN FAMILY.
CC -1- SIMILARITY: CONTAINS 1 SEMA DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC
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DR EMBL: U69535; AAC52964.1; -
 DR MGD; MGI:109244; Sema4d.
 DR InterPro: IPR003006; I9_MHC.
 DR InterPro: IPR003598; I9_C2.
 DR InterPro: IPR003659; PSI.
 DR InterPro: IPR002165; Plexin_repeat.
 DR InterPro: IPR001627; Sema.
 DR Pfam: PF00047; I9; 1.
 DR Pfam: PF01437; Plexin_repeat; 1.
 DR SMART: SM00403; Sema; 1.
 DR SMART: SM00408; IGC2; 1.
 DR SMART: SM00423; PSI; 1.
 DR Signal; transmembrane; Immunoglobulin domain; Multigene family;
 KW Neurogenesis; Developmental protein; Glycoprotein.
 FT SIGNAL 1 23
 FT CHAIN 24 861
 FT DOMAIN 24 733
 FT TRANSMEM 734 754
 FT DOMAIN 755 861
 FT DOMAIN 228 523
 FT DOMAIN 569 630
 FT DISULFID 576 624
 FT CARBOHYD 49 49
 FT CARBOHYD 77 77
 FT CARBOHYD 139 139
 FT CARBOHYD 191 191
 FT CARBOHYD 379 379
 FT CARBOHYD 419 419
 FT CARBOHYD 613 613
 FT CARBOHYD 632 632
 SQ SEQUENCE 861 AA; 95714 MW; 533C6D271A6D79B CRC64;

Query Match
 Best Local Similarity 52.5%; Score 42; DB 1; Length 861;
 Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 QLSCKRSPLSNVV 14
 Db 573 ELKCFKSLNLRV 586
 : |||: ||| : |||
 : |||: ||| : |||

RESULT 6
 YS97_CAEEL STANDARD; PRT; 863 AA.
 AC 009966;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE PUTATIVE G PROTEIN-COUPLED RECEPTOR B0244.7.
 GN B0244.7.
 OS Caenorhabditis elegans.
 CC Eukaryota; Metazoa; Chordata; Rhabditiida; Rhabditiidae;
 CC Rhabditiidae; Peloderinae; Caenorhabditis.
 CC NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA Favello T., Waterston R.;
 RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
 CC -1- SUPERCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC SUPFAMILY B0244.
 CC -----
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 CC -----

DR EMBL: U28971; AAA68378.1; -
 DR Wormpep; B0244.7; CE02416.
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PROSITE: PS00237; G_PROTEIN_RECPT_FL_1; FALSE_NEG.
 DR PROSITE: PS50262; G_PROTEIN_RECPT_FL_2; 2.
 KW Hypothetical protein; G-protein coupled receptor; Transmembrane;
 KW Glycoprotein.
 FT DOMAIN 596 599
 FT TRANSMEM 49 69
 FT TRANSMEM 107 127
 FT TRANSMEM 131 151
 FT TRANSMEM 166 186
 FT TRANSMEM 206 226
 FT TRANSMEM 262 282
 FT TRANSMEM 313 333
 FT TRANSMEM 352 372
 FT TRANSMEM 393 413
 FT TRANSMEM 536 556
 FT TRANSMEM 579 599
 FT TRANSMEM 612 632
 FT TRANSMEM 660 680
 FT TRANSMEM 698 718
 FT TRANSMEM 749 769
 FT TRANSMEM 787 807
 FT CARBOHYD 28 28
 FT CARBOHYD 521 521
 FT CARBOHYD 731 731
 FT CARBOHYD 812 812
 SQ SEQUENCE 863 AA; 97228 MW; B56BB2B63327683D CRC64;

Query Match
 Best Local Similarity 52.5%; Score 42; DB 1; Length 863;
 Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 3 SCRRKSPLSNVVC 15
 Db 430 SIFRKNKLTNIAC 442
 : |||: ||| : |||
 : |||: ||| : |||

RESULT 7
 Z294_HUMAN STANDARD; PRT; 1818 AA.
 ID 2294_HUMAN
 AC 094822;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 20-AUG-2001 (Rel. 40, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE ZINC FINGER PROTEIN 294.
 GN ZNF294 OR KIA0714.
 GN Homo sapiens (Human).
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 CC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20289799; PubMed=10830953;
 RA Hattori M., Fujiyama A., Taylor T.D., Watanabe H., Yada T.,
 RA Park H.-S., Toyoda A., Ishii K., Totoki Y., Choi D.-K., Soeda E.,
 RA Ohki M., Takagi T., Sakaki Y., Taudien S., Blechschmidt K., Polley A.,
 RA Wenzel U., Delabar J., Kumpf K., Lehmann R., Patterson D.,
 RA Reichwald K., Rump A., Schilhabel M., Schudy A., Zimmermann W.,
 RA Rosenthal A., Kudoh J., Shibuya K., Kawasaki K., Asakawa S.,
 RA Shintani A., Sasaki T., Nagamine K., Mitsuyama S., Antonarakis S.E.,
 RA Minoshima S., Shimizu N., Nordstiek G., Hornischer K., Brandt P.,
 RA Scharfe M., Schoen O., Desario A., Reichelt J., Kauer G., Bloeker H.,
 RA Ramser J., Beck A., Klages S., Hennig S., Riesseltmann L., Dagand E.,
 RA Wehmeyer S., Borzym K., Gardiner K., Nizetic D., Francis F.,
 RA Lehnach H., Reinhardt R., Yaspo M.-L.;
 RT "The DNA sequence of human chromosome 21.";

RL Nature 405:311-319(2000).
 RN [2]
 CC SEQUENCE OF 707-1818.
 RC TISSUE-Brain;
 RX MEDLINE-99087487; Pubmed-9872452;
 RA Nagase T., Ishikawa K.-I., Suyama M., Kikuno R., Miyajima N.,
 RA Tanaka A., Kotani H., Nomura N., Ohara O.;
 RT Prediction of the coding sequences of unidentified human genes. XI.
 RT The complete sequences of 100 new cDNA clones from brain which code
 RT for large proteins in vitro.*;
 RL DNA Res. 5:277-286(1998).
 CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
 CC -1- SIMILARITY: STRONG. NO YEAST YMR247C.
 CC -----
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 CC -----
 DR EMBL: AL163249; CAB90430.1; -
 DR EMBL: AL163248; CAB90429.3; -
 DR EMBL: AB018257; BA034434.1; -
 DR InterPro: IPR001841; Znf_fing.
 DR SMART: SM00184; RING; 1.
 KW Zinc-finger.
 FT ZN.FING 1767 1813 RING-TYPE.
 SQ SEQUENCE 1818 AA; 205732 MW; 416E3E7DADAC4705 CRC64;

Query Match 51.2%; Score 41; DB 1; Length 1818;
 Best Local Similarity 57.1%; Pred. No. 23;
 Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 LSCFRKSPLSNYVC 15
 DB 634 LSPLRKKPLEDLVC 647

RESULT 8
 GBB5_CAEEL STANDARD; PRT; 356 AA.
 AC Q20636;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, last sequence update)
 DT 15-DEC-1998 (Rel. 37, last annotation update)
 DE GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT 5.
 GN P52A8.2.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 NC NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA Wilkinson J.;
 RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: GUANINE NUCLEOTIDE-BINDING PROTEINS (G PROTEINS) ARE
 CC INVOLVED AS A MODULATOR OR TRANSDUCER IN VARIOUS TRANSMEMBRANE
 CC SIGNALING SYSTEMS. THE BETA AND GAMMA CHAINS ARE REQUIRED FOR THE
 CC GTPASE ACTIVITY, FOR REPLACEMENT OF GDP BY GTP, AND FOR G PROTEIN-
 CC EFFECTOR INTERACTION.
 CC -1- SUBUNIT: G PROTEINS ARE COMPOSED OF 3 UNITS (ALPHA, BETA & GAMMA).
 CC -1- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
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 CC -----
 DR EMBL: Z71263; CA95824.1; -
 DR HSSP: P04901; ITBG.
 DR WormPep: F52A8.2; CE17845.
 DR InterPro: IPR001632; Gproteln_B.
 DR InterPro: IPR001680; WD40.
 DR Pfam: PF00400; WD40; 7.
 DR PRINTS: PR00319; GPROTEINB.
 DR PRINTS: PR00320; GPROTEINBPT.
 DR SMART: SM00320; WD40; 7.
 DR PROSITE: PS00678; WD_REPEATS_1; 3.
 DR PROSITE: PS50082; WD_REPEATS_2; 5.
 DR PROSITE: PS50294; WD_REPEATS_REGION; 1.
 KW Transducer; Repeat; WD Repeat; Multigene family.
 FT REPEAT 66 96 WD 1.
 FT REPEAT 108 138 WD 2.
 FT REPEAT 154 184 WD 3.
 FT REPEAT 196 228 WD 4.
 FT REPEAT 240 270 WD 5.
 FT REPEAT 284 314 WD 6.
 FT REPEAT 326 356 WD 7.
 SQ SEQUENCE 356 AA; 39453 MW; 293AA6DCE317D832 CRC64;

Query Match 50.0%; Score 40; DB 1; Length 356;
 Best Local Similarity 46.7%; Pred. No. 6.4;
 Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 QLSCFKSPLSNYVC 15
 DB 330 RISCLRTSPDGTAVC 344

RESULT 9
 METK_MYCPN STANDARD; PRT; 383 AA.
 AC P78003;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, last sequence update)
 DT 20-AUG-2001 (Rel. 40, last annotation update)
 DE S-ADENOSYLMETHIONINE SYNTHETASE (EC 2.5.1.6) (METHIONINE-
 DE ADENOSYLTRANSFERASE) (ADOMET SYNTHETASE).
 GN METK OR METX OR MPN060 OR MP094.
 OS Mycoplasma pneumoniae.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Molluscates;
 OC Mycoplasmataceae; Mycoplasma.
 NC NCBI_TaxID=2104;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-ATCC 29342 / M129;
 RX MEDLINE-97105885; Pubmed-6948633;
 RA Himmelreich R., Hilbert H., Plagens H., Pirk E., Li B.-C.,
 RA Herrmann R.;
 RT "Complete sequence analysis of the genome of the bacterium Mycoplasma
 RT pneumoniae.";
 RL Nucleic Acids Res. 24:4420-4449(1996).
 CC -1- FUNCTION: CATALYZES THE FORMATION OF S-ADENOSYLMETHIONINE FROM
 CC METHIONINE AND ATP (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: ATP + L-METHIONINE + H(2)O = ORTHOPHOSPHATE +
 CC S-ADENOSYLMETHIONINE.
 CC -1- PATHWAY: ACTIVATED METHYL CYCLE.
 CC -1- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC -1- SIMILARITY: BELONGS TO THE ADOMET SYNTHETASE FAMILY.
 CC -----
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 CC -----

```
CC EMBL: AE000011: AAB95742.1; -.
DR HSSP: P04384; 1XRC.
DR InterPro: IPR002133: S-AdoMet_synth.
DR Pfam: PF00438; S-AdoMet_synth; 1.
DR PROSITE: PS00376; ADOMET_SYNTHETASE_1; 1.
DR PROSITE: PS00377; ADOMET_SYNTHETASE_2; 1.
DR Transferrase: One-carbon metabolism: ATP-binding; Complete proteome.
FT NP_BIND 114 119 ATP (POTENTIAL).
SQ SEQUENCE 383 AA; 42560 MW; 6E5817BAFAE65051 CRC64;

Query Match
Best Local Similarity 50.0%; Score 40; DB 1; Length 383;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 4 CRRKSPLSNVC 15
   1:11111111
DB 38 CTKOSPTSHVAC 49

RESULT 10
MS12_AGRHH STANDARD; PRT; 430 AA.
AC P50201;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE AGROPINE SYNTHESIS REDUCTASE (EC 1.-.-.-).
GN MAS1.
OS Agrobacterium rhizogenes.
OC Plasmid pRi8196.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Rhizobiaceae; Rhizobium.
OX NCBI_TaxID=359;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE-91352070; PubMed-1909028;
RA Hansen G., Larribe M., Vaubert D., Tempe J., Blermann B.J.,
RA Montoya A.L., Chilton M.D., Brevet J.,
RT Agrobacterium rhizogenes pRi8196 T-DNA: mapping and DNA sequence of
RT functions involved in mannopine synthesis and hairy root
RT differentiation.
RL Proc. Natl. Acad. Sci. U.S.A. 88:7763-7767(1991).
CC -1- FUNCTION: REDUCES DEOXY-FRUCTOSYL-GLUTAMINE TO MANNOPINE.
CC -1- PATHWAY: AGROPINE / MANNOPINE SYNTHESIS
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC (SDR) FAMILY.
-----
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-----
CC EMBL: M60490; AAA22101.1; -.
DR HSSP: P14061; 1FDV.
DR InterPro: IPR002198; ADH_short.
DR InterPro: IPR001345; PG_mutase.
DR Pfam: PF00106; adh_short; 1.
DR Pfam: PF00300; PGAM; 1.
DR PROSITE: PS00061; ADH_SHORT; 1.
DR Plasmid: Oxidoreductase.
FT NP_BIND 203 227
FT ACT_SITE 346 346 NAD OR NADP (BY SIMILARITY).
FT SEQUENCE 430 AA; 47583 MW; DD1B7EBD92854D2C CRC64;

Query Match
Best Local Similarity 48.8%; Score 39; DB 1; Length 430;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 6 RRSPLSNVC 15
   1:1:1111
DB 70 RKLPISSVC 79

RESULT 11
CC48_CAPAN STANDARD; PRT; 805 AA.
ID CC48_CAPAN
AC 096372;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE CELL DIVISION CYCLE PROTEIN 48 HOMOLOG.
GN CAP.
OS Capsicum annuum (Bell pepper).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; easterids I; Solanales; Solanaceae; Capsicum.
OX NCBI_TaxID=4072;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. YELLOW WONDER; TISSUE=fruit;
RA Akim S., Houine G., Schantz M.L., Schantz R.;
RL Submitted (NOV-1996) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: PROBABLY FUNCTIONS IN CELL DIVISION AND GROWTH
CC PROCESSES.
CC -1- SIMILARITY: BELONGS TO THE AAA FAMILY OF ATPASES.
-----
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-----
DR EMBL: X09396; CAA70565.1; -.
DR InterPro: IPR003593; AAA.
DR InterPro: IPR001939; AAA_subfam.
DR InterPro: IPR003338; VAT-Nn.
DR Pfam: PF00004; AAA; 2.
DR Pfam: PF02359; VAT-Nn; 1.
DR SMART: SM00382; AAA; 2.
DR SMART: SM00674; AAA; 2.
DR PROSITE: PS00674; AAA; 2.
KW Cell cycle; ATP-binding; Repeat.
FT NP_BIND 249 256 ATP (POTENTIAL).
FT NP_BIND 522 529 ATP (POTENTIAL).
FT SEQUENCE 805 AA; 89331 MW; 58EB975F38F2B6AD CRC64;

Query Match
Best Local Similarity 48.8%; Score 39; DB 1; Length 805;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 CRRKSPLS 11
   1:111111
DB 663 ACLRKSPLS 671

RESULT 12
HD RAT STANDARD; PRT; 3110 AA.
ID HD_RAT
AC P51111;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE HUNTINGTIN (HUNTINGTON'S DISEASE PROTEIN HOMOLOG) (HD PROTEIN).
GN HD
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
```

RN SEQUENCE FROM N.A.
 RC TISSUE-BRAIN;
 RX MEDLINE-96133292; PubMed-8528205;
 RA Schmitt I., Baechner D., Megow D., Henklein P., Boulter J.,
 RT *Expression of the Huntington disease gene in rodents: cloning the
 RT rat homologue and evidence for downregulation in non-neuronal tissues
 RT during development.";
 RL Hum. Mol. Genet. 4:1173-1182(1995).
 RN [2]
 RP SEQUENCE OF 1773-1926 FROM N.A.
 RC TISSUE-BRAIN;
 RX MEDLINE-94100980; PubMed-8275091;
 RA Strong T.V., Tagle D.A., Valdes J.M., Elmer L.W., Boehm K.,
 RA Swarcop M., Kaatz K.W., Collins F.S., Albin R.L.;
 RT *Widespread expression of the human and rat Huntington's disease gene
 RT in brain and nonneural tissues.";
 RL Nat. Genet. 5:259-265(1993).
 CC -1- FUNCTION: MAY PLAY A ROLE IN MICROTUBULE-MEDIATED TRANSPORT OR
 CC VESICLE FUNCTION.
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
 CC -1- TISSUE SPECIFICITY: EXPRESSED TO A HIGH DEGREE IN ALL THE REGIONS
 CC OF THE BRAIN OF ADULTS AND IN METABOLIC CELLS OF THE TESTIS. IN
 CC ADDITION, VERY LOW LEVELS ARE DETECTED IN VARIOUS NON-NEURONAL
 CC TISSUES (HEART, MUSCLE, LIVER, LUNG AND KIDNEY).
 CC -1- DEVELOPMENTAL STAGE: IDENTIFIED AT HIGH LEVELS IN NEURONAL TISSUES
 CC OF EMBRYOS AS EARLY AS DAY 14.5. THIS EXPRESSION REMAINS CONSTANT
 CC IN ALL FURTHER DEVELOPMENT STAGES (UP TO THE ADULT). ON THE OTHER
 CC HAND THE EXPRESSION IN NON-NEURONAL TISSUES IS DOWN-REGULATED FROM
 CC STAGE 17.5 DAY OLD EMBRYOS.
 CC -1- POLYMORPHISM: THE POLY-GLN REGION DOES NOT APPEAR TO BE
 CC POLYMORPHIC, EXPLAINING THE ABSENCE OF A RODENT HD-LIKE DISORDER.
 CC -1- SIMILARITY: CONTAINS 10 HEAT REPEATS.
 CC -1- SIMILARITY: BELONGS TO THE HUNTINGTIN FAMILY.
 CC -----
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 CC -----
 DR EMBL; U18650; AAA90987.1; ALT_SEQ.
 DR EMBL; U01022; AAC52133.1; -
 DR InterPro: IPR000091; Huntingtin.
 DR PRINTS; PRO0375; HUNTINGTIN.
 KM Repeat.
 FT DOMAIN 173 297 HEAT REPEATS DOMAIN 1.
 FT DOMAIN 714 911 HEAT REPEATS DOMAIN 2.
 FT DOMAIN 1503 1544 HEAT REPEATS DOMAIN 3.
 FT DOMAIN 11 18 POLY-GLN.
 FT DOMAIN 19 38 POLY-PRO.
 FT DOMAIN 42 51 POLY-THR.
 FT DOMAIN 1408 1411 POLY-GLU.
 FT DOMAIN 2606 2611 POLY-GLU.
 SQ SEQUENCE 3110 AA; 343757 MW; 33C357E8FC141550 CRC64;
 Query Match 48.8%; Score 39; DB 1; Length 3110;
 Best Local Similarity 46.2%; Pred. No. 91;
 Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE HUNTINGTIN (HUNTINGTON'S DISEASE PROTEIN HOMOLOG) (HD PROTEIN).
 GN HD OR HDL.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-C57BL/6; TISSUE-BRAIN, and Spleen;
 RX MEDLINE-94214482; PubMed-8162057;
 RA Lin B., Nasir J., Macdonald H., Hutchinson G., Graham R.K.,
 RA Rommens J.M., Hayden M.R.;
 RT *Sequence of the murine Huntington disease gene: evidence for
 RT conservation, alternate splicing and polymorphism in a triplet (CCG)
 RT repeat.";
 RL Hum. Mol. Genet. 3:85-92(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-94278649; PubMed-8009370;
 RA Barnes G.T., Duyao M.P., Ambrose C.M., McNeil S., Persichetti F.,
 RA Strindahl J., Gusella J.F., Macdonald M.E.;
 RT *Mouse Huntington's disease gene homolog (Hdh)."
 RL Somat. Cell Mol. Genet. 20:87-97(1994).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-95375771; PubMed-7647777;
 RA Trotter Y., Devys D., Imbert G., Saudou F., An I., Lutz Y.,
 RA Weber C., Agid Y., Hirsch E.C., Mandel J.L.;
 RT *Cellular localization of the Huntington's disease protein and
 RT discrimination of the normal and mutated form.";
 RL Nat. Genet. 10:104-110(1995).
 RN [4]
 RP SEQUENCE OF 1-181 FROM N.A.
 RX MEDLINE-95278941; PubMed-7759106;
 RA Lin B., Nasir J., Katchman M.A., McDonald H., Zelsler J.,
 RA Goldberg Y.P., Hayden M.R.;
 RT *Structural analysis of the 5' region of mouse and human Huntington
 RT disease genes reveals conservation of putative promoter region and
 RT di- and trinucleotide polymorphisms.";
 RL Genomics 25:707-715(1995).
 CC -1- FUNCTION: MAY PLAY A ROLE IN MICROTUBULE-MEDIATED TRANSPORT OR
 CC VESICLE FUNCTION.
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC -1- ALTERNATIVE PRODUCTS: ALTERNATIVE SPLICING SEEMS TO GIVE RISE TO A
 CC 480 AMINO ACIDS SHORTER ISOFORM. THIS PRODUCT CANNOT BE EXPLAINED
 CC BY A SIMPLE SPLICING EVENT.
 CC -1- TISSUE SPECIFICITY: THE HIGHEST LEVEL IS SEEN THROUGHOUT THE
 CC BRAIN, BUT IT IS ALSO FOUND IN THE STOMACH, HEART, TESTIS, ADIPOSE
 CC TISSUE, MUSCLE, SPLEEN, LIVER, AND KIDNEY.
 CC -1- DEVELOPMENTAL STAGE: PREDOMINANT EXPRESSION IN NEURONAL TISSUES AT
 CC ALL DEVELOPMENTAL STAGES. IN 14.5 DAY OLD EMBRYOS, IT IS ALSO
 CC DETECTED IN NON-NEURONAL TISSUES. THIS EXPRESSION IS DOWN-
 CC REGULATED IN LATER STAGES OF DEVELOPMENT.
 CC -1- POLYMORPHISM: THE FIRST POLY-PRO REPEAT STRETCH DIFFERS IN LENGTH
 CC BY ONE UNIT (THREE) IN MDS SPRETUS STRAIN COMPARED TO OTHER
 CC STRAINS (FOUR). THE POLY-GLN REGION DOES NOT APPEAR TO BE
 CC POLYMORPHIC, EXPLAINING THE ABSENCE OF A MURINE HD-LIKE DISORDER.
 CC -1- SIMILARITY: CONTAINS 10 HEAT REPEATS.
 CC -1- SIMILARITY: BELONGS TO THE HUNTINGTIN FAMILY.
 CC -----
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 CC -----
 DR EMBL; L23312; AAA37799.1; -
 DR EMBL; L23313; AAA37800.1; -

DR EMBL: L28827; AAA89100.1; ALT_SEQ.
 DR EMBL: U2423; AAC52218.1; -
 DR EMBL: L34024; AAA91085.1; -
 DR EMBL: L34008; AAA91085.1; JOINED.
 DR EMBL: L34021; AAA91085.1; JOINED.
 DR EMBL: L34022; AAA91085.1; JOINED.
 DR EMBL: L34023; AAA91085.1; JOINED.
 DR MGD: MGI:96067; Hdh.
 DR InterPro: IPR00091; Huntingtin.
 DR PRINTS: PR00375; HUNTINGTIN.
 KW Alternative splicing; Polymorphism; Repeat.
 FT DOMAIN 182 306
 FT DOMAIN 723 920
 FT DOMAIN 1512 1553
 FT DOMAIN 18 24
 FT DOMAIN 25 45
 FT DOMAIN 49 59
 FT DOMAIN 1417 1420
 FT DOMAIN 1696 1699
 FT DOMAIN 2615 2620
 FT VARSPLIC 1522 2001
 FT CONFLICT 2 2
 FT CONFLICT 29 29
 FT CONFLICT 116 116
 FT CONFLICT 138 138
 FT CONFLICT 521 521
 FT CONFLICT 524 524
 FT CONFLICT 533 533
 FT CONFLICT 607 607
 FT CONFLICT 769 769
 FT CONFLICT 972 972
 FT CONFLICT 1106 1106
 FT CONFLICT 1240 1240
 FT CONFLICT 1384 1384
 FT CONFLICT 1827 1827
 FT CONFLICT 1827 1827
 FT CONFLICT 1979 1980
 FT CONFLICT 2062 2062
 FT CONFLICT 2570 2570
 FT CONFLICT 2866 2866
 FT CONFLICT 2877 2877
 FT CONFLICT 2882 2882
 FT CONFLICT 2887 2887
 FT CONFLICT 2915 2915
 FT CONFLICT 3025 3025
 FT CONFLICT 3062 3063
 FT CONFLICT 3095 3096
 FT CONFLICT 3119 AA; 344685 MW; ECAA2B5916F50E4F CRC64;
 SQ SEQUENCE

Query Match 48.8%; Score 39; DB 1; Length 3119;
 Best Local Similarity 46.2%; Pred. No. 91;
 Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 3 SCFRKSPISNVVC 15
 DB 1279 SCFRSPMMAVVC 1291

RESULT 14
 HD HUMAN STANDARD; PRT: 3144 AA.
 AC P42858;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE HUNTINGTIN (HUNTINGTON'S DISEASE PROTEIN) (HD PROTEIN).
 GN HD OR IT15.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.

RC TISSUE=Retina;
 RX MEDLINE=93208892; PubMed=8458085;
 RA Macdonald M., Ambrose C.M., Duyao M.P., Myers R.H., Lin C.S.,
 RA Striudh J., Barnes G., Taylor S.A., James M., Groot N., McFarlane H.,
 RA Jenkins B., Anderson M.A., Wexler N.S., Gusella J.F., Bates G.P.,
 RA Baxendale S., Hummerich H., Kirby S., North M., Youngman S., Mott R.,
 RA Zehetner G., Sedlacek Z., Poustka A., Fritschauf A.-M., Leiraich H.,
 RA Buckler A.J., Church D., Doucette-Stamm L., O'Donovan M.C.,
 RA Riba-Ramirez U., Shan M., Stanton V.P., Strobel S.A., Drach K.M.,
 RA Wales J.L., Dervan P., Hausman D.E., Altherr M., Shiang R.,
 RA Thompson L., Fielder T., Wasmuth J.J., Tagle D., Valdes J., Elmer L.,
 RA Allard M., Callilla L., Swarcop M., Blanchard K., Collins F.S.,
 RA Snell R., Holloway T., Gillespie K., Danson N., Shaw S., Harper P.S.;
 RT *A novel gene containing a trinucleotide repeat that is expanded and
 RT unstable on Huntington's disease chromosomes. The Huntington's
 RT Disease Collaborative Research Group.*;
 RL Cell 72:971-983(1993).
 RN [2]
 RP SEQUENCE OF 1-90 FROM N.A.
 RX MEDLINE=95278941; PubMed=7759106;
 RA Lin B., Nasir J., Katchman M.A., McDonald H., Zeisler J.,
 RA Goldberg Y.P., Hayden M.R.;
 RT *Structural analysis of the 5' region of mouse and human Huntington
 RT disease genes reveals conservation of putative promoter region and
 RT di- and trinucleotide polymorphisms.*;
 RL Genomics 25:707-715(1995).
 RN [3]
 RP SEQUENCE OF 1-205 FROM N.A.
 RX MEDLINE=9425787; PubMed=8197474;
 RA Ambrose C.M., Duyao M.P., Barnes G., Bates G.P., Lin C.S.,
 RA Striudh J., Baxendale S., Hummerich H., Leiraich H., Altherr M.,
 RA Wasmuth J., Buckler A., Church D., Hausman D., Berts M., Micklem G.,
 RA Durbin R., Dodge A., Read A., Gusella J.F., Macdonald M.E.;
 RT *Structure and expression of the Huntington's disease gene: evidence
 RT against simple inactivation due to an expanded CAG repeat.*;
 RL Somatic. Cell Mol. Genet. 20:27-38(1994).
 RN [4]
 RP SEQUENCE OF 1-117 FROM N.A.
 RX Matthews P.;
 RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE OF 119-934 FROM N.A.
 RX Lloyd C.;
 RL Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE OF 1212-1290 FROM N.A.
 RX Mungall A., Odell C.;
 RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP SEQUENCE OF 1291-1860 FROM N.A.
 RX Mungall A.;
 RL Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.
 RN [8]
 RP SEQUENCE OF 1862-2820 FROM N.A.
 RX Buck D.;
 RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
 RN [9]
 RP SEQUENCE OF 2563-3144 FROM N.A.
 RX TISSUE=Frontal cortex, Brain, Retina, Caudate, and Muscles;
 RX MEDLINE=94093536; PubMed=7903579;
 RA Lin B., Rommens J.M., Graham R.K., Katchman M., Macdonald H.,
 RA Nasir J., Delaney A., Goldberg Y.P., Hayden M.R.;
 RT *Differential 3' polyadenylation of the Huntington disease gene
 RT results in two mRNA species with variable tissue expression.*;
 RL Hum. Mol. Genet. 2:1541-1545(1993).
 RN [10]
 RP SUBCELLULAR LOCATION.
 RX MEDLINE=95375771; PubMed=7647777;
 RA Trotter Y., Devys D., Imbert G., Saudou F., An I., Lutz Y., Weber C.,
 RA Agid Y., Hirsch E.C., Mandel J.-L.;
 RT *Cellular localization of the Huntington's disease protein and
 RT discrimination of the normal and mutated form.*;
 RL Nat. Genet. 10:104-110(1995).

Best Local Similarity 66.7%; Pred. No. 6.5;
Matches 6; Conservative 1; Mismatches

2; Indels 0; Gaps 0;

QY 4 CRRKSPLSN 12
|||||:

Db 104 CRRKFPFGN 112

Search completed: December 19, 2001, 16:26:15
Job time: 370 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: December 19, 2001, 16:25:20 ; Search time 157.32 Seconds
(without alignments)
13.947 Million cell updates/sec

Title: US-09-202-104A-4
Perfect score: 80
Sequence: 1 OLSCFKSPISNVVC 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues
Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: SPTEMBL_17:*
2: sp.archaea:*
3: sp.fungi:*
4: sp.human:*
5: sp.invertebrate:*
6: sp.mammal:*
7: sp.mhc:*
8: sp.organelle:*
9: sp.phage:*
10: sp.plant:*
11: sp.todent:*
12: sp.virus:*
13: sp.vertebrate:*
14: sp.unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	43	53.8	205	10	080328 nicotiana s
2	43	53.8	215	6	09N1Z4
3	43	53.8	215	6	09N1Z0
4	43	53.8	215	6	09N1Y8
5	43	53.8	1436	2	09PKP1
6	42	52.5	176	6	077551
7	42	52.5	263	4	09UPJ1
8	42	52.5	264	4	043789
9	42	52.5	402	5	09GN14
10	41	51.2	158	11	09GWN4
11	41	51.2	216	6	09N203
12	41	51.2	228	7	095591
13	41	51.2	348	7	031387
14	41	51.2	630	4	09NUY5
15	41	51.2	807	3	094275
16	40	50.0	165	7	098207
17	40	50.0	171	2	053728
18	40	50.0	379	10	041108
19	40	50.0	395	13	042481

20	40	50.0	1270	5	09VRV2	09VRV2 drosophila
21	40	50.0	5081	13	013054	013054 makaira nig
22	39	48.8	359	3	012642	012642 neurospora
23	39	48.8	412	5	09Q222	09Q222 caenorhabdi
24	39	48.8	454	10	09S7B0	09S7B0 oryza sativ
25	39	48.8	852	10	09L1I8	09L1I8 oryza sativ
26	39	48.8	977	5	019950	019950 caenorhabdi
27	39	48.8	3144	4	09Q0B7	09Q0B7 homo sapien
28	38.5	48.1	695	13	09PW85	09PW85 carassius a
29	38.5	48.1	695	5	09V712	09V712 drosophila
30	38.5	48.1	787	10	048847	048847 arabidopsis
31	38	47.5	97	10	09LP10	09LP10 arabidopsis
32	38	47.5	170	2	057501	057501 escherichia
33	38	47.5	172	11	09D0E6	09D0E6 mus musculu
34	38	47.5	175	7	031352	031352 barbus inte
35	38	47.5	175	7	09MM47	09MM47 barbus acut
36	38	47.5	242	5	09VYM8	09VYM8 drosophila
37	38	47.5	258	4	095012	095012 homo sapien
38	38	47.5	527	5	09W4N5	09W4N5 drosophila
39	38	47.5	557	5	009654	009654 caenorhabdi
40	38	47.5	630	4	09UNH9	09UNH9 homo sapien
41	38	47.5	630	4	09UBV7	09UBV7 homo sapien
42	38	47.5	630	4	09NZV8	09NZV8 homo sapien
43	38	47.5	630	11	063881	063881 rattus norv
44	38	47.5	630	11	0920V2	0920V2 mus musculu
45	38	47.5	686	12	09WRU0	09WRU0 macaca mula

ALIGNMENTS

RESULT	ID	PRELIMINARY	PRT	205 AA.
080328	080328			
AC	080328			
DT	01-NOV-1998 (TREMBLrel. 08, Created)			
DT	01-NOV-1998 (TREMBLrel. 08, last sequence update)			
DT	01-JUN-2001 (TREMBLrel. 17, last annotation update)			
DE	HEAT SHOCK PROTEIN 26 (FRAGMENT).			
GN	HSP26.			
OS	Nicotiana glauca (wood tobacco).			
OC	Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;			
OC	Asteridae; easterids I; Solanales; Solanaceae; Nicotiana.			
OX	NCBI_TaxId=4096;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=GREEN LEAF;			
RX	MEDLINE=98363655; PubMed=9700075;			
RA	Lee B.-H., Tanaka Y., Iwasaki T., Yamamoto N., Kayano T., Miyao M.,			
RT	"Evolutionary origin of two genes for chloroplast small heat shock			
RL	Plant Mol. Biol. 37:1035-1043(1998).			
DR	EMBL; AB06043; BAA29066.1; -			
DR	Mendel; 30994; NicSY:2971;30994.			
DR	InterPro: IPR002068; CrystalIn_HSP20.			
DR	Pfam: PF00011; HSP20; 1.			
KW	Heat shock.			
FT	NON_TER			
FT	NON_TER			
SO	SEQUENCE			

Query Match 53.8%; Score 43; DB 10; Length 205;
Best local Similarity 69.2%; Pred. No. 2.5;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 LSCFKSPISNV 14
DB 1 LTCSAASPLSNV 13

```
RESULT 2
ID Q9N1Z4 PRELIMINARY; PRT; 215 AA.
AC Q9N1Z4;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE OLFACTORY RECEPTOR (FRAGMENT).
GN SMO28.
OS Saimiri boliviensis (Bolivian squirrel monkey).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Cebinae; Saimiri.
OX NCBI_TaxID=27679;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20183981; PubMed=10706615;
RA Rouquier S., Blancher A., Giorgi D.;
RT "The olfactory receptor gene repertoire in primates and mouse;
RT Evidence for reduction of the functional fraction in primates.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:2870-2874(2000).
DR EMBL; AF127904; AAF40291.1; -.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_FL_2; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 215
SQ SEQUENCE 215 AA; 23705 MW; FE073BCC58D712B9 CRC64;

Query Match 53.8%; Score 43; DB 6; Length 215;
Best Local Similarity 46.7%; Pred. No. 2.6;
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

OY 1 QLSCFRKSPLSNVVC 15
Db 98 QFSCKFKIKISNFEC 112

RESULT 3
ID Q9N1Z0 PRELIMINARY; PRT; 215 AA.
AC Q9N1Z0;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE OLFACTORY RECEPTOR (FRAGMENT).
GN SSC32.
OS Saimiri sciureus (Common squirrel monkey).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Cebinae; Saimiri.
OX NCBI_TaxID=9521;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20183981; PubMed=10706615;
RA Rouquier S., Blancher A., Giorgi D.;
RT "The olfactory receptor gene repertoire in primates and mouse;
RT Evidence for reduction of the functional fraction in primates.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:2870-2874(2000).
DR EMBL; AF127902; AAF40295.1; -.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_FL_2; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 215
SQ SEQUENCE 215 AA; 23663 MW; EA5870CF40DC01B1 CRC64;

Query Match 53.8%; Score 43; DB 6; Length 215;
Best Local Similarity 46.7%; Pred. No. 2.6;
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
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```
OY 1 QLSCFRKSPLSNVVC 15
Db 98 QFSCKFKIKISNFEC 112

RESULT 4
ID Q9N1Y8 PRELIMINARY; PRT; 215 AA.
AC Q9N1Y8;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE OLFACTORY RECEPTOR (FRAGMENT).
GN SSC34.
OS Saimiri sciureus (Common squirrel monkey).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Cebinae; Saimiri.
OX NCBI_TaxID=9521;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20183981; PubMed=10706615;
RA Rouquier S., Blancher A., Giorgi D.;
RT "The olfactory receptor gene repertoire in primates and mouse;
RT Evidence for reduction of the functional fraction in primates.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:2870-2874(2000).
DR EMBL; AF127904; AAF40297.1; -.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_FL_2; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 215
SQ SEQUENCE 215 AA; 23695 MW; FE073BCF5BD711BA CRC64;

Query Match 53.8%; Score 43; DB 6; Length 215;
Best Local Similarity 46.7%; Pred. No. 2.6;
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

OY 1 QLSCFRKSPLSNVVC 15
Db 98 QFSCKFKIKISNFEC 112

RESULT 5
ID Q9PKP1 PRELIMINARY; PRT; 1436 AA.
AC Q9PKP1;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE HYPOTHETICAL PROTEIN TC0424.
GN TC0424.
OS Chlamydia muridarum.
OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=83560;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MOPN / NRG;
RX MEDLINE=20150255; PubMed=10684935;
RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
RA White O., Hickey E.K., Peterson J., Ulfersack T., Berry K., Bass S.,
RA Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
RA Gwin M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
RA Eisen J., Fraser C.M.;
RT "Genome sequences of Chlamydia trachomatis MOPN and Chlamydia
RT pneumoniae AR39.";
RL Nucleic Acids Res. 28:1397-1406(2000).
DR EMBL; AE002309; AAF39280.1; -.
DR TIGR; TC0424; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 1436 AA; 161977 MW; F3CD62603DCC287C CRC64;
```

Query Match 53.8%; Score 43; DB 2; Length 1436;
Best Local Similarity 46.7%; Pred. No. 15;
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

OY 1 QUSCFRKSPLSNVC 15
DB 771 ELSSSRKDPIDNLC 785

RESULT 6
ID 077551 PRELIMINARY; PRT; 176 AA.
AC 077551;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE OLFATORY RECEPTOR (FRAGMENT).
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
OX NCBI_TaxID=96823;

RN [1]
RP SEQUENCE FROM N.A.
RA Matarazzo V., Tizard A., Renucci M., Belaich A., Clement J.L.;
RT "Isolation of putative olfactory receptor sequences from pig nasal
epithelium."
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL, AF042026; AAC24802.1; -
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PROSITE: PS50262; G_PROTEIN_RECEP_F1_2; 1.
FT NON_TER 1 176
FT SEQUENCE 176 AA; 19122 MW; A859CB3CE40B65F CRC64;

Query Match 52.5%; Score 42; DB 6; Length 176;
Best Local Similarity 46.7%; Pred. No. 3;
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

OY 1 QUSCFRKSPLSNVC 15
DB 50 QLTCEKDVDSNFC 64

RESULT 7
ID 090P1 PRELIMINARY; PRT; 263 AA.
AC 090P1;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE BC319430_5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;

RN [1]
RP SEQUENCE FROM N.A.
RA Lamerdin J.E., McCready P.M., Skowronski E., Viswanathan V.,
RA Burkhart-Schultz K., Gordon L., Dias J., Ramirez M., Stillwagen S.,
RA Phan H., Velasco N., Do L., Regala W., Terry A., Garnes J.,
RA Dandapani L., Erlar A., Christensen M., Georgescu A., Ayala J., Liu S.,
RA Attix C., Andreise T., Frankheim M., Amico-Keller G., Coefield J.,
RA Duarte S., Lucas R., Bruce R., Thomas P., Quan G., Kronmiller B.,
RA Arellano A., Sanders C., Ow D., Nolan M., Trong S., Kobayashi A.,
RA Olsen A.S., Carriero A.V.;
RT "Sequence analysis of a 2.5 Mb region in 19p13.2 between D19S461 and
PRKSH";
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL, AC006271; AAD03353.1; -
DR InterPro: IPR000276; GPCR_Rhodpsn.

DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCR_Rhodpsn.
DR PROSITE: PS50262; G_PROTEIN_RECEP_F1_2; 1.
SO SEQUENCE 263 AA; 29791 MW; 16586C73601F3B0C CRC64;

Query Match 52.5%; Score 42; DB 4; Length 263;
Best Local Similarity 46.7%; Pred. No. 4.8;
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

OY 1 QUSCFRKSPLSNVC 15
DB 107 QLTCEKDVDSNFC 121

RESULT 8
ID 043789 PRELIMINARY; PRT; 264 AA.
AC 043789;
DT 01-JUN-1998 (TREMBlrel. 06, Created)
DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE OLFATORY RECEPTOR (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;

RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=TESTIS;
RX MEDLINE=97415789; PubMed=9268701;
RA Vandenheghen P., Schumann S., Vassart G., Parmentier M.;
RT "Molecular cloning and chromosomal mapping of olfactory receptor genes
expressed in the male germ line: evidence for their wide distribution
in the human genome."
RL Biochem. Biophys. Res. Commun. 237:283-287(1997).
DR EMBL, Y10529; CAAT1557.1; -
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCR_Rhodpsn.
DR PROSITE: PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor.
FT NON_TER 1 264
FT SEQUENCE 264 AA; 29888 MW; 43086C5D1B1F3B10 CRC64;

Query Match 52.5%; Score 42; DB 4; Length 264;
Best Local Similarity 46.7%; Pred. No. 4.8;
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

OY 1 QUSCFRKSPLSNVC 15
DB 108 QLTCEKDVDSNFC 122

RESULT 9
ID 09GN14 PRELIMINARY; PRT; 402 AA.
AC 09GN14;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE S-ADENOSYLMETHYLTRANSFERASE (METHYLTRANSFERASE)
(EC 2.5.1.6).
GN MAT.
OS Plasmodium falciparum (isolate 3D7), and
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=36329, 5833;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES-P.falciparum (isolate 3D7);
RX MEDLINE=20036339; PubMed=10567242;

RA Chiang P.K., Chamberlin M.E., Nicholson D., Scubes S., Su X.,
 RA Subramanian G., Lanar D.E., Prigge S.T., Scovilli J.P., Miller L.H.,
 RA Chou J.Y.;
 RT "Molecular characterization of Plasmodium falciparum S-
 RT adenosylmethionine synthetase.";
 RL Biochem. J. 344:571-576(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC SPECIES=P.falciparum; STRAIN=FCUPL/RSA;
 RA Clark K., Joubert F., Neitz A.W.H., Louw A.I.;
 RT "Molecular characterization of the Plasmodium falciparum methionine
 RT adenosyltransferase cDNA.";
 RL Submitted (Aug-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF097923; AAC13449.1; -
 DR EMBL: AF180426; AAC02013.1; -
 DR InterPro: IPR002133; S-Adomet_synth.
 DR Pfam: PF00438; S-Adomet_synth.1.
 DR PROSITE: PS00376; ADOMET_SYNTHETASE_1; 1.
 KW Transferrase.
 SQ SEQUENCE 402 AA; 44844 MW; EB76C6023494A16C CRC64;
 SQ

Query Match 52.5%; Score 42; DB 5; Length 402;
 Best Local Similarity 53.8%; Pred. No. 7.2;
 Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 3 SCFRKPSPLSNVVC 15
 Db 37 SCLRDPEPSKVAC 49

RESULT 10
 ID 09CWN4 PRELIMINARY; PRT; 158 AA.
 AC 09CWN4;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE 2410016A19RIK PROTEIN.
 GN 2410016A19RIK.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=EMBRYONIC STEM CELLS;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Atakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Atakawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
 RA Saito T., Okazaki Y., Gotohori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochwa H.,
 RA Knehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
 RA Schirml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carlini P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Guslinich S., Hill D., Hofmann M., Hume D.A., Kamiya K., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
 RA Wyszewski-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohlsuki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 DR EMBL: AK010511; BAB26994.1; -
 DR MGI:1923730; 2410016A19RIK.
 SQ SEQUENCE 158 AA; 16352 MW; E3B96D06F2800B6 CRC64;

Query Match 51.2%; Score 41; DB 11; Length 158;
 Best Local Similarity 50.0%; Pred. No. 4.6;
 Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 2 LSCFRKPSPLSNVVC 15
 Db 24 LSCLDPEPSKVAC 37

RESULT 11
 ID 09N203 PRELIMINARY; PRT; 216 AA.
 AC 09N203;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE OLFACORY RECEPTOR (FRAGMENT).
 GN CUA26.
 OS Callithrix jacchus (Common marmoset).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Callitrich.
 OX NCBI_TaxID=9483;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20183981; PubMed=10706615;
 RA Rouquier S., Blancher A., Giorgi D.;
 RT "The olfactory receptor gene repertoire in primates and mouse:
 RT Evidence for reduction of the functional fraction in primates.";
 RL Proc. Natl. Acad. Sci. U.S.A. 97:2870-2874(2000).
 DR EMBL: AF127880; AAF40282.1; -
 DR InterPro: IPR00276; GPCR_Rhodpsn.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PROSITE: PS50262; G_PROTEIN_RECPT_FL_2; 1.
 KW Receptor.
 FT NON_TER 1 1
 FT NON_TER 216 216
 SQ SEQUENCE 216 AA; 23829 MW; B09E9D74296D2A8 CRC64;

Query Match 51.2%; Score 41; DB 6; Length 216;
 Best Local Similarity 46.7%; Pred. No. 6.2;
 Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 QLSFRKPSPLSNVVC 15
 Db 98 QSCFRKPSPLSNVVC 112

RESULT 12
 ID 095591 PRELIMINARY; PRT; 228 AA.
 AC 095591;
 DT 01-FEB-1997 (TrEMBLrel. 02, Created)
 DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE MHC CLASS I PROTEIN (FRAGMENT).
 GN CYCA-UAI*02.
 OS Cyprinus carpio (Common carp).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
 OC Cypriniformes; Cyprinidae; Cyprininae; Cyprinus.
 OX NCBI_TaxID=7962;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86217555; PubMed=8613142;
 RA Van Ert S.H., Dixon B., Figueroa F., Egberts E., Stet R.J.;
 RT "Identification and characterization of a new major histocompatibility
 RT complex class I gene in carp (Cyprinus carpio L.).";
 RL Immunogenetics 44:49-61(1996).
 CC -1- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE
 CC IMMUNE SYSTEM (BY SIMILARITY).
 CC -1- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
 CC MICROGLOBULIN) (BY SIMILARITY).


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CC -1 SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL: X91027: CAA62499.1: -.
DR EMBL: X91028: CAA62499.1: JOINED.
DR InterPro: IPR003597; Ig_C1.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR001039; MHC_I.
DR Pfam: PF00047; Ig_1.
DR Pfam: PF00129; MHC_I_1.
DR ProDom: PD00050; MHC_I_1.
DR SMART: SM00407; IgC1_1.
DR PROSITE: PS00290; IG_MHC; UNKNOWN_1.
KW Glycoprotein; MHC; Transmembrane.
FT NON_TER 1
FT SEQUENCE 228 AA; 25817 MW; 6D30DF0010A53076 CRC64;

Query Match 51.2%; Score 41; DB 7; Length 228;
Best Local Similarity 53.3%; Pred. No. 6.5;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 QLSCFKSPLSNYVC 15
DB 95 QVSLQKDPLEDPVTC 109

RESULT 13
Q31387 PRELIMINARY; PRT; 348 AA.
ID Q31387;
AC Q31387;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE MHC CLASS I PROTEIN PRECURSOR.
CYCA-V0A1*01.
GN Cyprinus carpio (Common carp).
OS Cyprinidae; Cypriniformes; Cyprinidae; Cyprinus.
OC Actinopterygii; Neopterygii; Teleostei; Osteichthyes;
OC Cypriniformes; Cyprinidae; Cyprinidae; Cyprinus.
NCBI_TaxID=962;
RX MEDLINE-96217555; PubMed-8613142;
RA van Erp S.H., Dixon B., Figueroa F., Egberts E., Stet R.J.;
RT Identification and characterization of a new major histocompatibility
RT complex class I gene in carp (Cyprinus carpio L.).
RL Immunogenetics 44:49-61(1996).
CC -1 FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE
CC IMMUNE SYSTEM (BY SIMILARITY).
CC -1 SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN) (BY SIMILARITY).
CC -1 SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL: X91015: CAA62497.1: -.
DR InterPro: IPR003597; Ig_C1.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR001039; MHC_I.
DR Pfam: PF00047; Ig_1.
DR Pfam: PF00129; MHC_I_1.
DR ProDom: PD00050; MHC_I_1.
DR SMART: SM00407; IgC1_1.
DR PROSITE: PS00290; IG_MHC; UNKNOWN_1.
KW Glycoprotein; MHC; Signal; Transmembrane.
FT SIGNAL 1
FT CHAIN 17 348 MHC CLASS I PROTEIN.
FT SEQUENCE 348 AA; 39008 MW; 0A1F3C97F22B1A5C CRC64;

Query Match 51.2%; Score 41; DB 7; Length 348;
Best Local Similarity 53.3%; Pred. No. 9.7;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

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QY 1 QLSCFKSPLSNYVC 15
DB 199 QVSLQKDPLEDPVTC 213

RESULT 14
Q9NUY5 PRELIMINARY; PRT; 630 AA.
ID Q9NUY5;
AC Q9NUY5;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE CDNA FLJ1053 FIS, CLONE PLACE1004664 (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
RX TISSUE-PLACENTA;
RN [1]
RP SEQUENCE FROM N.A.
RA Isogai T., Ota T., Hayaashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sugano S., Aotsuka S., Yoshikawa Y.,
RA Matsunawa H., Ishii S., Kawai Y., Saito K., Yamamoto J., Wakamatsu A.,
RA Nakamura Y., Nagahara K., Masubo Y., Sasaki N.;
RT "NEDO human cDNA sequencing project."
RT Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AK001915; BAA91976.1; -.
FT NON_TER 630
FT SEQUENCE 630 AA; 71539 MW; C8C0E85198DE90 CRC64;

Query Match 51.2%; Score 41; DB 4; Length 630;
Best Local Similarity 57.1%; Pred. No. 17;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 LSCFRKSPLSNYVC 15
DB 516 LSPLRKKPLEDLVC 529

RESULT 15
Q94275 PRELIMINARY; PRT; 807 AA.
ID Q94275;
AC Q94275;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE PUTATIVE UBIQUITIN-PROTEIN LIGASE.
GN SPBPB7.27.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
NCBI_TaxID=4896;
RX [1]
RP SEQUENCE FROM N.A.
RC STRAIN-972H-;
RA Beck A., Reinhardt R., Lyne M., Rajandream M.A., Barrell B.G.;
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AL032684: CAA21812.1; -.
DR InterPro: IPR000569; HECT.
DR InterPro: IPR001607; zf-UBP.
DR InterPro: IPR003662; sub_transporter.
DR Pfam: PF00632; HECT_1.
DR PROSITE: PS0237; HECT_1.
DR PROSITE: PS00217; SUGAR_TRANSPORT_2; UNKNOWN_1.
DR SMART: SM00119; HECTC_1.
DR SMART: SM00290; Znf-UBP_1.
KW Ligase.
FT SEQUENCE 807 AA; 93414 MW; 7203EB267E2D3AB CRC64;

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Query Match 51.2%; Score 41; DB 3; Length 807;
 Best Local Similarity 54.5%; Pred. No. 21;
 Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 2 LSCFRKSPLSN 12
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 Db 288 ISCFKOPYN 298

Search completed: December 19, 2001, 16:25:21
 Job time: 546 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 19, 2001, 16:20:59 ; Search time 78.52 Seconds
(without alignments)
4.299 Million cell updates/sec

Title: US-09-202-104A-4

Perfect score: 80

Sequence: 1 QLSCFRKSPLSNVVC 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA:*
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2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/PCYUS.COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/Backfilest1.pep:*

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	80	100.0	210	4	US-09-043-785-1
2	80	100.0	323	6	Sequence 1, Appl1
3	80	100.0	323	6	Patent No. 5171840
4	80	100.0	323	6	Patent No. 5480796
5	80	100.0	344	6	Patent No. 5171840-7
6	80	100.0	344	6	Patent No. 5480796-7
7	80	100.0	386	6	Patent No. 5171840-5
8	80	100.0	386	6	Patent No. 5480796-5
9	80	100.0	468	6	US-08-795-473B-5
10	80	100.0	468	6	Sequence 5, Appl1
11	67	83.8	188	1	Patent No. 5171840-2
12	67	83.8	188	1	Patent No. 5480796-2
13	67	83.8	188	1	Sequence 8, Appl1
14	67	83.8	188	1	Sequence 8, Appl1
15	67	83.8	188	2	Sequence 8, Appl1
16	52	65.0	201	6	Sequence 8, Appl1
17	39	48.8	3119	2	Patent No. 5171840
18	39	48.8	3119	2	Sequence 8, Appl1
19	39	48.8	3119	1	Sequence 16, Appl1
20	39	48.8	3144	1	Sequence 16, Appl1
21	39	48.8	3144	1	Sequence 6, Appl1
22	39	48.8	3144	2	Sequence 6, Appl1
23	39	48.8	3144	3	Sequence 42, Appl1
24	39	48.8	3144	4	Sequence 21, Appl1
25	39	48.8	3144	4	Sequence 15, Appl1
26	38	47.5	2594	4	Sequence 9, Appl1
27	37	46.2	2485	5	Sequence 7, Appl1

28	37	46.2	2485	5	PCT-US94-00198-2	Sequence 2, Appl1
29	37	46.2	2818	1	US-08-510-284-1	Sequence 1, Appl1
30	37	46.2	2818	1	US-08-411-389-2	Sequence 2, Appl1
31	37	46.2	2818	2	US-08-449-933-2	Sequence 2, Appl1
32	37	46.2	2818	4	US-07-966-049A-2	Sequence 2, Appl1
33	37	46.2	2818	4	US-09-542-331-2	Sequence 2, Appl1
34	36	45.0	262	1	US-08-292-045-11	Sequence 11, Appl1
35	36	45.0	3289	2	US-08-477-451-2	Sequence 2, Appl1
36	35	43.8	337	4	US-09-044-404A-2	Sequence 2, Appl1
37	35	43.8	388	4	US-09-188-930-275	Sequence 275, App
38	35	43.8	428	4	US-09-423-340-2	Sequence 2, Appl1
39	35	43.8	462	3	US-08-875-944B-5	Sequence 2, Appl1
40	35	43.8	462	4	US-09-116-049-4	Sequence 4, Appl1
41	35	43.8	555	2	US-08-780-835B-2	Sequence 2, Appl1
42	35	43.8	555	4	US-09-303-268-2	Sequence 2, Appl1
43	35	43.8	555	4	US-09-116-049-2	Sequence 2, Appl1
44	35	43.8	656	1	US-08-444-005-15	Sequence 2, Appl1
45	35	43.8	1561	3	US-08-894-017-23	Sequence 23, Appl1

ALIGNMENTS

RESULT 1
US-09-043-785-1
; Sequence 1, Application US/09043785
; Patent No. 6172042
; GENERAL INFORMATION:
; APPLICANT: CHEBATH, Judith
; APPLICANT: HALIMI, Hubert
; APPLICANT: REVEL, Michel
; TITLE OF INVENTION: SYNTHETIC PEPTIDES THAT INHIBIT IL-6 ACTIVITY
; FILE REFERENCE: Chebath-1
; CURRENT APPLICATION NUMBER: US/09/043,785
; CURRENT FILING DATE: 1998-09-02
; EARLIER APPLICATION NUMBER: PCT/IL96/00119
; EARLIER FILING DATE: 1996-09-26
; EARLIER APPLICATION NUMBER: 115,453
; EARLIER FILING DATE: 1995-09-26
; EARLIER APPLICATION NUMBER: 118,097
; EARLIER FILING DATE: 1996-05-01
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 1
; LENGTH: 210
; TYPE: PRT
; ORGANISM: Human
US-09-043-785-1

Query Match 100.0%; Score 80; DB 4; Length 210;
Best Local Similarity 100.0%; Pred. No. 5.8e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QLSCFRKSPLSNVVC 15
DB 6 QLSCFRKSPLSNVVC 20
RESULT 2
5171840-6
; APPLICANT: KISHIMOTO, TADAMITSU
; TITLE OF INVENTION: RECEPTOR PROTEIN FOR HUMAN B CELL
; STIMULATORY FACTOR-2
; NUMBER OF SEQUENCES: 11
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/298,694
; FILING DATE: 19-JAN-1989
; SEQ ID NO: 6
; LENGTH: 323
5171840-6

Query Match 100.0%; Score 80; DB 6; Length 323;
Best Local Similarity 100.0%; Pred. No. 9.4e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QLSCFRKSPLSNVVC 15
Db 118 QLSCFRKSPLSNVVC 132

RESULT 3

5480796-6
; Patent No. 5480796
; APPLICANT: KISHIMOTO, TADAMITSU
; TITLE OF INVENTION: ANTIBODIES AGAINST THE RECEPTOR PROTEIN
; . FOR HUMAN B CELL STIMULATORY FACTOR-2
; . NUMBER OF SEQUENCES: 8
; . CURRENT APPLICATION DATA:
; . APPLICATION NUMBER: US/07/907,650
; . FILING DATE: 02-JUL-1992
; . PRIOR APPLICATION DATA:
; . APPLICATION NUMBER: 298,694
; . FILING DATE: 19-JAN-1989
; SEQ ID NO:6:
; LENGTH: 323
5480796-6

Query Match 100.0%; Score 80; DB 6; Length 323;
Best Local Similarity 100.0%; Pred. No. 9.4e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QLSCFRKSPLSNVVC 15
Db 118 QLSCFRKSPLSNVVC 132

RESULT 4

5171840-7
; Patent No. 5171840
; APPLICANT: KISHIMOTO, TADAMITSU
; TITLE OF INVENTION: RECEPTOR PROTEIN FOR HUMAN B CELL
; . STIMULATORY FACTOR-2
; . NUMBER OF SEQUENCES: 11
; . CURRENT APPLICATION DATA:
; . APPLICATION NUMBER: US/07/298,694
; . FILING DATE: 19-JAN-1989
; SEQ ID NO:7:
; LENGTH: 344
5171840-7

Query Match 100.0%; Score 80; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 1e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QLSCFRKSPLSNVVC 15
Db 118 QLSCFRKSPLSNVVC 132

RESULT 5

5480796-7
; Patent No. 5480796
; APPLICANT: KISHIMOTO, TADAMITSU
; TITLE OF INVENTION: ANTIBODIES AGAINST THE RECEPTOR PROTEIN
; . FOR HUMAN B CELL STIMULATORY FACTOR-2
; . NUMBER OF SEQUENCES: 8
; . CURRENT APPLICATION DATA:
; . APPLICATION NUMBER: US/07/907,650
; . FILING DATE: 02-JUL-1992
; . PRIOR APPLICATION DATA:
; . APPLICATION NUMBER: 298,694
5480796-7

; FILING DATE: 19-JAN-1989
; SEQ ID NO:7:
; LENGTH: 344
5480796-7

Query Match 100.0%; Score 80; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 1e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QLSCFRKSPLSNVVC 15
Db 118 QLSCFRKSPLSNVVC 132

RESULT 6

5171840-5
; Patent No. 5171840
; APPLICANT: KISHIMOTO, TADAMITSU
; TITLE OF INVENTION: RECEPTOR PROTEIN FOR HUMAN B CELL
; . STIMULATORY FACTOR-2
; . NUMBER OF SEQUENCES: 11
; . CURRENT APPLICATION DATA:
; . APPLICATION NUMBER: US/07/298,694
; . FILING DATE: 19-JAN-1989
; SEQ ID NO:5:
; LENGTH: 386
5171840-5

Query Match 100.0%; Score 80; DB 6; Length 386;
Best Local Similarity 100.0%; Pred. No. 1.1e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QLSCFRKSPLSNVVC 15
Db 36 QLSCFRKSPLSNVVC 50

RESULT 7

5480796-5
; Patent No. 5480796
; APPLICANT: KISHIMOTO, TADAMITSU
; TITLE OF INVENTION: ANTIBODIES AGAINST THE RECEPTOR PROTEIN
; . FOR HUMAN B CELL STIMULATORY FACTOR-2
; . NUMBER OF SEQUENCES: 8
; . CURRENT APPLICATION DATA:
; . APPLICATION NUMBER: US/07/907,650
; . FILING DATE: 02-JUL-1992
; . PRIOR APPLICATION DATA:
; . APPLICATION NUMBER: 298,694
; . FILING DATE: 19-JAN-1989
; SEQ ID NO:5:
; LENGTH: 386
5480796-5

Query Match 100.0%; Score 80; DB 6; Length 386;
Best Local Similarity 100.0%; Pred. No. 1.1e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QLSCFRKSPLSNVVC 15
Db 36 QLSCFRKSPLSNVVC 50

RESULT 8

US-08-795-473B-5
; Sequence 5, Application US/08795473B
; Patent No. 6217858
; GENERAL INFORMATION:
; APPLICANT: Galun, Elhan
; APPLICANT: Nahot, Orit

APPLICANT: Blum, Herbert E.
TITLE OF INVENTION: A Pharmaceutical Composition for Treating
TITLE OF INVENTION: Hepatitis B Virus (HBV) Infection
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Davidson, Davidson and Kappel, LLC
STREET: 1140 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS-DOS EDITOR
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/795,473B
FILING DATE: 11-FEB-1997
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Davidson, Clifford M.
REGISTRATION NUMBER: 32,728
REFERENCE/DOCKET NUMBER: 963,1007
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)-997-1028
TELEFAX: (212)-997-1037
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 468 amino acids
TYPE: amino acid
TOPOLOGY: unknown
US-08-795-473B-5

Query Match 100.0%; Score 80; DB 4; Length 468;
Best Local Similarity 100.0%; Pred. No. 1.4e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 QLSCFRKSPLSNVC 15
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Db 118 QLSCFRKSPLSNVC 132

RESULT 9
5171840-2
PATENT No. 5171840
APPLICANT: KISHIMOTO, TADAMITSU
TITLE OF INVENTION: RECEPTOR PROTEIN FOR HUMAN B CELL
STIMULATORY FACTOR-2
NUMBER OF SEQUENCES: 11
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/298,694
FILING DATE: 19-JAN-1989
SEQ ID NO: 2;
LENGTH: 468
5171840-2

Query Match 100.0%; Score 80; DB 6; Length 468;
Best Local Similarity 100.0%; Pred. No. 1.4e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 QLSCFRKSPLSNVC 15
|||||
Db 118 QLSCFRKSPLSNVC 132

RESULT 10
5480796-2
PATENT No. 5480796
APPLICANT: KISHIMOTO, TADAMITSU
TITLE OF INVENTION: ANTIBODIES AGAINST THE RECEPTOR PROTEIN

FOR HUMAN B CELL STIMULATORY FACTOR-2
NUMBER OF SEQUENCES: 8
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/907,650
FILING DATE: 02-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 298,694
FILING DATE: 19-JAN-1989
SEQ ID NO: 2;
LENGTH: 468
5480796-2

Query Match 100.0%; Score 80; DB 6; Length 468;
Best Local Similarity 100.0%; Pred. No. 1.4e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 QLSCFRKSPLSNVC 15
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Db 118 QLSCFRKSPLSNVC 132

RESULT 11
US-07-676-647-8
Sequence 8, Application US/07676647
Patent No. 5426177
GENERAL INFORMATION:
APPLICANT: Davis, Samuel
APPLICANT: Squinto, Stephen P.
APPLICANT: Futh, Mark E.
APPLICANT: Yancopoulos, George D.
TITLE OF INVENTION: The Ciliary Neurotrophic Factor Receptor
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/676,647
FILING DATE: 19910328
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 6526-048
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEFAX: 212 8698864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 188 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-676-647-8

Query Match 83.8%; Score 67; DB 1; Length 188;
Best Local Similarity 100.0%; Pred. No. 0.00011;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 CFRKSPLSNVVC 12

RESULT 12

US-08-449-329-8

Sequence 8, Application US/08449329

Patent No. 5848334

GENERAL INFORMATION:

APPLICANT: Davis, Samuel

APPLICANT: Squinto, Stephen P.

APPLICANT: Furch, Mark E.

APPLICANT: Yancopoulos, George D.

TITLE OF INVENTION: The Ciliary Neurotrophic Factor Receptor

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: U.S.A.

ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/449,329

FILING DATE:

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/700,677

FILING DATE: 15-MAY-1991

ATTORNEY/AGENT INFORMATION:

NAME: Mistock, S. Leslie

REGISTRATION NUMBER: 18,872

REFERENCE/DOCKET NUMBER: 6526-065

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212 790-9090

TELEFAX: 212 8698864/9741

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 188 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: unknown

MOLECULE TYPE: peptide

US-08-449-329-8

Query Match 83.8%; Score 67; DB 1; Length 188;

Best Local Similarity 100.0%; Pred. No. 0.00011;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CFRKSPLSNVVC 15

Db 1 CFRKSPLSNVVC 12

RESULT 13

US-08-445-073-8

Sequence 8, Application US/08445073

Patent No. 5849897

GENERAL INFORMATION:

APPLICANT: Davis, Samuel

APPLICANT: Squinto, Stephen P.

APPLICANT: Furch, Mark E.

APPLICANT: Yancopoulos, George D.

TITLE OF INVENTION: The Ciliary Neurotrophic Factor Receptor

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: U.S.A.

ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/445,073

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/676,647

FILING DATE: 28-MAR-1991

ATTORNEY/AGENT INFORMATION:

NAME: Mistock, S. Leslie

REGISTRATION NUMBER: 18,872

REFERENCE/DOCKET NUMBER: 6526-048

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212 790-9090

TELEFAX: 212 8698864/9741

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 188 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-445-073-8

Query Match 83.8%; Score 67; DB 2; Length 188;

Best Local Similarity 100.0%; Pred. No. 0.00011;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CFRKSPLSNVVC 15

Db 1 CFRKSPLSNVVC 12

RESULT 14

US-08-585-258-8

Sequence 8, Application US/08585258

Patent No. 5892003

GENERAL INFORMATION:

APPLICANT: Davis, Samuel

APPLICANT: Squinto, Stephen P.

APPLICANT: Furch, Mark E.

APPLICANT: Yancopoulos, George D.

TITLE OF INVENTION: The Ciliary Neurotrophic Factor Receptor

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: U.S.A.

ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/585,258

FILING DATE: 11-JAN-1996

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/001,904

FILING DATE:
APPLICATION NUMBER: US/07/700,677
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 6526-065
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEFAX: 212 8698864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 188 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-585-258-8

Query Match 83.8%; Score 67; DB 2; Length 188;
Best Local Similarity 100.0%; Pred. No. 0.00011;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CFRKSPLSNVC 15
|||||
DB 1 CFRKSPLSNVC 12

RESULT 15
PCT-US91-03896-8
Sequence 8, Application.PC/TUS9103896
GENERAL INFORMATION:
APPLICANT: Davis, Samuel
APPLICANT: Squinto, Stephen P.
APPLICANT: Furth, Mark E.
APPLICANT: Yancopoulos, George D.
TITLE OF INVENTION: The Ciliary Neurotrophic Factor Receptor
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/03896
FILING DATE: 19910603
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 6526-065-228
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEFAX: 212 8698864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 188 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
PCT-US91-03896-8

Query Match 83.8%; Score 67; DB 5; Length 188;
Best Local Similarity 100.0%; Pred. No. 0.00011;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 CFRKSPLSNVC 15
|||||
DB 1 CFRKSPLSNVC 12

Search completed: December 19, 2001, 16:20:59
Job time: 404 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: December 19, 2001, 16:19:34 ; Search time 170.68 seconds
(without alignments)
8.680 Million cell updates/sec

Title: US-09-202-104A-6
Perfect score: 105
Sequence: 1 MCVASSVGSKFKTQFGCC 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: A_Geneseq_1101.*
2: /SIDS8/gcgdata/geneseq/geneseqp/AA1980.DAT.*
3: /SIDS8/gcgdata/geneseq/geneseqp/AA1981.DAT.*
4: /SIDS8/gcgdata/geneseq/geneseqp/AA1982.DAT.*
5: /SIDS8/gcgdata/geneseq/geneseqp/AA1983.DAT.*
6: /SIDS8/gcgdata/geneseq/geneseqp/AA1984.DAT.*
7: /SIDS8/gcgdata/geneseq/geneseqp/AA1985.DAT.*
8: /SIDS8/gcgdata/geneseq/geneseqp/AA1987.DAT.*
9: /SIDS8/gcgdata/geneseq/geneseqp/AA1988.DAT.*
10: /SIDS8/gcgdata/geneseq/geneseqp/AA1989.DAT.*
11: /SIDS8/gcgdata/geneseq/geneseqp/AA1990.DAT.*
12: /SIDS8/gcgdata/geneseq/geneseqp/AA1991.DAT.*
13: /SIDS8/gcgdata/geneseq/geneseqp/AA1992.DAT.*
14: /SIDS8/gcgdata/geneseq/geneseqp/AA1993.DAT.*
15: /SIDS8/gcgdata/geneseq/geneseqp/AA1994.DAT.*
16: /SIDS8/gcgdata/geneseq/geneseqp/AA1995.DAT.*
17: /SIDS8/gcgdata/geneseq/geneseqp/AA1996.DAT.*
18: /SIDS8/gcgdata/geneseq/geneseqp/AA1997.DAT.*
19: /SIDS8/gcgdata/geneseq/geneseqp/AA1998.DAT.*
20: /SIDS8/gcgdata/geneseq/geneseqp/AA1999.DAT.*
21: /SIDS8/gcgdata/geneseq/geneseqp/AA2000.DAT.*
22: /SIDS8/gcgdata/geneseq/geneseqp/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	105	100.0	20	19	AAW52206
2	105	100.0	182	17	AAW00403
3	105	100.0	315	20	AAW70805
4	105	100.0	315	21	AAV92200
5	105	100.0	323	10	AAV90527
6	105	100.0	325	21	AAV15389
7	105	100.0	325	21	AAV15390
8	105	100.0	344	10	AAV90528
9	105	100.0	345	21	AAV55071
10	105	100.0	360	20	AAW70804
11	105	100.0	360	21	AAV92199

12	105	100.0	386	10	AAV90526	B cell stimulating
13	105	100.0	419	20	AAV30938	Human IL-6 recepto
14	105	100.0	468	10	AAV90525	B cell stimulating
15	105	100.0	468	10	AAV90284	Sequence of a rece
16	105	100.0	468	14	AAV37215	IL-6 receptor. Sy
17	105	100.0	468	17	AAV83664	Interleukin-6 rece
18	105	100.0	468	19	AAV71371	Human interleukin-
19	105	100.0	468	21	AAV92196	Human IL-6R-alpha-
20	105	100.0	468	22	AAV36655	Human IL-6 recepto
21	105	100.0	477	21	AAV32197	Human IL-6R-alpha-
22	105	100.0	500	18	AAV36847	Human fusion polyp
23	105	100.0	515	21	AAV15404	IL-6R/IL-6 fusion
24	105	100.0	525	18	AAV36846	Human fusion polyp
25	105	100.0	543	20	AAV03164	Chimeric sIL-6R/IL
26	105	100.0	592	20	AAV70797	Human interleukin-
27	105	100.0	592	21	AAV32185	Human IL-6R-alpha-
28	105	100.0	690	21	AAV92195	Human IL-6R-alpha-
29	105	100.0	1042	16	AAV70122	IL8-R type 1-GBP 1
30	105	100.0	1158	21	AAV92205	Fusion polypeptide
31	105	100.0	1168	21	AAV92204	Fusion polypeptide
32	54	51.4	460	12	AAV13318	IL-6 receptor. Mu
33	52	49.5	460	13	AAV22616	IL-6R for soluble
34	52	49.5	460	13	AAV36656	Mouse IL-6 recepto
35	47.5	45.2	311	22	AAV66701	Human GPCR1 polype
36	47.5	45.2	315	22	AAV71546	Human olfactory re
37	47	44.8	70	21	AAV63162	Human secreted pro
38	47	44.8	70	22	AAV01655	Human secreted pro
39	47	44.8	97	21	AAV73386	HTRM clone 32/9329
40	45	42.9	342	20	AAV36967	Chlamydia trachoma
41	44	41.9	55	21	AAV07485	Arabidopsis thalia
42	44	41.9	55	21	AAV19980	Arabidopsis thalia
43	44	41.9	55	21	AAV50989	Arabidopsis thalia
44	44	41.9	73	21	AAV07484	Arabidopsis thalia
45	44	41.9	73	21	AAV19799	Arabidopsis thalia

ALIGNMENTS

RESULT 1	
AAW52206	
ID	AAW52206 standard; peptide: 20 AA.
XX	
AC	AAW52206;
XX	
DT	09-JUN-1998 (first entry)
XX	
DE	Interleukin-6 antagonist peptide.
XX	
KW	Interleukin-6, IL-6; antagonist; IL-6 related disease; multiple myeloma;
KW	acquired immune deficiency syndrome-related lymphoma; immune response;
KW	rheumatoid arthritis; psoriasis; sepsis; osteoporosis; therapy;
XX	Alzheimer's disease.
XX	
OS	Synthetic.
OS	Homo sapiens.
XX	
PN	W09748728-A1.
XX	
PD	24-DEC-1997.
XX	
PF	19-JUN-1997; 97WO-NL00345.
XX	
PR	20-JUN-1996; 96EP-0201720.
XX	
PA	(KOST/) KOSTER H W.
XX	
PI	Hoebel KHN, Van Leengoed LAMG;
XX	
DR	WPI, 1998-063080/06.
XX	
PT	New peptide(s) with Interleukin-6 agonist or antagonist activity -
PT	useful for treatment, prevention and diagnosis of IL-6 associated

Query Match 100.0%; Score 105; DB 20; Length 315;
 Best Local Similarity 100.0%; Pred. No. 5.6e-09;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MCVASSVSGSKFSKTQTFQGC 20
 |||
 DB 192 mcvassvsgskfskttqtfqgc 211

RESULT 4

AAV92200 standard; protein: 315 AA.

AC AAV92200;

DT 01-AUG-2000 (first entry)

DE Soluble human IL-6-R-alpha-313.

KM Soluble IL-6-R-alpha-313; cytokine; antagonist; CNTF; receptor;
 fusion protein; cytosolic; immunomodulator; osteopontin.

OS Homo sapiens.

Key Location/Qualifiers

FT Protein 1..313
 FT /label= truncated_IL-6-R-alpha
 FT Peptide 314..315
 FT /note= "Thr-Gly bridge"

PN WO200018932-A2.

PD 06-APR-2000.

PF 22-SEP-1999; 99WO-US22045.

PR 25-SEP-1998; 98US-0101858.
 PR 19-MAY-1999; 99US-0313942.

PA (REGE-) REGENERON PHARM INC.

PI Stahl N, Yancopoulos GD;

DR WPI; 2000-293165/25.

Isolated nucleic acid molecule for treating cytokine-related diseases or disorders encodes a fusion polypeptide capable of binding a cytokine to form a nonfunctional complex

Example 4; Fig 16; 152pp; English.

The invention concerns production of antagonists to any cytokine that utilizes an alpha specificity determining component, which when combined with the cytokine, binds to a first beta signal transducing component to form a non-functional intermediate which then binds to a second beta signal transducing component causing beta-receptor dimerization, the soluble alpha specificity determining component of the receptor (SR-alpha) and the extracellular domain of the first beta signal transducing component of the cytokine receptor (beta-1) are combined to form heterodimers (SR-alpha:beta-1) that act as antagonist to the cytokine by binding the cytokine to form a non-functional complex. The receptor components are shared by cytokines such as the CNTF (ciliary neurotrophic factor) family of cytokines. The invention provides the basis for the development of IL-6 antagonists, as they show that if, in the presence of a ligand, a non-functional intermediate complex, consisting of the ligand, its alpha receptor and its beta-1 receptor component, can be formed, it will effectively block the action of the ligand. Effective antagonists of IL-6 or CNTF consist of heterodimers of the extracellular domains of the alpha specificity determining components of their receptors and the extracellular domain of gp130. The resultant heterodimers, function as high-affinity traps, rendering

CC the cytokine inaccessible to form a signal transducing complex with the
 CC native membrane-bound forms of their receptor. The nucleic acids and
 CC polypeptides are useful for treating cytokine-related diseases or
 CC disorders such as osteoporosis and primary and secondary effects of
 CC cancer including multiple myeloma or cachexia.

SQ Sequence 315 AA;

Query Match 100.0%; Score 105; DB 21; Length 315;
 Best Local Similarity 100.0%; Pred. No. 5.6e-09;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MCVASSVSGSKFSKTQTFQGC 20
 |||
 DB 192 mcvassvsgskfskttqtfqgc 211

RESULT 5

AAV90527 standard; protein: 323 AA.

AC AAV90527;

DT 25-JAN-1990 (first entry)

DE B cell stimulating factor-2 receptor.

KM B cell stimulating factor-2 receptor; monocytic U937 cell line.

OS Homo sapiens.

PN AU8928720-A.

PD 27-JUL-1989.

PF 23-JAN-1989; 89AU-0028720.

PR 22-JAN-1988; 88JP-0012387.
 PR 25-JAN-1988; 88JP-0012599.
 PR 04-AUG-1988; 88JP-0194885.
 PR 14-JAN-1989; 89JP-0007461.

PA (KISH) TADAMITSU KISHIMOTO.

PI Kishimoto T;

DR WPI; 1989-264012/37.

DR N-PSDB; AAV90525.

Receptor protein for human B cell stimulating factor-2 - used for developing prophylactic, therapeutic and diagnostic agents for associated disorders.

Claim 6, page 39; 76pp; english.

The BSF2 receptor has amino acids at the C-terminal deleted. The receptor is derived from a monocytic U937 cell line. It can be used to develop prophylactic and therapeutic pharmaceuticals, as agents to relate diseases and disorders to abnormal BSF-2 prodn. It can also be used to study an immune mechanism with which BSF-2 or the receptor is concerned.

SQ Sequence 323 AA;

Query Match 100.0%; Score 105; DB 10; Length 323;
 Best Local Similarity 100.0%; Pred. No. 5.8e-09;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MCVASSVSGSKFSKTQTFQGC 20
 |||
 DB 192 mcvassvsgskfskttqtfqgc 211

```

RESULT      6
AAB15389
ID AAB15389 standard; Protein; 325 AA.
XX
AC AAB15389;
XX
DT 11-DEC-2000 (first entry)
XX
DE Human Interleukin 6 receptor protein.
XX
KM Human; interleukin-6 receptor; fungus; Pichia pastoris; PCR primer;
XX expression vector; immunoglobulin-like region; cytokine receptor region.
XX Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 57 /note= "encoded by GGC"
FT Misc-difference 281 /note= "encoded by CAA"
FT
XX JP2000157280-A.
XX
PD 13-JUN-2000.
XX
PF 26-NOV-1998; 98JP-0335464.
XX
PR 26-NOV-1998; 98JP-0335464.
XX
PA (WOJY ) TOSOH CORP.
XX
XX WPI: 2000-468203/41.
DR N-PSDB; AAA70701.
XX
XX Yeasts transformed with IL-6 receptor gene -
PT
XX
XX Example 1; Page 6-8; 10pp; Japanese.
XX
CC The invention relates to the production of human interleukin-6 receptor
CC (IL-6R) protein in the fungus Pichia pastoris. The fungus was
CC transformed with an expression vector (pOTC9-A201L) containing a gene
CC encoding an IL-6R protein having an immunoglobulin-like region and
CC cytokine receptor region and spanning amino acids from Leu20-Ala323. The
CC human IL-6R region was PCR amplified using the primers AAA70702-A70703.
CC This sequence represents the recombinant IL-6R protein of the invention.
CC
XX
SQ Sequence 325 AA;

Query Match 100.0%; Score 105; DB 21; Length 325;
Best Local Similarity 100.0%; Pred. No. 5.8e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MCVASVSGSKFKSTQTFQGC 20
   |||||||||||||||||||
Db 173 mcvassvsgskfktqtlgqc 192

RESULT      7
AAB15390
ID AAB15390 standard; Protein; 325 AA.
XX
AC AAB15390;
XX
DT 15-DEC-2000 (first entry)
XX
DE Bovine Interleukin-12 p35 subunit protein.
XX
KM AntiInfective; bovine; Interleukin 12; IL12; heterodimer; infection.
XX
OS Bos taurus.
XX

```

```

PN JP2000157274-A.
XX
PD 13-JUN-2000.
XX
XX 20-NOV-1998; 98JP-0331052.
XX
PR 20-NOV-1998; 98JP-0331052.
XX
XX (DADC ) DAICHI PHARM CO LTD.
XX
PA WPI: 2000-468201/41.
XX
DR N-PSDB; AAA70708.
XX
XX Preparation of bovine interleukin 12 comprising using a vector
XX containing the gene encoding it, useful for the prevention and
XX treatment of chronic and opportunistic infections -
XX
PS Example 1; Page 8; 11pp; Japanese.
XX
XX The invention relates to a method for the preparation of bovine
XX interleukin 12 (BoiIL12). BoiIL12 consists of a heterodimer of p35
XX and p40 subunits. BoiIL12 is produced by introducing into a host cell,
XX recombinant vectors containing genes encoding the p35 and p40 subunits.
XX This sequence represents the bovine IL12 p35 subunit. Interleukin 12
XX is used for the prevention and treatment of chronic infections and
XX opportunistic infections.
XX
SQ Sequence 325 AA;

Query Match 100.0%; Score 105; DB 21; Length 325;
Best Local Similarity 100.0%; Pred. No. 5.8e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MCVASVSGSKFKSTQTFQGC 20
   |||||||||||||||||||
Db 173 mcvassvsgskfktqtlgqc 192

RESULT      8
AAP90528
ID AAP90528 standard; protein; 344 AA.
XX
AC AAP90528;
XX
DT 25-JAN-1990 (first entry)
XX
XX B cell stimulating factor-2 receptor.
DE
XX B cell stimulating factor-2 receptor.
XX
KM B cell stimulating factor-2 receptor; monocycle U937 cell line.
XX
OS Homo sapiens.
XX
PN A08928720-A.
XX
PD 27-JUL-1989.
XX
PF 23-JAN-1989; 89AU-0028720.
XX
PR 22-JAN-1988; 88JP-0012387.
PR 25-JAN-1988; 88JP-0012599.
PR 04-AUG-1988; 88JP-0194885.
PR 14-JAN-1989; 89JP-0007461.
XX
XX (KISH ) TADAMITSU KISHIMOTO.
XX
XX Kishimoto T;
XX
XX WPI: 1989-264012/37.
DR N-PSDB; AAP90525.
XX
XX Receptor protein for human B cell stimulating factor-2 - used for
XX developing prophylactic, therapeutic and diagnostic agents for
PT

```

PT associated disorders.
 XX
 XX
 PS Claim 7; page 40; 76pp; English.
 XX
 CC The BSR2 receptor has amino acids at the C-terminal deleted. The receptor
 CC is derived from a monocyle U937 cell line. It can be used to develop
 CC prophylactic and therapeutic pharmaceuticals, as agents to relate
 CC diseases and disorders to abnormal BSR-2 prodn. It can also be used to
 CC study an immune mechanism with which BSR-2 or the receptor is concerned.
 XX
 SQ Sequence 344 AA:
 Query Match 100.0%; Score 105; DB 10; Length 344;
 Best Local Similarity 100.0%; Pred. No. 6.2e-09;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 MCVASSVSGSKFSTQTFQGC 20
 DB 192 mcvassvsgskfktqfkgc 211
 RESULT 9
 AAY55071
 ID AAY55071 standard; Protein; 345 AA.
 XX
 AC AAY55071;
 XX
 DT 25-FEB-2000 (first entry)
 XX
 DE SR345 protein sequence.
 XX
 KW Gene isolation: membrane-bound protein; fusion protein; drug production;
 KW antigen binding cell; secretable functional protein; antigenic protein;
 KW protein isolation; diagnosis; SR345 protein.
 XX
 OS Homo sapiens.
 XX
 PN MO9960113-A1.
 PD 25-NOV-1999.
 XX
 PF 30-APR-1999; 99WO-JP02341.
 XX
 PR 20-MAY-1998; 98JP-0138652.
 PR 01-OCT-1998; 98JP-0279876.
 XX
 PA (CHUS) CHUGAI SEIYAKU KK.
 XX
 PI Tsuchiya M, Saito M, Ohtomo T;
 XX
 DR WPI: 2000-039382/03.
 DR N-PSDB: AAL40288.
 XX
 PT Efficient and selective isolation of a gene encoding membrane protein
 PT with low or no antigenic binding activity, for diagnosis, study of, and
 PT production of drugs creating abnormal functions of the protein -
 XX
 PS Example 1; Page 49-52; 120pp; Japanese.
 XX
 CC This sequence represents the SR345 protein.
 CC The invention relates to a method for isolating a gene encoding a
 CC membrane-bound protein, comprising introducing a vector into a cell,
 CC contacting an antigen with the cell expressing the fused protein encoded
 CC by the vector on its surface to select an antigen-binding cell, and
 CC isolating the cDNA. The vector contains DNA encoding a secretable
 CC functional protein with antigenicity and binding affinity, and a cDNA
 CC ligated to DNA downstream of the 3' end of the coding sequence. The
 CC method can be used to isolate a membrane-bound protein for diagnosis and
 CC study. It can also be used for producing drugs treating abnormal
 CC functions of the protein. Such a technique is efficient and selective,
 CC which is different from the prior-art transmembrane trap (TMT) method
 CC wherein an epitope recognised by an antibody is carried in a fused

CC protein.
 XX
 XX
 SQ Sequence 345 AA:
 Query Match 100.0%; Score 105; DB 21; Length 345;
 Best Local Similarity 100.0%; Pred. No. 6.2e-09;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 MCVASSVSGSKFSTQTFQGC 20
 DB 192 mcvassvsgskfktqfkgc 211
 RESULT 10
 AAW70804
 ID AAW70804 standard; Protein; 360 AA.
 XX
 AC AAW70804;
 XX
 DT 03-FEB-1999 (first entry)
 XX
 DE Amino acid sequence of the interleukin (IL)-6R-alpha domain.
 XX
 KW gp130; cytokine antagonist; interleukin; gamma-interferon;
 KW granulocyte macrophage colony-stimulating factor; J peptide;
 KW transforming growth factor-beta.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Protein 1..358
 FT /note="soluble interleukin (IL)-6R-alpha domain"
 PN US5844099-A.
 PD 01-DEC-1998.
 XX
 PF 27-NOV-1995; 95US-0563105.
 XX
 PR 27-NOV-1995; 95US-0563105.
 PR 20-OCT-1993; 93US-0140222.
 XX
 PA (REGF-) REGENERON PHARM INC.
 XX
 PI Economides A, Stahl N, Yancopoulos GD;
 XX
 DR WPI: 1999-044669/04.
 XX
 PT Cytokine antagonists - comprising extracellular domains of
 PT specificity-determining and signal-transducing components of
 PT cytokine receptor
 XX
 PS Example 4; Fig 15; 46pp; English.
 XX
 CC The present sequence represents the amino acid sequence of interleukin
 CC (IL)-6R-alpha domain. The protein is used in the course of the invention.
 CC The specification describes cytokine antagonists comprising only the
 CC extracellular domain of the specificity-determining component of
 CC the cytokine receptor and the extracellular domain of a
 CC signal-transducing component of the cytokine receptor. The cytokine
 CC is an interleukin (IL-1, IL-2, IL-3, IL-4, IL-5 or IL-15),
 CC granulocyte macrophage colony-stimulating factor (GM-CSF),
 CC gamma-interferon or transforming growth factor-beta (TGF-beta). The
 CC antagonist is capable of binding the cytokine to form a nonfunctional
 CC complex. The compounds have therapeutic activity as cytokine antagonists
 CC and can also be used in assays for identifying novel agonists and
 CC antagonists of cytokines.
 XX
 SQ Sequence 360 AA:
 Query Match 100.0%; Score 105; DB 20; Length 360;


```

DE Human IL-6 receptor/IL-6 fusion protein.
XX
XX IL-6; interleukin-6; receptor; human; fusion protein; bone marrow;
KM stem cell; platelet; reduced antigenicity.
XX
XX Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Protein 1..420
FT /note="No start codon given"
XX
XX JP1196867-A.
XX
XX 27-JUL-1999.
XX
XX 09-JAN-1998; 98JP-0002921.
XX
XX 09-JAN-1998; 98JP-0002921.
XX
XX (TOYO ) TOSOH CORP.
XX
XX WPI: 1999-496648/42.
XX
XX N-PSDB; AA09202.
XX
XX New interleukin-6 receptor-interleukin-6 fused protein and gene -
PT used for growth of bone marrow stem cells and platelets
XX
XX Example 1; Page 5-8; 8pp; Japanese.
XX
XX This invention describes a novel gene which encodes a fusion protein of
CC Interleukin-6 (IL-6) receptor and bound with a gene sequence encoding
CC for IL-6 at the downstream of IL-6 receptor gene. The gene and its
CC encoding protein has applications for the growth of bone marrow stem
CC cells and platelets. Transmission of a signal of IL-6 to target cells for
CC stimulation with reduced antigenicity is possible. This sequence
CC represents the IL-6 receptor/IL-6 fusion protein described in the
CC invention.
XX
XX Sequence 419 AA;
SQ

```

Query Match 100.0%; Score 105; DB 20; Length 419;
Best Local Similarity 100.0%; Pred. No. 7.6e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

OY 1 MCVASSVSGSKFKTQTFQGC 20
    |||||||
DB 77 mcvassvsgskfktqtfqgc 96

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RESULT 14
AAP90525
ID AAP90525 standard; protein; 468 AA.
XX
XX AAP90525;
AC
XX 23-JAN-1990 (first entry)
DT
XX B cell stimulating factor-2 receptor.
DE
XX B cell stimulating factor-2 receptor; monocytic U937 cell line.
KM
XX Homo sapiens.
OS
XX AU8928720-A.
PN
XX 27-JUL-1989.
PD
XX 23-JAN-1989; 89AU-0028720.
PF
XX 22-JAN-1988; 88JP-0012387.
PR 25-JAN-1988; 88JP-0012599.
PR

```

PR 04-AUG-1988; 88JP-0194885.
PR 14-JAN-1989; 89JP-0007461.
XX
XX (KISH ) TADAMITSU KISHIMOTO.
XX
XX Kishimoto T;
XX
XX WPI: 1989-264012/37.
XX
XX N-PSDB; AAP90525.
XX
XX Receptor protein for human B cell stimulating factor-2 - used for
PT developing prophylactic, therapeutic and diagnostic agents for
PT associated disorders.
XX
XX Claim 2; page 36; 76pp; english.
XX
XX The BSF2 receptor is derived from a monocytic U937 cell line. It can be
CC used to develop prophylactic and therapeutic pharmaceuticals, as agents to
CC relate diseases and disorders to abnormal BSF-2 prodn. It can also be
CC used to study an immune mechanism with which BSF-2 or the receptor is
CC concerned.
XX
XX Sequence 468 AA;
SQ

```

Query Match 100.0%; Score 105; DB 10; Length 468;
Best Local Similarity 100.0%; Pred. No. 8.5e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

OY 1 MCVASSVSGSKFKTQTFQGC 20
    |||||||
DB 192 mcvassvsgskfktqtfqgc 211

```

RESULT 15
AAP90284
ID AAP90284 standard; protein; 468 AA.
XX
XX AAP90284;
AC
XX 31-MAR-1992 (first entry)
DT
XX Sequence of a receptor protein for human B cell stimulating
DE factor-2 (BSF2 receptor).
XX
XX B cell; immune disorder; therapy; diagnosis; prophylaxis.
KM
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH Region 2..22
FT /label= hydrophobic region
FT Region 362..386
FT /label= hydrophobic region
XX
XX EP325474-A.
PN
XX 26-JUL-1989.
PD
XX 20-JAN-1989; 89EP-0300536.
PF
XX 14-JAN-1989; 89JP-0017461.
PR 22-JAN-1988; 88JP-0012387.
PR 25-JAN-1988; 88JP-0012599.
PR 04-AUG-1988; 88JP-0194885.
PR 20-JAN-1989; 89JP-0009774.
XX
XX (KISH/) KISHIMOTO T.
XX
XX Kishimoto T;
PI
XX WPI: 1989-214667/30.
DR N-PSDB; AAN90340.
DR

XX Receptor protein for human B cell stimulating factor-2 - obtd. by
 PT recombinant DNA techniques and used as diagnostic, prophylactic or
 PT therapeutic agent
 XX
 PS Claim 2; Page 19-21; 63pp; English.
 XX
 CC The cDNA in AAN90340 was derived from monocyte cell line U937.
 CC Isolated BSF2 receptor and DNA encoding it are claimed, as are
 CC (b) expression vectors; (c) host organisms; (d) antibodies; and
 CC (e) hybridomas.
 XX
 SO Sequence 468 AA;

Query Match 100.0%; Score 105; DB 10; Length 468;
 Best Local Similarity 100.0%; Pred. No. 8.5e-09;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MCVASSVSGSKFSKTQTFQGC 20
 |||
 Db 192 mcvassvsgskfsktqtfqgc 211

Search completed: December 19, 2001, 16:19:35
 Job time: 360 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: December 19, 2001, 16:22:38 ; Search time 88.82 Seconds
(without alignments)
17.153 Million cell updates/sec

Title: US-09-202-104A-6

Perfect score: 105

Sequence: 1 MCVASSVGSKFSKTRFGC 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

PIR_68:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	105	100.0	468	1 A41242	interleukin-6 rece
2	52	49.5	440	2 JL0144	interleukin-6 rece
3	52	49.5	460	2 JL0145	interleukin-6 rece
4	50	47.6	462	1 A37986	interleukin-6 rece
5	46	43.8	415	2 B71541	probable amino aci
6	43	41.0	218	2 B25193	C-reactive protein
7	43	41.0	218	2 C25193	C-reactive protein
8	43	41.0	242	2 C25192	C-reactive protein
9	43	41.0	242	2 B25192	C-reactive protein
10	43	41.0	479	2 S60924	hypothetical prote
11	43	41.0	687	2 T49226	hypothetical prote
12	42	40.0	1081	1 WZBBA6	119k DNA helicase/
13	42	40.0	1369	2 T38495	hypothetical prote
14	41	39.0	323	2 A64054	selenophosphate sy
15	41	39.0	519	2 S78196	probable maturase
16	41	39.0	601	2 F81074	thiol-disulfide in
17	41	39.0	613	2 B81868	thiol-disulfide in
18	41	39.0	722	2 E86725	conserved hypotet
19	41	39.0	747	2 T47285	hypothetical prote
20	41	39.0	2034	2 T22147	hypothetical prote
21	40	38.1	153	2 B26889	T-cell receptor al
22	40	38.1	722	2 T00049	hemocyte protein A
23	40	38.1	918	2 S45872	hypothetical prote
24	40	38.1	1374	2 T30809	plasmaingogen relat
25	40	38.1	2180	2 A46182	polyprotein - echo
26	39	37.1	49	2 S65722	hemoglobin, extrac
27	39	37.1	113	2 S40138	T-cell receptor V-
28	39	37.1	131	1 RMHUA	T-cell receptor al
29	39	37.1	223	1 YLHUP	serum amyloid P-co

30	39	37.1	238	2 T31680	back protein - Bac
31	39	37.1	285	2 G71552	hypothetical prote
32	39	37.1	287	2 S74944	hypothetical prote
33	39	37.1	300	2 S60538	envelope polyprote
34	39	37.1	300	2 S60526	envelope polyprote
35	39	37.1	341	2 T45124	hypothetical prote
36	39	37.1	661	2 T40056	nadph-cytochrome p
37	39	37.1	678	1 S29123	NADPH--ferritinopr
38	39	37.1	700	2 B81266	DNA topoisomerase
39	39	37.1	790	2 T12203	transcription fact
40	39	37.1	1076	2 S50536	hypothetical prote
41	38.5	36.7	646	2 C86441	probable ABC trans
42	38	36.2	132	2 S37965	hypothetical prote
43	38	36.2	136	2 T47982	hypothetical prote
44	38	36.2	169	2 S67636	probable membrane
45	38	36.2	179	2 T49757	hypothetical prote

ALIGNMENTS

RESULT 1
A41242
interleukin-6 receptor precursor - human
N:Contains: interleukin-6 receptor, soluble form
C:Species: Homo sapiens (man)
C:Date: 27-Mar-1992 #Sequence-Revision 02-Dec-1994 #text-change 21-Jul-2000
C:Accession: A41242; J00080; S17468; A61459; S14621
R:Yamasaki, K.; Taga, T.; Hirata, Y.; Yawata, H.; Kawanishi, Y.; Seed, B.; Taniguchi, Science 241, 825-828, 1988
A:Title: Cloning and expression of the human Interleukin-6 (BSF-2/IFNbeta 2) receptor
A:Reference number: A41242; M0ID:88305347
A:Accession: A41242
A:Molecule type: mRNA
A:Residues: 1-468 <YAM>
A:Cross-references: GB:M20566; NID:933845; PIDN:CAA31312.1; PID:933846
R:Yamasaki, K.; Taga, T.; Hirata, Y.; Yawata, H.; Kawanishi, Y.; Seed, B.; Taniguchi, Proc. Jpn. Acad. 64, 209-211, 1988
A:Title: Molecular structure of Interleukin 6 receptor.
A:Reference number: J00080
A:Accession: J00080
A:Molecule type: mRNA
A:Residues: 1-468 <YAZ>
R:Schmidt, H.; Stoyan, T.; Lenz, D.; Schmitz, H.; Hirano, T.; Kishimoto, T.; Heine Biochem. J. 277, 659-664, 1991
A:Title: Structural and functional studies on the human hepatic Interleukin-6 recepto
A:Reference number: S17468; M0ID:91336983
A:Accession: S17468
A:Molecule type: mRNA
A:Residues: 1-468 <SCH>
A:Cross-references: EMBL:X58298; NID:932580; PIDN:CAA41231.1; PID:932581
A:Experimental source: Hepatoma cell line HepG2
R:Novick, D.; Engelmann, H.; Wallach, D.; Rubinstein, M. J. Exp. Med. 170, 1409-1414, 1989
A:Title: Soluble cytokine receptors are present in normal human urine.
A:Reference number: A61459; M0ID:90010793
A:Accession: A61459
A:Molecule type: protein
A:Residues: 20-49 <NOV>
C:Comment: Through this receptor, interleukin-6 induces proliferation, activation, an
C:Comment: This growth factor receptor does not have a tyrosine kinase domain.
C:Genetics:
A:Gene: GDB:IL6R
A:Cross-references: GDB:127966; OMIM:147880
A:Map position: 1q21-1q21
C:Superfamily: ciliary neurotrophic factor receptor; cytokine receptor homology; immu
C:Keywords: acute phase; cytokine receptor; glycoprotein; transmembrane protein
F:1-19/Domain: signal sequence #status predicted <Sig>
F:20-468/Product: interleukin-6 receptor #status predicted <Mat>
F:20-363/Domain: extracellular #status predicted <Ext>
F:40-98/Domain: immunoglobulin homology <IMM2>
F:121-309/Domain: cytokine receptor homology <CRS>
F:364-386/Domain: transmembrane #status predicted <TM>

F:387-468/Domain: intracellular #status predicted <INT>
F:47-96/Disulfide bonds: #status predicted
F:55,93,221,245,350/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 105; DB 1; Length 468;
Best Local Similarity 100.0%; Pred. No. 4,8e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MCVASSVSGSKFSKTQTFGC 20
|||||
Db 192 MCVASSVSGSKFSKTQTFGC 211

RESULT 2
JL0144
Interleukin-6 receptor precursor (clone lambda p1) - mouse
C:Species: Mus musculus (house mouse)
C>Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 21-Jan-2000
C:Accession: JL0144
R: Sugita, T.; Totsuka, T.; Saito, M.; Yamasaki, K.; Taga, T.; Hirano, T.; Kishimoto, T.
J. Exp. Med. 171, 2001-2009, 1990
A: Title: Functional murine interleukin 6 receptor with the intracisternal a particle get
A: Reference number: JL0144; MUID:90278354
A: Accession: JL0144
A: Status: nucleic acid sequence not shown
A: Molecule type: mRNA
A: Residues: 1-440 <SIG>
A: Cross-references: GB:51976; NID:953548; PIDN:CAA36238.1; PID:953549
C: Superfamily: ciliary neurotrophic factor receptor; cytokine receptor homology; immunog
C: Keywords: cytokine receptor; transmembrane protein
F: 1-19/Domain: signal sequence #status predicted <SIG>
F: 20-440/Product: Interleukin-6 receptor #status predicted <MAT>
F: 40-94/Domain: immunoglobulin homology <IMM>
F: 117-306/Domain: cytokine receptor homology <CRS>
F: 358-385/Domain: transmembrane #status predicted <TRA>

Query Match 49.5%; Score 52; DB 2; Length 440;
Best Local Similarity 58.8%; Pred. No. 0.53;
Matches 10; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 1 MCVASSVSGSKFSKTQTF 17
|||||
Db 189 LCVANSVSGSKSHNEAF 205

RESULT 3
JL0145
Interleukin-6 receptor precursor (clone lambda 301) - mouse
C:Species: Mus musculus (house mouse)
C>Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 21-Jan-2000
C:Accession: JL0145; S14543
R: Sugita, T.; Totsuka, T.; Saito, M.; Yamasaki, K.; Taga, T.; Hirano, T.; Kishimoto, T.
J. Exp. Med. 171, 2001-2009, 1990
A: Title: Functional murine interleukin 6 receptor with the intracisternal a particle get
A: Reference number: JL0144; MUID:90278354
A: Accession: JL0145
A: Status: nucleic acid sequence not shown
A: Molecule type: mRNA
A: Residues: 1-460 <SIG>
A: Cross-references: GB:X1975; NID:948725; PIDN:CAA36237.1; PID:949726
A: Experimental source: clone lambda 301
R: Fiorillo, M.T.; Ciliberto, G.; Dente, L.
submitted to the EMBL data library, July 1990
A: Description: Cloning and expression of murine IL-6 receptor.
A: Reference number: S14543
A: Accession: S14543
A: Status: preliminary
A: Molecule type: mRNA
A: Residues: 1-373; 'R', 375-460 <PIO>
A: Cross-references: EMBL:X53802; NID:952692; PIDN:CAA37810.1; PID:952693
C: Superfamily: ciliary neurotrophic factor receptor; cytokine receptor homology; immunog

C: Keywords: cytokine receptor; transmembrane protein
F: 1-19/Domain: signal sequence #status predicted <SIG>
F: 20-460/Product: Interleukin-6 receptor #status predicted <MAT>
F: 40-94/Domain: immunoglobulin homology <IMM>
F: 117-306/Domain: cytokine receptor homology <CRS>
F: 358-385/Domain: transmembrane #status predicted <TRA>

Query Match 49.5%; Score 52; DB 2; Length 460;
Best Local Similarity 58.8%; Pred. No. 0.55;
Matches 10; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 1 MCVASSVSGSKFSKTQTF 17
|||||
Db 189 LCVANSVSGSKSHNEAF 205

RESULT 4
A37986
Interleukin-6 receptor precursor - rat
N: Alternate names: IL-6 receptor
C: Species: Rattus norvegicus (Norway rat)
C: Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 22-Jun-1999
C: Accession: A37986
R: Baumann, M.; Baumann, H.; Fey, G.H.
J. Biol. Chem. 265, 19853-19867, 1990
A: Title: Molecular cloning, characterization and functional expression of the rat 11v
A: Reference number: A37986; MUID:91060602
A: Accession: A37986
A: Molecule type: mRNA
A: Residues: 1-462 <RNA>
A: Cross-references: GB:58587; GB:J05668; NID:9204921; PIDN:AAA1431.1; PID:9204922
C: Comment: After binding IL-6, this chain associates with a 130k glycoprotein that is
C: Superfamily: ciliary neurotrophic factor receptor; cytokine receptor homology; immu
C: Keywords: acute phase; cytokine receptor; transmembrane protein
F: 1-19/Domain: signal sequence #status predicted <SIG>
F: 20-462/Product: Interleukin-6 receptor #status predicted <MAT>
F: 20-362/Domain: extracellular #status predicted <EXT>
F: 40-94/Domain: immunoglobulin homology <IMM>
F: 117-306/Domain: cytokine receptor homology <CRS>
F: 353-385/Domain: transmembrane #status predicted <TMN>
F: 386-462/Domain: intracellular #status predicted <INT>
F: 47-92/Disulfide bonds: #status predicted

Query Match 47.6%; Score 50; DB 1; Length 462;
Best Local Similarity 55.6%; Pred. No. 1.2;
Matches 10; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

OY 1 MCVASSVSGSKFSKTQTF 18
|||||
Db 189 LCVANSVSGSKSHNVFQ 206

RESULT 5
B71541
Probable amino acid (glutamate) transporter - Chlamydia trachomatis (serotype D, stra
C: Species: Chlamydia trachomatis
C: Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 18-Feb-2000
C: Accession: B71541
R: Stephens, R.S.; Kaiman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitche
Science 282, 754-759, 1998
A: Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia t
A: Reference number: A71570; MUID:9900809
A: Accession: B71541
A: Status: preliminary
A: Molecule type: DNA
A: Residues: 1-415 <ARN>
A: Cross-references: GB:AE001296; GB:AE001273; NID:93328630; PIDN:AA067822.1; PID:9332
A: Experimental source: serotype D, strain UW-3/Cx
C: Genetics:
A: Gene: CT230
C: Superfamily: C4-dicarboxylate carrier protein

Query Match 43.8%; Score 46; DB 2; Length 415;
Best Local Similarity 42.1%; Pred. No. 5.3;
Matches 8; Conservative 3; Mismatches 8; Indels 0; Gaps 0;
QY 2 CVASVSGKFSKQTQTFQGC 20
||| | : ||| | : |
Db 392 CVMVSVINKKRFEDLPFC 410

RESULT 6
B25193
C-reactive protein chain 3.3 - Atlantic horseshoe crab
C/Species: Limulus polyphemus (Atlantic horseshoe crab)
C/Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 18-Jun-1993
C/Accession: B25193
R:Nguyen, N.Y.; Suzuki, A.; Boykins, R.A.; Liu, T.Y.
J. Biol. Chem. 261, 10456-10465, 1986
A/Title: The amino acid sequence of Limulus C-reactive protein. Evidence of polymorphism
A/Reference number: A25193; MID:86278106
A/Accession: B25193
A/Molecule type: DNA
A/Residues: 1-218 <NGU>
A/Cross-references: GB:M14024
C/Superfamily: C-reactive protein

Query Match 41.0%; Score 43; DB 2; Length 218;
Best Local Similarity 57.1%; Pred. No. 9.2;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
QY 6 SVGSKFSKQTQTFQGC 19
||| | | : : |
Db 147 SVGKFPDQSLG 160

RESULT 7
C25193
C-reactive protein chain 1.1 - Atlantic horseshoe crab
C/Species: Limulus polyphemus (Atlantic horseshoe crab)
C/Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 18-Jun-1993
C/Accession: C25193
R:Nguyen, N.Y.; Suzuki, A.; Boykins, R.A.; Liu, T.Y.
J. Biol. Chem. 261, 10456-10465, 1986
A/Title: The amino acid sequence of Limulus C-reactive protein. Evidence of polymorphism
A/Reference number: A25193; MID:86278106
A/Accession: C25193
A/Molecule type: DNA
A/Residues: 1-218 <NGU>
A/Cross-references: GB:M14024
C/Superfamily: C-reactive protein

Query Match 41.0%; Score 43; DB 2; Length 218;
Best Local Similarity 57.1%; Pred. No. 9.2;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
QY 6 SVGSKFSKQTQTFQGC 19
||| | | : : |
Db 147 SVGKFPDQSLG 160

RESULT 8
C25192
C-reactive protein chain 1.1 precursor - Atlantic horseshoe crab
C/Species: Limulus polyphemus (Atlantic horseshoe crab)
C/Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 20-Aug-1999
C/Accession: C25192
R:Nguyen, N.Y.; Suzuki, A.; Cheng, S.M.; Zon, G.; Liu, T.
J. Biol. Chem. 261, 10450-10455, 1986
A/Title: Isolation and characterization of Limulus C-reactive protein genes.
A/Reference number: A92551; MID:86278105

A/Accession: C25192
A/Molecule type: DNA
A/Residues: 1-242 <NGU>
A/Cross-references: GB:M14026; MID:g156635; PIDN:AAA28270.1; PID:g156636
C/Genetics:
A/Start codon: ATG
C/Superfamily: C-reactive protein

Query Match 41.0%; Score 43; DB 2; Length 242;
Best Local Similarity 57.1%; Pred. No. 10;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
QY 6 SVGSKFSKQTQTFQGC 19
||| | | : : |
Db 171 SVGKFPDQSLG 184

RESULT 9
B25192
C-reactive protein chain 3.3 precursor - Atlantic horseshoe crab
C/Species: Limulus polyphemus (Atlantic horseshoe crab)
C/Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 20-Aug-1999
C/Accession: B25192
R:Nguyen, N.Y.; Suzuki, A.; Cheng, S.M.; Zon, G.; Liu, T.
J. Biol. Chem. 261, 10450-10455, 1986
A/Title: Isolation and characterization of Limulus C-reactive protein genes.
A/Reference number: A92551; MID:86278105
A/Accession: B25192
A/Molecule type: DNA
A/Residues: 1-242 <NGU>
A/Cross-references: GB:M14025; MID:g156633; PIDN:AAA28269.1; PID:g156634
C/Genetics:
A/Start codon: ATG
C/Superfamily: C-reactive protein

Query Match 41.0%; Score 43; DB 2; Length 242;
Best Local Similarity 57.1%; Pred. No. 10;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
QY 6 SVGSKFSKQTQTFQGC 19
||| | | : : |
Db 171 SVGKFPDQSLG 184

RESULT 10
S60924
hypothetical protein YPL066w - yeast (Saccharomyces cerevisiae)
N/Alternate names: hypothetical protein LPE4w
C/Species: Saccharomyces cerevisiae
C/Date: 15-Feb-1996 #sequence_revision 01-Mar-1996 #text_change 05-Nov-1999
C/Accession: S60924
R:Winnett, E.; Ahmed, A.; Bussey, H.; Fortin, N.; Friesen, J.D.; Hall, J.; Storms, R.
submitted to the EMBL Data Library, October 1995
A/Reference number: S60921
A/Accession: S60924
A/Molecule type: DNA
A/Residues: 1-479 <MIN>
A/Cross-references: EMBL:U39205; MID:g1079672; PID:g1079676; GSPDB:GN00016; MIPS:YPL0
C/Genetics:
A/Gene: MIPS:YPL066w
A/Map position: 16L

Query Match 41.0%; Score 43; DB 2; Length 479;
Best Local Similarity 72.7%; Pred. No. 20;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 10 KFSKQTQFQGC 20
||| | | | | |
Db 139 KFGKTFQFLDC 149

A:Experimental source: strain ad7-50h
R:Schaefer, B.; Merlos-Lange, A.M.; Anderl, C.; Welser, F.; Zimmer, M.; Wolf, K.
Mol. Gen. Genet. 225, 158-167, 1991
A:Title: The mitochondrial genome of fission yeast: inability of all introns to splice
A:Reference number: S13339; MUID:91155928
A:Accession: S13339
A>Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 132-152, 'L', 154-177, 'L', 179-186, 'L', 188-206, 'R', 208-262, 'I', 264-271, 'L', 273-
7, 'I', 409-421, 'LL', 424-429, 'L', 431-438, 'I', 440-448, 'T', 450-462, 'L', 464-494, 'L', 496-519
A:Experimental source: mutant strain ana(gamma)-14
C:Genetics:
A:Gene: cox11
A:Genome: mitochondrion
A:Genetic code: SGC2
C:Superfamily: COI intron 9 protein; COI intron 9 protein homology
C:Keywords: mitochondrion
F:1-135/Region: cox1 exon 1 encoded
F:136-519/Region: cox1 intron encoded

Query Match 39.0%; Score 41; DB 2; Length 519;
Best Local Similarity 55.6%; Pred. No. 48;
Matches 10; Conservative 1; Mismatches 7; Indels 0; Gaps 0;
QY 2 CVASSVGSKSKTKTFQF 19
1 :|| |||| ||
DB 231 CFSSSPSKSFQTQWLVG 248

Search completed: December 19, 2001, 16:22:39
Job time: 459 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: December 19, 2001, 16:26:15 ; Search time 48.45 Seconds

(without alignments)
15.135 Million cell updates/sec

Title: US-09-202-104A-6

Perfect score: 105

Sequence: 1 MCVASSVGSFKSTQTEQGC 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 3664827 residues

100059

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	ID	Description
1	105	100.0	468	1	IL6A_HUMAN
2	59	56.2	467	1	IL6A_PIG
3	52	49.5	460	1	IL6A_MOUSE
4	50	47.6	462	1	IL6A_RAT
5	44	41.9	77	1	IM08_ARATH
6	43	41.0	242	1	CRP1_LIMPO
7	43	41.0	242	1	CRP3_LIMPO
8	43	41.0	272	1	RPXA_HUMAN
9	43	41.0	479	1	YP66_YEAST
10	42	40.0	1081	1	UL52_HSVB
11	41	39.0	348	1	SELD_HAETN
12	41	39.0	384	1	YMC1_SCHRO
13	41	39.0	601	1	DSBD_NEIMA
14	41	39.0	601	1	DSBD_NEIMA
15	40	38.1	416	1	PXN1_XENLA
16	40	38.1	918	1	IMB2_YEAST
17	40	38.1	2180	1	POLG_EC2H
18	39	37.1	131	1	TYA1_HUMAN
19	39	37.1	223	1	SAMP_HUMAN
20	39	37.1	287	1	BTFA_SYNY3
21	39	37.1	512	1	VNN1_MOUSE
22	39	37.1	678	1	NCPK_SCHRO
23	39	37.1	700	1	TOP1_CAMEJ
24	39	37.1	1076	1	YEM3_YEAST
25	38	36.2	132	1	YK06_YEAST
26	38	36.2	211	1	XYN1_ASPAW
27	38	36.2	211	1	XYN1_ASPNG
28	38	36.2	211	1	XYN1_ASPNG
29	38	36.2	211	1	XYN3_ASPAK
30	38	36.2	264	1	SNAI_MOUSE
31	38	36.2	279	1	PSAI_DROME
32	38	36.2	281	1	YP52_BORBU
33	38	36.2	427	1	APEX_CAVPO

ALIGNMENTS

RESULT	ID	IL6A_HUMAN	STANDARD	PRT	468 AA.
AC	P08887	Q16202			
DT	01-NOV-1988	(rel. 09, Created)			
DT	01-NOV-1988	(rel. 09, Last sequence update)			
DT	20-AUG-2001	(rel. 40, Last annotation update)			
DE	INTERLEUKIN-6 RECEPTOR ALPHA CHAIN PRECURSOR (IL-6R-ALPHA) (IL-6R 1)				
DE	(CD126 ANTIGEN).				
GN	IL6R.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.				
OX	NCBI_TaxID-9606;				
RN	[1]				
RP	SEQUENCE FROM N.A. (LONG ISOFORM).				
RX	MEDLINE-8830547; PubMed-3136346;				
RA	Yamasaki K., Taga T., Hirata Y., Yawata H., Kawanishi Y., Seed B.,				
RA	Taniguchi T., Hirano T., Kishimoto T.;				
RT	"Cloning and expression of the human interleukin-6 (BSF-2/IFN beta 2)				
RT	receptor".				
RL	Science 241:825-828(1988).				
RN	[2]				
RP	SEQUENCE FROM N.A. (LONG ISOFORM).				
RA	Yamasaki K., Taga T., Hirata Y., Yawata H., Kawanishi Y., Seed B.,				
RA	Taniguchi T., Hirano T., Kishimoto T.;				
RT	"Molecular structure of interleukin 6 receptor".				
RL	Proc. Jpn. Acad., B, Phys. Biol. Sci. 64:209-211(1988).				
RN	[3]				
RP	SEQUENCE FROM N.A. (LONG ISOFORM).				
RX	MEDLINE-91336983; PubMed-1872801;				
RA	Schoolnik H., Stoyan T., Lenz D., Schmitz H., Hirano T.,				
RA	Kishimoto T., Heinrich P.C., Rose-John S.;				
RT	"Structural and functional studies on the human hepatic interleukin-6				
RT	receptor. Molecular cloning and overexpression in Hep2 cells.";				
RL	Biochem. J. 277:659-664(1991).				
RN	[4]				
RP	SEQUENCE OF 313-365 FROM N.A. (SHORT ISOFORM).				
RX	MEDLINE-9433499; PubMed-8056053;				
RA	Horiuchi S., Koyanagi Y., Zhou Y., Miyamoto H., Tanaka Y., Waki M.,				
RA	Matsumoto A., Yamamoto M., Yamamoto N.;				
RT	"Soluble interleukin-6 receptors released from T cell or				
RT	granulocyte/macrophage cell lines and human peripheral blood				
RT	mononuclear cells are generated through an alternative splicing				
RT	mechanism".				
RL	Eur. J. Immunol. 24:1945-1948(1994).				
RN	[5]				
RP	PARTIAL SEQUENCE, CARBOHYDRATE-LINKAGE SITES, AND DISULFIDE BONDS.				
RX	MEDLINE-99167486; PubMed-10066782;				
RA	Cole A.R., Hall N.E., Treutlein H.R., Eddes J.S., Reid G.E.,				
RA	Moritz R.L., Simpson R.J.;				
RT	"Disulfide bond structure and N-glycosylation sites of the				
RT	extracellular domain of the human Interleukin-6 receptor.";				
RL	J. Biol. Chem. 274:7207-7215(1999).				
RN	[6]				
RP	MUTAGENESIS.				

34 38 36.2 427 1 IRK2_CANFA Q9my9 canis fam1
35 38 36.2 427 1 IRK2_CAVPO P52185 cavia porce
36 38 36.2 427 1 IRK2_CHICK P52186 gallus gall
37 38 36.2 427 1 IRK2_HUMAN P48049 homo sapien
38 38 36.2 427 1 IRK2_RABIT P49656 oryctolagus
39 38 36.2 427 1 IRK2_RAT P35561 mus musculu
40 38 36.2 428 1 IRK2_MOUSE P47972 homo sapien
41 38 36.2 430 1 ENOA_BOVIN P49x14 bos taurus
42 38 36.2 433 1 PAC1_PSESV P15557 pseudomonas
43 38 36.2 557 1 PAC1_PSESV Q05053 pseudomonas
44 38 36.2 557 1 PAC1_PSESV Q9p117 chlamydia m
45 37 35.2 108 1 RU31_CHLMU

RX MEDLINE-9323711; PubMed-8467812;
 RA Yawata H., Yasukawa K., Natsuka S., Murakami M., Yamasaki K., Hibi M.,
 RA Taga T., Kishimoto T.;
 RT Structure-function analysis of human IL-6 receptor: dissociation of
 RT amino acid residues required for IL-6-binding and for IL-6 signal
 RT transduction through gp130.;
 RL EMBO J. 12:1705-1712(1993).
 CC -1- FUNCTION: PART OF THE RECEPTOR FOR INTERLEUKIN 6. BINDS TO IL-6
 CC WITH LOW AFFINITY, BUT DOES NOT TRANSDUCE A SIGNAL. SIGNAL
 CC ACTIVATION NECESSITATE AN ASSOCIATION WITH IL6ST. ACTIVATION MAY
 CC LEAD TO THE REGULATION OF THE IMMUNE RESPONSE. ACUTE-PHASE
 CC REACTIONS AND HEMATOPOIESIS.
 CC -1- FUNCTION: LOW CONCENTRATION OF A SOLUBLE FORM OF INTERLEUKIN-6
 CC RECEPTOR ACTS AS AN AGONIST OF IL-6 ACTIVITY.
 CC -1- SUBUNIT: HEXAMER OF 2 IL6, 2 IL6R-ALPHA AND 2 IL6ST.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (LONG FORM) AND
 CC SECRETED (SHORT FORM).
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A
 CC SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: THE SHORT FORM IS EXPRESSED IN PERIPHERAL
 CC BLOOD MONONUCLEAR CELLS AND WEAKLY FOUND IN URINE AND SERUM.
 CC -1- DOMAIN: THE TWO FIBROBLAST TYPE III-LIKE DOMAINS CONTAINED IN THE
 CC N-TERMINAL PART FORM TOGETHER A CYTOKINE-BINDING DOMAIN.
 CC -1- PTM: A SHORT SOLUBLE FORM MAY ALSO BE RELEASED FROM THE MEMBRANE
 CC BY PROTEOLYSIS.
 CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 FIBROBLAST TYPE III-LIKE DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 CC -1- DATABASE: NAME-PROX; NOTE-CD guide CD126 entry;
 CC WWW-<http://www.ncbi.nlm.nih.gov/prov/cd/cd126.htm>.
 CC -----
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 CC -----
 DR EMBL: X12830; CAA31312.1; -;
 DR EMBL: X58298; CAA41231.1; -;
 DR EMBL: S72848; AAC60635.1; -;
 DR PIR: A41242; A41242.
 DR PIR: J00080; J00080.
 DR PIR: S14621; S14621.
 DR PIR: S17468; S17468.
 DR MIM: 147880; -;
 DR InterPro: IPR002996; CRIA.
 DR InterPro: IPR001777; FN_III.
 DR InterPro: IPR003530; Hematopo_receptor_L_F3.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003598; Ig_C2.
 DR Pfam: PF00041; fn3; 1.
 DR Pfam: PF00047; Ig; 1.
 DR SMART: SM00060; FN3; 1.
 DR SMART: SM00408; IGC2; 1.
 DR PROSITE: PS01354; HEMATOPO_REC_L_F3; 1.
 KW Receptor; Transmembrane; Glycoprotein; Immunoglobulin domain; Repeat;
 KW Alternative splicing; Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 468 INTERLEUKIN-6 RECEPTOR ALPHA CHAIN.
 FT DOMAIN 20 365 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 366 386 POTENTIAL.
 FT DOMAIN 387 468 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 40 103 IG-LIKE C2-TYPE DOMAIN.
 FT DISULFID 25 193
 FT DISULFID 47 96
 FT DISULFID 121 132
 FT DISULFID 165 176
 FT CARBOHYD 55 55
 FT CARBOHYD 93 93 N-LINKED (GLCNAC. . .).
 FT CARBOHYD 221 221 N-LINKED (GLCNAC. . .).
 FT VASPLP 356 365 VODSSVPLP -> GSRKRGCGL (IN SHORT

FT VASPLP 366 468 ISOFORM).
 FT MUTAGEN 121 121 MISSING (IN SHORT ISOFORM).
 FT MUTAGEN 122 122 C->S: COMPLETE LOSS OF LIGAND-BINDING.
 FT MUTAGEN 132 132 F->A: NO CHANGE OF LIGAND-BINDING AND IL6
 FT MUTAGEN 133 133 SIGNALING.
 FT MUTAGEN 134 134 C->A: COMPLETE LOSS OF LIGAND-BINDING.
 FT MUTAGEN 140 140 W->L: COMPLETE LOSS OF LIGAND-BINDING.
 FT MUTAGEN 143 143 P->S: NO CHANGE OF LIGAND-BINDING AND IL6
 FT MUTAGEN 153 153 SIGNALING.
 FT MUTAGEN 153 153 F->L: NO CHANGE OF LIGAND-BINDING AND IL6
 FT MUTAGEN 165 165 SIGNALING.
 FT MUTAGEN 174 174 C->E: COMPLETE LOSS OF LIGAND-BINDING.
 FT MUTAGEN 176 176 F->L: NO CHANGE OF LIGAND-BINDING AND IL6
 FT MUTAGEN 184 184 SIGNALING.
 FT MUTAGEN 190 190 C->A: COMPLETE LOSS OF LIGAND-BINDING.
 FT MUTAGEN 193 193 D->T: 30% DECREASE OF LIGAND-BINDING AND
 FT MUTAGEN 211 211 IL6 SIGNALING.
 FT MUTAGEN 217 217 V->S: 80% DECREASE OF LIGAND-BINDING AND
 FT MUTAGEN 232 232 NO IL6 SIGNALING.
 FT MUTAGEN 233 233 C->D: COMPLETE LOSS OF LIGAND-BINDING.
 FT MUTAGEN 254 254 C->A: NO CHANGE OF LIGAND-BINDING AND IL6
 FT MUTAGEN 277 277 SIGNALING.
 FT MUTAGEN 278 278 D->S: 30% DECREASE OF LIGAND-BINDING AND
 FT MUTAGEN 279 279 IL6 SIGNALING.
 FT MUTAGEN 280 280 W->Q: 30% DECREASE OF LIGAND-BINDING AND
 FT MUTAGEN 281 281 INCREASE OF IL6 SIGNALING.
 FT MUTAGEN 285 285 E->A: 50% DECREASE OF LIGAND-BINDING AND
 FT MUTAGEN 291 291 IL6 SIGNALING.
 FT MUTAGEN 293 293 C->D: 30% INCREASE OF LIGAND-BINDING AND
 FT MUTAGEN 293 293 100% INCREASE IN IL6 SIGNALING.
 FT MUTAGEN 293 293 V->N: 50% DECREASE OF LIGAND-BINDING AND
 FT MUTAGEN 293 293 50% INCREASE IN IL6 SIGNALING.
 FT MUTAGEN 293 293 I->D: COMPLETE LOSS OF LIGAND-BINDING.
 FT MUTAGEN 293 293 H->I: NO CHANGE OF LIGAND-BINDING AND NO
 FT MUTAGEN 281 281 IL6 SIGNALING.
 FT MUTAGEN 281 281 D->S: 70% DECREASE OF LIGAND-BINDING AND
 FT MUTAGEN 285 285 NO IL6 SIGNALING.
 FT MUTAGEN 285 285 G->D: 80% DECREASE OF LIGAND-BINDING AND
 FT MUTAGEN 291 291 NO IL6 SIGNALING.
 FT MUTAGEN 293 293 O->K: COMPLETE LOSS OF LIGAND-BINDING.
 FT MUTAGEN 293 293 R->S: COMPLETE LOSS OF LIGAND-BINDING.
 FT SEQUENCE 468 AA; 51547 MW; 62AA239FA14F1BBB CRC64;
 QY 1 MCVAASVSGSKFSKTFQFGC 20
 DB 192 MCVAASVSGSKFSKTFQFGC 211
 Query Match 100.0%; Score 105; DB 1; Length 468;
 Best Local Similarity 100.0%; Pred. No. 9,2e-11;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 RESULT 2
 IL6A_PIG STANDARD; PRI: 467 AA.
 ID IL6A_PIG
 AC O18796;
 DT 20-AUG-2001 (Rel. 40, Created)
 DT 20-AUG-2001 (Rel. 40, Last sequence update)
 DE 20-AUG-2001 (Rel. 40, Last annotation update)
 DE INTERLEUKIN-6 RECEPTOR ALPHA CHAIN PRECURSOR (IL-6R-ALPHA) (IL-6R 1).
 GN IL6R.
 OS Sus scrofa (Pig).
 CC Eukaryota; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
 OX NCBI_TaxID=9623;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Morris K.R., Strom A.D.G.;
 RT "Cloning and expression of biologically active porcine IL-6 receptor
 RT alpha chain".
 RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.

[2]
 RN SEQUENCE OF 123-186 FROM N.A.
 RP TISSUE=Liver;
 RC Klotz J., Matterl R.L.;
 RT "Partial cDNA sequence of porcine interleukin 6 receptor.";
 RL Submitted (Jul-1997) to the EMBL/Genbank/DBJ databases.
 CC -1 FUNCTION: PART OF THE RECEPTOR FOR INTERLEUKIN 6. BINDS TO IL-6
 WITH LOW AFFINITY, BUT DOES NOT TRANSDUCE A SIGNAL. SIGNAL
 ACTIVATION NECESSITATE AN ASSOCIATION WITH IL6ST. ACTIVATION MAY
 LEAD TO THE REGULATION OF THE IMMUNE RESPONSE, ACUTE-PHASE
 REACTIONS AND HEMATOPOIESIS.
 CC -1 SUBUNIT: HEXAMER OF 2 IL6, 2 IL6R-ALPHA AND 2 IL6ST (BY
 SIMILARITY).
 CC -1 TISSUE SPECIFICITY: EXPRESSED IN LIVER.
 CC -1 DOMAIN: THE TWO FIBRONECTIN TYPE III-LIKE DOMAINS CONTAINED IN THE
 C-TERMINAL PART FORM TOGETHER A CYTOKINE-BINDING DOMAIN.
 CC -1 SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
 CC -1 SIMILARITY: CONTAINS 3 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC -1 SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.

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 CC EMBL; AF147881; AAF73109.1; -;
 DR EMBL; AF015116; AAB70916.1; -;
 DR HSSP; P16471; 1BP3.
 DR InterPro; IPR002996; CRIA.
 DR InterPro; IPR001777; FN_III.
 DR InterPro; IPR003530; Hematopo_rcptor_L_F3.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003598; Ig_C2.
 DR Pfam; PF00041; fn3; 1.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00060; FN3; 1.
 DR SMART; SM00408; IGC2; 1.
 DR PROSITE; PS00340; RECEPTOR_CYTOKINES_2; 1.
 DR KMW Receptor; Transmembrane; Glycoprotein; Immunoglobulin domain; Repeat;
 KW Signal.
 FT CHAIN. 1 19 BY SIMILARITY.
 FT DOMAIN 20 467 INTERLEUKIN-6 RECEPTOR ALPHA CHAIN.
 FT TRANSMEM 366 386 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 387 467 POTENTIAL.
 FT DOMAIN 40 103 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 47 193 IG-LIKE C2-TYPE DOMAIN.
 FT DISULFID 121 132 BY SIMILARITY.
 FT DISULFID 165 176 BY SIMILARITY.
 FT CARBOHYD 55 55 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 93 93 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 221 221 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 350 350 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 467 AA: 51066 MW: 42808848210502 CRC64;

Query Match 56.2%; Score 59; DB 1; Length 467;
 Best Local Similarity 57.9%; Pred. No. 0.011;

Matches 11; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

OY 1 MCVASSVGSKSKRTQTFQG 19
 :||:|:|:|:|:|:|:|:|
 DB 192 LCVANSAGSSSTPTQTFEG 210

RESULT 3
 IL6A_MOUSE STANDARD; PRT; 460 AA.
 ID IL6A_MOUSE

AC P22272;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE INTERLEUKIN-6 RECEPTOR ALPHA CHAIN PRECURSOR (IL-6R-ALPHA) (IL-6R 1).
 GN IL6RA OR IL6R.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/C; TISSUE=Spleen;
 RX MEDLINE=90278354; PubMed=2112585;
 RA Sugita T., Totsuka T., Saio M., Yamasaki K., Taga T., Hirano T.,
 RA Kishimoto T.;
 RT "Functional murine interleukin 6 receptor with the intracellular A
 particle gene product at its cytoplasmic domain. Its possible role in
 RT plasmacytogenesis";
 RL J. Exp. Med. 171:2001-2009(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C3H; TISSUE=Liver;
 RA Fiorillo M.T., Cliberto G., Dente L.;
 RL Submitted (Jul-1990) to the EMBL/Genbank/DBJ databases.
 CC -1 FUNCTION: PART OF THE RECEPTOR FOR INTERLEUKIN 6. BINDS TO IL-6
 WITH LOW AFFINITY, BUT DOES NOT TRANSDUCE A SIGNAL. SIGNAL
 ACTIVATION NECESSITATE AN ASSOCIATION WITH IL6ST. ACTIVATION MAY
 LEAD TO THE REGULATION OF THE IMMUNE RESPONSE, ACUTE-PHASE
 REACTIONS AND HEMATOPOIESIS.
 CC -1 SUBUNIT: HEXAMER OF 2 IL6, 2 IL6R-ALPHA AND 2 IL6ST (BY
 SIMILARITY).
 CC -1 SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1 DOMAIN: THE TWO FIBRONECTIN TYPE III-LIKE DOMAINS CONTAINED IN THE
 C-TERMINAL PART FORM TOGETHER A CYTOKINE-BINDING DOMAIN.
 CC -1 SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
 CC -1 SIMILARITY: CONTAINS 3 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC -1 SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.

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 CC EMBL; X51975; CAA36237.1; -;
 DR EMBL; X53802; CAA37810.1; -;
 DR PIR; J01044; J01044.
 DR PIR; J01045; J01045.
 DR PIR; S14543; S14543.
 DR HSSP; P16471; 1BP3.
 DR MGD; MGI:105304; IL6ra.
 DR InterPro; IPR002996; CRIA.
 DR InterPro; IPR001777; FN_III.
 DR InterPro; IPR003530; Hematopo_rcptor_L_F3.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003598; Ig_C2.
 DR Pfam; PF00041; fn3; 1.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00060; FN3; 1.
 DR SMART; SM00408; IGC2; 1.
 DR PROSITE; PS01354; HEMATOPO_REC_L_F3; 1.
 DR KMW Receptor; Transmembrane; Glycoprotein; Immunoglobulin domain; Repeat;
 KW Signal.
 FT CHAIN. 1 19
 FT DOMAIN 20 460 INTERLEUKIN-6 RECEPTOR ALPHA CHAIN.
 FT TRANSMEM 365 385 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 386 460 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 40 99 IG-LIKE C2-TYPE DOMAIN.
 FT DISULFID 25 190 BY SIMILARITY.

FT	DISULFID	47	92	BY SIMILARITY.
FT	DISULFID	117	128	BY SIMILARITY.
FT	DISULFID	162	173	BY SIMILARITY.
FT	CARBOHYD	32	32	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	55	55	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	150	150	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CONFLICT	374	374	A -> R (IN REF. 2).
SO	SEQUENCE	460 AA;	50454 MW;	P85C5906008525C4 CMC64;

Query Match	Best Local Similarity	49.5%;	Score 52;	DB 1;	Length 460;	
Matches 10;	Conservative	58.8%;	Pred. No. 0.18;	Mismatches 3;	Indels 4;	Gaps 0;
QY	1 MCVASSVGSKFSKTQTF	17				
Db	189 LCVANVSQSKSSHNEAF	205				

RESULT	4		
IL6A_RAT	STANDARD;	PRT;	462 AA.
AC	P22273;		
DT	01-AUG-1991 (Rel. 19, Created)		
DT	01-FEB-1995 (Rel. 31, Last sequence update)		
DT	20-AUG-2001 (Rel. 40, Last annotation update)		
DE	INTERLEUKIN-6 RECEPTOR ALPHA CHAIN PRECURSOR (IL-6R-ALPHA) (IL-6R 1).		
GN	IL6R.		
OS	Rattus norvegicus (Rat).		
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.		
OX	NCBI_TaxID=10116;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=FISCHER 344; TISSUE=Liver;		
RX	MEDLINE=91060602; PubMed=2174054;		
RA	Baumann M., Baumann H., Fey G.H.:		
RT	"Molecular cloning, characterization and functional expression of the		
RT	rat liver interleukin 6 receptor.";		
RL	J. Biol. Chem. 265:19853-19862(1990).		
RN	[2]		
RP	IDENTIFICATION OF PROBABLE FRAMESHIFT IN 227-261.		
RA	Gibson T.;		
RL	Unpublished observations (FEB-1995).		
CC	-1- FUNCTION: PART OF THE RECEPTOR FOR INTERLEUKIN 6. BINDS TO IL-6		
CC	WITH LOW AFFINITY, BUT DOES NOT TRANSDUCE A SIGNAL. SIGNAL		
CC	ACTIVATION NECESSITATE AN ASSOCIATION WITH IL6ST. ACTIVATION MAY		
CC	LEAD TO THE REGULATION OF THE IMMUNE RESPONSE, ACUTE-PHASE		
CC	REACTIONS AND HEMATOPOIESIS.		
CC	-1- SUBUNIT: HEXAMER OF 2 IL6, 2 IL6R-ALPHA AND 2 IL6ST (BY		
CC	SIMILARITY).		
CC	-1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.		
CC	-1- DOMAIN: THE TWO FIBROECTIN TYPE I/II-LIKE DOMAINS CONTAINED IN THE		
CC	C-TERMINAL PART FORM TOGETHER A CYPOKINE-BINDING DOMAIN.		
CC	-1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.		
CC	-1- SIMILARITY: CONTAINS 3 FIBROECTIN TYPE I/II-LIKE DOMAINS.		
CC	-1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.		
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CC	modified and this statement is not removed. Usage by and for commercial		
CC	entities requires a license agreement (See http://www.isb-sib.ch/annotation/		
CC	or send an email to license@isb-sib.ch).		
CC	-----		
DR	EMBL; M56587; AAA41431.1; -.		
DR	PIR; A37986; A37986.		
DR	HSSP; P16471; 1BP3.		
DR	InterPro; IPR002996; CRA.		
DR	InterPro; IPR001377; FN_III.		
DR	InterPro; IPR003530; Hematopo_rceptor_L_F3.		
DR	InterPro; IPR003006; I9_MHC.		

Query Match	41.9%	Score 44	DB 1	Length 77
Query Match	41.9%	Score 44	DB 1	Length 77

Best Local Similarity 46.7%; Pred. No. 0.7;
Matches 7; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

OY 2 CVAASVSGSKFKSTQQT 16
I: I: ||||| : : :
Db 39 CITSAPGSKFKSSSES 53

RESULT 6

CRP3_LIMPO STANDARD; PRT; 242 AA.
ID CRP3_LIMPO
AC P06205;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE C-REACTIVE PROTEIN 1.1 PRECURSOR.
OS Limulus polyphemus (Atlantic horseshoe crab).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Merostomata; Xiphosura;
OC Limulidae; Limulus.
OX NCBI_Taxid=6850;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86278105; PubMed=3015932;
RA Nguyen N.Y., Suzuki A., Cheng S.-M., Zon G., Liu T.-Y.;
RT *Isolation and characterization of Limulus C-reactive protein genes.";
RL J. Biol. Chem. 261:10450-10455(1986).
RN [2]
RP SEQUENCE OF 25-242, DISULFIDE BONDS, AND CARBOHYDRATE-LINKAGE SITE.
RX MEDLINE=86278106; PubMed=2426265;
RA Nguyen N.Y., Suzuki A., Boykins R.A., Liu T.-Y.;
RT *The amino acid sequence of Limulus C-reactive protein. Evidence of
RT polymorphism.";
RL J. Biol. Chem. 261:10456-10465(1986).
RN [3]
RP 3D-STRUCTURE MODELING.
RX MEDLINE=95187705; PubMed=7881902;
RA Sriivasan N., White H.E., Emsley J., Wood S.P., Pepys M.B.,
RA Blundell T.L.;
RT *Comparative analyses of pentraxins: implications for proteome
RT assembly and ligand binding.";
RL Structure 2:1017-1027(1994).
CC -1- FUNCTION: MIGHT SERVE THE ROLE OF IMMUNOGLOBULINS.
CC -1- SUBUNIT: HOMOPENTAMER. PENTAXIN (OR PENTAXIN) HAVE A DISCOID
CC ARRANGEMENT OF 5 NONCOVALENTLY BOUND SUBUNITS.
CC -1- SIMILARITY: BELONGS TO THE PENTAXIN FAMILY.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: M14026; AAA8270.1; -
DR PIR: C25192; C25192.
DR PIR: C25193; C25193.
DR PDB: 1LTM; 15-OCT-95.
DR InterPro: IPR001759; Pentaxin.
DR Pfam: PF00354; pentaxin.1.
DR PRINTS: PRO0895; PENTAXIN.
DR SMART: SM00159; PTX; 1.
DR PROSITE: PS00289; PENTAXIN; 1.
KW Pentaxin; Calcium; Glycoprotein; signal; 3D-structure.
FT CHAIN 1 24
FT SIGNAL 1 24
FT DOMAIN 25 242
FT DISULFID 62 125
FT DISULFID 112 144
FT DISULFID 207 241
FT CARBOHYD 147 147
FT DOMAIN 52 67
FT DOMAIN 59 60
N-LINKED (GLCNAC. . .).
BINDING OF PHOSPHORYLCHOLINE (POTENTIAL).
INTERACTION WITH PHOSPHATE GROUP OF

FT FT BINDING 63 63 PHOSPHORYLCHOLINE (POTENTIAL).
FT FT QUATERNARY AMONIUM GROUP OF
FT FT PHOSPHORYLCHOLINE (POTENTIAL).
SQ SIMILAR 139 153 STRONG WITH CA-BINDING EF-HAND SEQUENCE.
SQ SEQUENCE 242 AA; 26773 MW; A572B982FA8FDB92 CRC64;

Query Match 41.0%; Score 43; DB 1; Length 242;

Best Local Similarity 57.1%; Pred. No. 3.4;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 6 SVGSKFKSTQQTQFG 19
I: I: ||||| : : :
Db 171 SVGSKFKSTQQTQFG 184

RESULT 7

CRP3_LIMPO STANDARD; PRT; 242 AA.
ID CRP3_LIMPO
AC P06207;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE C-REACTIVE PROTEIN 3.3 PRECURSOR.
OS Limulus polyphemus (Atlantic horseshoe crab).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Merostomata; Xiphosura;
OC Limulidae; Limulus.
OX NCBI_Taxid=6850;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86278105; PubMed=3015932;
RA Nguyen N.Y., Suzuki A., Cheng S.-M., Zon G., Liu T.-Y.;
RT *Isolation and characterization of Limulus C-reactive protein genes.";
RL J. Biol. Chem. 261:10450-10455(1986).
RN [2]
RP SEQUENCE OF 25-242, DISULFIDE BONDS, AND CARBOHYDRATE-LINKAGE SITE.
RX MEDLINE=86278106; PubMed=2426265;
RA Nguyen N.Y., Suzuki A., Boykins R.A., Liu T.-Y.;
RT *The amino acid sequence of Limulus C-reactive protein. Evidence of
RT polymorphism.";
RL J. Biol. Chem. 261:10456-10465(1986).
CC -1- FUNCTION: MIGHT SERVE THE ROLE OF IMMUNOGLOBULINS.
CC -1- SUBUNIT: HOMOPENTAMER. PENTAXIN (OR PENTAXIN) HAVE A DISCOID
CC ARRANGEMENT OF 5 NONCOVALENTLY BOUND SUBUNITS.
CC -1- SIMILARITY: BELONGS TO THE PENTAXIN FAMILY.
CC -----
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CC -----
DR EMBL: M14025; AAA8269.1; -
DR PIR: B25192; B25192.
DR PIR: B25193; B25193.
DR HSSP: P06205; 1LTM.
DR InterPro: IPR001759; Pentaxin.
DR Pfam: PF00354; pentaxin.1.
DR PRINTS: PRO0895; PENTAXIN.
DR SMART: SM00159; PTX; 1.
DR PROSITE: PS00289; PENTAXIN; 1.
KW Pentaxin; Calcium; Glycoprotein; signal.
FT CHAIN 1 24
FT SIGNAL 1 24
FT DOMAIN 25 242
FT DISULFID 62 125
FT DISULFID 112 144
FT DISULFID 207 241
FT CARBOHYD 147 147
FT DOMAIN 52 67
FT DOMAIN 59 60
N-LINKED (GLCNAC. . .).
BINDING OF PHOSPHORYLCHOLINE (POTENTIAL).
INTERACTION WITH PHOSPHATE GROUP OF

FT BINDING 63 63 PHOSPHORYLCHOLINE (POTENTIAL).
 FT SIMILAR 139 153 QUATERNARY AMMONIUM GROUP OF
 FT SEQUENCE 242 AA; 26720 MM; C45E47E5F4B8C869 CRC64;
 SO
 Query Match 41.0%; Score 43; DB 1; Length 242;
 Best Local Similarity 57.1%; Pred. No. 3.4;
 Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 Oy 6 SVSGSKSTOTFOG 19
 Db 171 SVGGKFDATQSLGG 184
 RESULT 8
 ID RFXA_HUMAN STANDARD; PRT: 272 AA.
 AC 000287;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE REGULATORY FACTOR X-ASSOCIATED PROTEIN (RFX DNA-BINDING COMPLEX 36 KDA
 SUBUNIT) (RFX-ASSOCIATED PROTEIN).
 GN RFXAP.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RA MEDLINE-97224131; PubMed-9118943;
 RA Durand B., Sperisen P., Barras E., Zuferey M., Mach B.,
 RA Reith W.;
 RT "RFXAP, a novel subunit of the RFX DNA binding complex is mutated in
 RT MHC class II deficiency";
 RL EMO J. 16:1045-1055(1997).
 RN [2]
 RP PARTIAL SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE-Lymphoblast;
 RX MEDLINE-99170284; PubMed-10072068;
 RX Negarajan U.M., Louis-Pence P., Desandro A., Nilsen R., Bushey A.,
 RA Boss J.M.;
 RA "RFX-B is the gene responsible for the most common cause of the bare
 RA lymphocyte syndrome, an MHC class II immunodeficiency.";
 RL Immunity 10:153-162(1999).
 RN [3]
 RP ERRATUM.
 RA Negarajan U.M., Louis-Pence P., Desandro A., Nilsen R., Bushey A.,
 RA Boss J.M.;
 RL Immunity 10:399-399(1999).
 CC -1- FUNCTION: PART OF THE RFX COMPLEX THAT BINDS TO THE X-BOX OF MHC
 CC II PROMOTERS.
 CC -1- SUBUNIT: RFX CONSISTS OF AT LEAST 3 DIFFERENT SUBUNITS: RFXAP,
 CC COMPLEMENTATION GROUP. RFX FORMS COOPERATIVE DNA BINDING COMPLEXES
 CC WITH X2BP AND CBF/NF-Y. RFX ASSOCIATES WITH C/ITTA TO FORM AN
 CC ACTIVE TRANSCRIPTIONAL COMPLEX.
 CC -1- SUBCELLULAR LOCATION: NUCLEAR.
 CC -1- TISSUE SPECIFICITY: UBIQUITOUS.
 CC -1- PTM: PHOSPHORYLATED.
 CC -1- DISEASE: DEFECTS IN RFXAP ARE A CAUSE OF HEREDITARY MHC CLASS II
 CC DEFICIENCY (ALSO KNOWN AS BARE LYMPHOCYTE SYNDROME (BLS) OR HLA
 CC CLASS II-DEFICIENT COMBINED IMMUNODEFICIENCY); A FORM OF SEVERE
 CC COMBINED IMMUNODEFICIENCY DISEASE (SCID). RFXAP IS LINKED WITH
 CC BLS COMPLEMENTATION GROUP D.
 CC
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 CC
 CC -----
 DR EMBL: Y12812; CA73338.1; -.
 DR MIM: 601861; -.
 DR MIM: 209920; -.
 KW Nuclear protein; DNA-binding; SCID; Phosphorylation.
 FT DOMAIN 38 41 POLY-ALA.
 FT DOMAIN 171 178 POLY-LYS.
 FT DOMAIN 163 178 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
 SO SEQUENCE 272 AA; 28232 MM; A6757E5F03D5F905 CRC64;
 Oy 6 SVSGSKSTOTFOGC 20
 Db 132 SVGGSKSTOTYEGC 146
 Query Match 41.0%; Score 43; DB 1; Length 272;
 Best Local Similarity 53.3%; Pred. No. 3.9;
 Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
 RESULT 9
 ID YP66_YEAST STANDARD; PRT: 479 AA.
 AC Q12194;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE HYPOTHETICAL 54.9 KDA PROTEIN IN VPS28-BTS1 INTERGENIC REGION.
 GN YPL066W OR LPEAW.
 OS Saccharomyces cerevisiae (Baker's yeast).
 CC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 CC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 NX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Winnett E., Ahmed A., Bussey H., Fortin N., Friesen J.D., Hall J.,
 RA Storms R.K., Vo D.H., Wang Y.;
 RL Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.
 CC
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 CC
 CC -----
 DR EMBL: U50630; -; NOT_ANNOTATED_COS.
 DR EMBL: U39205; AAB68299.1; -.
 DR SGD: S0005987; YPL066W.
 KW Hypothetical protein.
 SO SEQUENCE 479 AA; 54893 MM; D6C9FA7AEBACF74 CRC64;
 Oy 10 KFSKSTOTFOGC 20
 Db 139 KFGKSTOTFLDC 149
 Query Match 41.0%; Score 43; DB 1; Length 479;
 Best Local Similarity 72.7%; Pred. No. 6.9;
 Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 RESULT 10
 ID UL52_HSVB STANDARD; PRT: 1081 AA.
 AC P28962;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE DNA HELICASE/PRIMASE COMPLEX PROTEIN (DNA REPLICATION PROTEIN UL52).

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GN 7.
OS Equine herpesvirus type 1 (strain Ab4p) (EHV-1).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Varicelloviruses.
OX NCBI_TaxID=31520;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=92295566; PubMed=1318606;
RA Telford E.A.R., Watson M.S., McBride K., Davison A.J.;
RT "The DNA sequence of equine herpesvirus-1.";
RL Virology 189:304-316(1992).
CC -1- FUNCTION: INVOLVED IN DNA REPLICATION.
CC -1- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL52,
CC EHV-1 7, EBV BSFL1, HSV-1 56, HCMV UL70 AND VZV 6.
CC -----
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CC -----
CC EMBL, M86664; AAB02442.1; -.
CC PIR, H36795; WZBEA6.
CC DNA replication.
CC SEQUENCE 1081 AA; 118962 MW; C76D42F36ADC7BC3 CRC64;
SQ

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Query Match 40.0%; Score 42; DB 1; Length 1081;
Best Local Similarity 29.4%; Pred. No. 24;
Matches 5; Conservative 10; Mismatches 2; Indels 0; Gaps 0;

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OY 1 MCVASSVSGSKESKTQTE 17
DB 423 VCLPASIGSGYADKTY 439

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RESULT 11

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SELD_HAEIN STANDARD; PRT; 348 AA.
ID SELD_HAEIN
AC P43911;
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 40, Last annotation update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE SELDENIUM, WATER DIKINASE (EC 2.7.9.3) (SELENOPHOSPHATE SYNTHETASE)
GN SELD OR HI0200.
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Haemophilus.
OX NCBI_TaxID=727;
RN (1)
RP SEQUENCE FROM N.A.
RX STRAIN=RD / KW20 / ATCC 51907;
RX MEDLINE=95350630; PubMed=7542800;
RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
RA Kervatage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
RA Scott J.D., Shirley R., Liu L.-I., Glodet A., Kelley J.M.,
RA Weisman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
RA Fine L.D., Fritchman J.L., Fuhmann J.L., Geoghegan N.S.M.,
RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA Venter J.C.;
RT "Whole-genome random sequencing and assembly of Haemophilus
RT influenzae Rd.";
RL Science 269:496-512(1995).
CC [2]
CC CONCEPTUAL TRANSLATION.
RP Bairoch A.;
RL Unpublished observations (AUG-1995).
CC -1- FUNCTION: SYNTHESIZES SELENOPHOSPHATE FROM SELENIDE AND ATP

```

```

CC (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: ATP + SELENIDE + H(2)O = AMP + SELENOPHOSPHATE
CC + PHOSPHATE.
CC -1- COFACTOR: REQUIRES MAGNESIUM (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE SELENOPHOSPHATE SYNTHETASE 1 FAMILY.
CC CLASS 1 SUBFAMILY.
CC -1- CAUTION: THIS IS A CONCEPTUAL TRANSLATION; A UGA STOP CODON HAD TO
CC BE SKIPPED IN POSITION 16 TO PRODUCE THIS ORF. WE (REF.2) BELIEVE
CC THAT THIS RESIDUES IS MOST PROBABLY AN ACTIVE-SITE SELENOCYSTEINE.
CC -----
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CC -----
CC EMBL, U32705; AAC21869.1; ALT_FRAME.
CC TIGR, HI0200; -.
CC InterPro, IPR000728; ATRS_related.
CC Pfam, PF00586; ATRS; 1.
CC Transferase; Selenium; Magnesium; ATP-binding; Selenocysteine;
CC Complete proteome.
CC ACT_SITE 16 16 POTENTIAL.
CC SE_CYS 16 16 POTENTIAL.
CC SITE 19 19 IMPORTANT FOR CATALYTIC ACTIVITY (BY
CC SIMILARITY).
CC NP_BIND 231 237 ATP (POTENTIAL).
CC SEQUENCE 348 AA; 36523 MW; A7B1F534C57C264A CRC64;
SQ

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Query Match 39.0%; Score 41; DB 1; Length 348;
Best Local Similarity 53.8%; Pred. No. 11;
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

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OY 1 MCVASSVSGSKESK 13
DB 207 MCOMNISTGSOFSQ 219

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RESULT 12

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YMC1_SCHPO STANDARD; PRT; 384 AA.
ID YMC1_SCHPO
AC P22191;
DT 01-AUG-1991 (Rel. 19, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE HYPOHETICAL COX1 INTRON-1 45.6 KDA PROTEIN (PROBABLE MATURASE).
OS Schizosaccharomyces pombe (Flission yeast).
OG Mitochondrion.
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OX NCBI_TaxID=4896;
RN (1)
RP SEQUENCE FROM N.A.
RX STRAIN=AD7-50;
RA Lang B.F.;
RT Submitted (AUG-1990) to the EMBL/Genbank/DBJ databases.
CC -1- MISCELLANEOUS: THIS PROTEIN IS CODED IN GROUP-1 INTRON 1 OF COX1.
CC -----
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CC -----
CC EMBL, X54421; CAA38285.1; -.
CC InterPro, IPR001982; Intron_endonuc.
CC Pfam, PF00961; Intron_maturase; 2.

```

KW Hypothetical protein; Mitochondrion.
 SQ SEQUENCE 384 AA; 45637 MW; C670AC92C78110D CRC64;

Query Match 39.0%; Score 41; DB 1; Length 384;
 Best Local Similarity 55.6%; Pred. No. 12;
 Matches 10; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 2 CVA5VSGSKFSTQTFQGC 19
 1 : 11 1111 11 1
 Db 96 CFS5SPSKFSTQTFQWVG 113

RESULT 13
 DSD_NEIMA STANDARD; PRT; 601 AA.

AC 09JYL9;
 DT 20-AUG-2001 (Rel. 40, Created)
 DT 20-AUG-2001 (Rel. 40, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE THIO:DISULFIDE INTERCHANGE PROTEIN DSD PRECURSOR.
 GN DSD OR NMA1719.
 OS Neisseria meningitidis (serogroup A).
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
 OX NCBI_TaxID=65699;

[1]
 SEQUENCE FROM N.A.
 RP STRAIN=22491 / SEROGROUP A / SEROTYPE 4A;
 RX MEDLINE=20222556; PubMed=10761919;
 RA Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.,
 RA Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
 RA Davies R.M., Davis P., Devlin K., Felwell T., Hamlin N., Holtroyd S.,
 RA Jajelski K., Leather S., Moule S., Mungall K., Quail M.A.,
 RA Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
 RA Whitehead S., Spratt B.G., Barrell B.G.;
 RT "Complete DNA sequence of a serogroup A strain of Neisseria
 meningitidis 22491".
 RL Nature 404:502-506(2000).

CC -1- FUNCTION: REQUIRED TO FACILITATE THE FORMATION OF CORRECT
 CC DISULFIDE BONDS IN SOME PERIPLASMIC PROTEINS AND FOR THE ASSEMBLY
 CC OF THE PERIPLASMIC C-TYPE CYTOCHROMES. ACTS BY TRANSFERRING
 CC ELECTRONS FROM CYTOPLASMIC THIOREDOXIN TO THE PERIPLASM. THIS
 CC TRANSFER INVOLVES A CASCADE OF DISULFIDE BOND FORMATION AND
 CC REDUCTION STEPS (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE
 CC (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE THIOREDOXIN FAMILY. DSD SUBFAMILY.
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DR EMBL; AL162756; CAB84947.1; ALT_INIT.
 DR InterPro: IPR000063; ThioRed.
 DR InterPro: IPR003834; DsdD_DfpZ.
 DR Pfam; PF02683; DsdD; 1.
 DR Pfam; PF02085; ThioRed; 1.
 DR PROSITE; PS00194; THIOREDOXIN; FALSE_NEG.
 KW Redox-active center; Electron transport; Transmembrane;
 KW Inner membrane; Cytochrome c-type biogenesis; Signal;
 KW Complete proteome.

FT SIGNAL 1 20 POTENTIAL.
 FT CHAIN 21 601 THIO:DISULFIDE INTERCHANGE PROTEIN DSD.
 FT DOMAIN 21 191 PERIPLASMIC (POTENTIAL).
 FT TRANSSEM 192 212 POTENTIAL.
 FT DOMAIN 213 242 CYTOPLASMIC (POTENTIAL).
 FT TRANSSEM 243 263 POTENTIAL.
 FT DOMAIN 264 266 PERIPLASMIC (POTENTIAL).
 FT TRANSSEM 267 287 POTENTIAL.

FT DOMAIN 288 310 CYTOPLASMIC (POTENTIAL).
 FT TRANSSEM 311 331 POTENTIAL.
 FT DOMAIN 332 346 PERIPLASMIC (POTENTIAL).
 FT TRANSSEM 347 367 POTENTIAL.
 FT DOMAIN 368 380 CYTOPLASMIC (POTENTIAL).
 FT TRANSSEM 381 401 POTENTIAL.
 FT DOMAIN 402 406 PERIPLASMIC (POTENTIAL).
 FT TRANSSEM 407 427 POTENTIAL.
 FT DOMAIN 428 438 CYTOPLASMIC (POTENTIAL).
 FT TRANSSEM 439 459 POTENTIAL.
 FT DOMAIN 460 601 PERIPLASMIC (POTENTIAL).
 FT DISULFID 120 126 REDOX-ACTIVE (BY SIMILARITY).
 FT DISULFID 207 328 REDOX-ACTIVE (BY SIMILARITY).
 FT DISULFID 519 522 REDOX-ACTIVE (BY SIMILARITY).
 SQ SEQUENCE 601 AA; 64865 MW; 22FE3062AD5C78E CRC64;

Query Match 39.0%; Score 41; DB 1; Length 601;
 Best Local Similarity 41.2%; Pred. No. 20;
 Matches 7; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 4 ASSVSGSKFSTQTFQGC 20
 1 : 11 1111
 Db 104 AKAVGEPIKLVTFQGC 120

RESULT 14
 DSD_NEIMA STANDARD; PRT; 601 AA.

AC 09JYMO;
 DT 20-AUG-2001 (Rel. 40, Created)
 DT 20-AUG-2001 (Rel. 40, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE THIO:DISULFIDE INTERCHANGE PROTEIN DSD PRECURSOR.
 GN DSD OR NMB1519.
 OS Neisseria meningitidis (serogroup B).
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
 OX NCBI_TaxID=491;

[1]
 SEQUENCE FROM N.A.
 RP STRAIN=MC58 / SEROGROUP B;
 RX MEDLINE=20175755; PubMed=10710307;
 RA Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E.,
 RA Eisen J.A., Ketchum K.A., Hood B.W., Peden J.F., Dodson R.J.,
 RA Nelson W.C., Gwin M.L., Deboy R., Peterson J.D., Hickey E.K.,
 RA Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A.,
 RA Mason T., Ciecko A., Parksey D.S., Blair E., Clifton H., Clark E.B.,
 RA Cotton M.D., Uitterlinden T.R., Khouri H., Qian H., Yamthuevan J.,
 RA Gill J., Scarlato V., Masignani V., Pizza M., Grandi G., Sun L.,
 RA Smith H.O., Fraser C.M., Moxon F.R., Rappuoli R., Venter J.C.;
 RT "Complete genome sequence of Neisseria meningitidis serogroup B strain
 MC58".
 RL Science 287:1809-1815(2000).

CC -1- FUNCTION: REQUIRED TO FACILITATE THE FORMATION OF CORRECT
 CC DISULFIDE BONDS IN SOME PERIPLASMIC PROTEINS AND FOR THE ASSEMBLY
 CC OF THE PERIPLASMIC C-TYPE CYTOCHROMES. ACTS BY TRANSFERRING
 CC ELECTRONS FROM CYTOPLASMIC THIOREDOXIN TO THE PERIPLASM. THIS
 CC TRANSFER INVOLVES A CASCADE OF DISULFIDE BOND FORMATION AND
 CC REDUCTION STEPS (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE
 CC (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE THIOREDOXIN FAMILY. DSD SUBFAMILY.
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DR EMBL; AE002501; AAF41875.1; -.
 DR TIGR; NMB1519; -.

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DR InterPro: IPR000063; ThioRed.
DR InterPro: IPR003834; Dsbd_Dlpz.
DR Pfam: PF02683; Dsbd; 1.
DR Pfam: PF00085; thioRed; 1.
DR PROSITE: PS00194; THIOREDOXIN; FALSE NEG.
DR Redox-active center; Electron transport; Transmembrane;
KW Inner membrane; Cytochrome c-type biogenesis; Signal;
KM Complete proteome.
FT SIGNAL 1 20 POTENTIAL.
FT CHAIN 21 601 THIO-DISULFIDE INTERCHANGE PROTEIN Dsbd.
FT DOMAIN 21 191 PERIPLASMIC (POTENTIAL).
FT TRANSMEM 192 212 POTENTIAL.
FT DOMAIN 213 242 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 243 263 POTENTIAL.
FT DOMAIN 264 266 PERIPLASMIC (POTENTIAL).
FT TRANSMEM 267 287 POTENTIAL.
FT DOMAIN 288 310 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 311 331 POTENTIAL.
FT DOMAIN 332 346 PERIPLASMIC (POTENTIAL).
FT TRANSMEM 347 367 POTENTIAL.
FT DOMAIN 368 380 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 381 401 POTENTIAL.
FT DOMAIN 402 406 PERIPLASMIC (POTENTIAL).
FT TRANSMEM 407 427 POTENTIAL.
FT DOMAIN 428 437 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 438 458 POTENTIAL.
FT DOMAIN 459 601 PERIPLASMIC (POTENTIAL).
FT DISULFID 120 126 REDOX-ACTIVE (BY SIMILARITY).
FT DISULFID 207 328 REDOX-ACTIVE (BY SIMILARITY).
FT DISULFID 519 522 REDOX-ACTIVE (BY SIMILARITY).
SQ SEQUENCE 601 AA; 64925 MW; AC19CBBP9E763A04 CRC64;

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Query Match 39.0%; Score 41; DB 1; Length 601;
Best Local Similarity 41.2%; Pred. No. 20;
Matches 7; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

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QY 4 ASSVGSFKSTQTFQGC 20
DB 104 AKAVGEPIKLVLYQGC 120

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RESULT 15
PXXL XENLA STANDARD; PRT; 416 AA.
AC P49263;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE PENTRAXIN FUSION PROTEIN PRECURSOR.
GN PXXL
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=94052237; PubMed=7694301;
RA Seery L.T., Schoenberg D.R., Barbaux S., Sharp P.M., Whitehead A.S.;
RT Identification of a novel member of the pentraxin family in Xenopus
RT laevis.
RL Proc. R. Soc. Lond., B, Biol. Sci. 253:263-270(1993).
CC - SIMILARITY: BELONGS TO THE PENTRAXIN FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
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CC or send an email to license@isb-sib.ch).

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CC EMBL: L19881; AAC38013.1; -
DR HSSP: P02743; ILGN.
DR InterPro: IPR001759; Pentaxin.
DR Pfam: PF00354; pentaxin; 1.
DR PRINTS: PR00895; PENTRAXIN.
DR SMART: SM00159; PTX; 1.
DR PROSITE: PS00289; PENTRAXIN; 1.
KW Pentaxin; Signal.
FT SIGNAL 1 14 POTENTIAL.
FT CHAIN 15 416 PENTRAXIN FUSION PROTEIN.
FT DOMAIN 232 416 PENTRAXIN.
FT DISULFID 251 311 BY SIMILARITY.
FT CARBOHYD 129 129 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 221 221 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 416 AA; 47241 MW; 62EDE45B913A2BD7 CRC64;

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Query Match 38.1%; Score 40; DB 1; Length 416;
Best Local Similarity 57.1%; Pred. No. 20;
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

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QY 6 SVGSFKSTQTFQGC 19
DB 355 SYGADFQKTSFVG 368

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Search completed: December 19, 2001, 16:26:16
Job time: 571 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: December 19, 2001, 16:25:22 ; Search time 157.32 Seconds
(without alignments)
18.596 Million cell updates/sec

Title: US-09-202-104A-6
Perfect score: 105
Sequence: 1 MCVASVSGSKFKTQTFQGC 20

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: SP-archaea:*
2: SP-bacteria:*
3: SP-fungi:*
4: SP-human:*
5: SP_invertebrate:*
6: SP_mammal:*
7: SP_mhc:*
8: SP_organelle:*
9: SP-phage:*
10: SP-plant:*
11: SP-rodent:*
12: SP-virus:*
13: SP-vertebrate:*
14: SP_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	49	46.7	415	2	09PKG4 chlamydia m
2	46	43.8	415	2	084233 chlamydia t
3	43	41.0	687	10	091Y34 arabidopsis
4	43	41.0	688	5	09GMP2 ciona savig
5	43	41.0	770	5	09GMP1 ciona savig
6	42	40.0	801	12	099BY7 human immun
7	42	40.0	801	12	099BX7 human immun
8	42	40.0	1995	3	014029 schizosacch
9	41	39.0	101	2	09F3Y8
10	41	39.0	255	12	09F3Y8 oscillator
11	41	39.0	687	5	09U7F6 entamoeba h
12	41	39.0	722	2	09CHC7 lactococcus
13	41	39.0	747	10	09M227 arabidopsis
14	41	39.0	850	2	09CKA8 pasteurella
15	41	39.0	2034	3	017388 caenorhabd
16	40	38.1	71	10	09XGY3 malus domes
17	40	38.1	106	10	09FK87 arabidopsis
18	40	38.1	138	5	09BMA6 paramoecium
19	40	38.1	312	5	09U3T2 caenorhabd

20	40	38.1	551	10	09LEZ2 spinacia ol
21	40	38.1	555	10	09FXX8 mesembryant
22	40	38.1	655	12	09E203 cercopithe
23	40	38.1	722	5	015983 halocynthia
24	40	38.1	866	12	076868 human immun
25	40	38.1	1374	13	09YGN0 fugu rubrip
26	40	38.1	1839	12	09DQ92 pineapple m
27	39.5	37.6	497	3	092460 usillaigo ma
28	39.5	37.6	509	5	076924 drosophila
29	39	37.1	224	6	019063 sus scrofa
30	39	37.1	238	2	09X2L0 bacillus li
31	39	37.1	258	2	09RA41 trichodesm
32	39	37.1	285	2	084144 chlamydia t
33	39	37.1	300	12	076206 human immun
34	39	37.1	300	12	076204 human immun
35	39	37.1	300	12	076205 human immun
36	39	37.1	300	12	076207 human immun
37	39	37.1	341	2	09X962 salmonella
38	39	37.1	483	10	09LQ76 staphylococ
39	39	37.1	518	2	099UT9 streptomyce
40	39	37.1	590	5	097392 brugia mala
41	39	37.1	790	10	080394 mesembryant
42	38.5	36.7	93	2	09L0D6 streptomyce
43	38.5	36.7	204	12	037356 barley yell
44	38.5	36.7	349	13	09W6A6 brachydanio
45	38.5	36.7	646	10	09C6R7 arabidopsis

ALIGNMENTS

RESULT	ID	PRELIMINARY	PRT	415 AA.
09PKG4	09PKG4			
AC	01-OCT-2000 (TREMblrel. 15, Created)			
DT	01-OCT-2000 (TREMblrel. 15, Last sequence update)			
DT	01-JUN-2001 (TREMblrel. 17, Last annotation update)			
DE	SODIUM:DICARBOXYLATE SYMPORTER FAMILY PROTEIN.			
GN	TC0501.			
OS	Chlamydia muridarum.			
OC	Bacteria: Chlamydiales; Chlamydiaceae; Chlamydia.			
OX	NCBI_TaxID=83560;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=MOPN / NIGG;			
RX	MEDLINE=20150255; PubMed=10684935;			
RA	Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,			
RA	White O., Hickey E.K., Peterson J., Ueterbach T., Berry K., Bass S.,			
RA	Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,			
RA	Gwin M., Nelson W., Deboy R., Kolonay J., McClarty G., Salzberg S.L.,			
RA	Eisen J., Fraser C.M.;			
RT	"Genome sequences of Chlamydia trachomatis Mopn and Chlamydia			
RT	pneumoniae AR39."			
RL	Nucleic Acids Res. 28:1397-1406(2000).			
EMBL:	AE002318; AAF7365.1; -.			
DR	TIGR, TC0501; -.			
DR	InterPro: IPR001991; Na_dicarboxyl_symp.			
DR	Pfam: PF00375; SDF: 1.			
DR	PRINTS: PR00173; EDFRNSPORT.			
KW	Complete proteome.			
SO	SEQUENCE 415 AA; 45069 MW; 19BB188D6D74FDFC CRC64;			

Query Match
Best local Similarity 46.7%; Score 49; DB 2; Length 415;
Matches 8; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

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RESULT 2
ID 084233 PRELIMINARY; PRT; 415 AA.
AC 084233;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DE 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE NEUTRAL AMINO ACID (GLUTAMATE) TRANSPORTER (GLUTAMATE).
GN Chlamydia trachomatis.
OS Chlamydia trachomatis.
OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=813;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=D/UM-3/CX;
RX MEDLINE=9900809; PubMed=9784136;
RA Stephens R.S., Kalman S., Lammel C.J., Fan J., Marathe R., Aravind L.,
RA Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V.,
RA Davis R.W.;
RT "Genome sequence of an obligate intracellular pathogen of humans:
RT Chlamydia trachomatis."
RL Science 282:754-759(1998).
DR EMBL: AF001296; AAC67822.1; -
DR InterPro: IPR001991; Ne_dicarboxyl_symp.
DR Pfam: PF00375; SDF; 1.
DR Complete proteome.
KW SEQUENCE 415 AA; 45086 MW; 627AF1671F8FBF74 CRC64;
SQ

Query Match 43.8%; Score 46; DB 2; Length 415;
Best Local Similarity 42.1%; Pred. No. 7.1;
Matches 8; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 2 CVASSVGSFKFTQFGC 20
Db 392 CVSVINKKFSFETEDLPKC 410

RESULT 3
ID 09LY34 PRELIMINARY; PRT; 687 AA.
AC 09LY34;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DE 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE HYPOTHETICAL 76.5 KDA PROTEIN.
GN F27H5_100.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eustosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC Rieger M., Mueller-Auer S., Zipp M., Schaefer M., Meyes H.W., Rudd S.,
RA Lemcke K., Mayer K.F.X., Queller F., Salanoubat M.;
RL Submitted (APR-2000) to the EMBL/Genbank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Submitted (APR-2000) to the EMBL/Genbank/DBJ databases.
RL EMBL: AL163852; CAB87868.1; -
DR InterPro: IPR000179; Cyt_b_b6.
DR PROSITE: PS00193; CYTOCHROME_B_OO; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 687 AA; 76489 MW; 61BBA489B620F17 CRC64;

Query Match 41.0%; Score 43; DB 10; Length 687;
Best Local Similarity 36.8%; Pred. No. 39;
Matches 7; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 1 MCVASSVGSFKFTQFG 19
```

```
Db 446 ICISKSGSEAVRTETITG 464

RESULT 4
ID 09GNP2 PRELIMINARY; PRT; 688 AA.
AC 09GNP2;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DE 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE VASA HOMOLOG.
GN CSDEAD1B(CSVH).
OS Clona savignyi.
OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Phlebobranchia;
OC Clonidae; Clona.
OX NCBI_TaxID=51511;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=OVARY;
RX MEDLINE=20130953; PubMed=10664149;
RA Fujimura M., Takamura K.;
RT "Characterization of an ascidian DEAD-box gene, Cl-DEAD1: specific
RT expression in the germ cells and its mRNA localization in the
RT posterior-most blastomeres in early embryos."
RL Dev. Genes Evol. 210:64-72(2000).
CC -1- SIMILARITY: BELONGS TO ZN-FINGER CCHC TYPE FAMILY.
CC -1- SIMILARITY: TO DEAD/DEAH BOX HELICASE FAMILY.
CC -1- SIMILARITY: TO HELICASE C-TERMINAL DOMAIN.
DR EMBL: AB047802; BAB12216.1; -
DR InterPro: IPR001410; DEAD
DR InterPro: IPR001650; Helicase_C.
DR InterPro: IPR001878; Znf_CCHC.
DR Pfam: PF00270; DEAD; 1.
DR Pfam: PF00271; Helicase_C; 1.
DR Pfam: PF00098; zf-CCHC; 3.
DR SMART: SM00487; DEXDC; 1.
DR SMART: SM00490; HELICG; 1.
DR SMART: SM00343; Znf_C2HC; 3.
DR ARP-binding; Helicase; Zinc-finger.
KW SEQUENCE 688 AA; 73744 MW; 7EE70CFE04A681B9 CRC64;
SQ

Query Match 41.0%; Score 43; DB 5; Length 688;
Best Local Similarity 50.0%; Pred. No. 39;
Matches 9; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 2 CVASSVGSFKFTQFG 19
Db 619 CAESAVGSSFKRGSGFG 636

RESULT 5
ID 09GNP1 PRELIMINARY; PRT; 770 AA.
AC 09GNP1;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DE 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE VASA HOMOLOG.
GN CSDEAD1B(CSVH).
OS Clona savignyi.
OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Phlebobranchia;
OC Clonidae; Clona.
OX NCBI_TaxID=51511;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=OVARY;
RX MEDLINE=20130953; PubMed=10664149;
RA Fujimura M., Takamura K.;
RT "Characterization of an ascidian DEAD-box gene, Cl-DEAD1: specific
RT expression in the germ cells and its mRNA localization in the
RT posterior-most blastomeres in early embryos."
RL Dev. Genes Evol. 210:64-72(2000).
```


RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: A401186; CAC10075.1; -
DR InterPro: IPR001659; Phycobllisome.
DR InterPro: IPR001230; Preylin.
DR Pfam: PF00502; Phycobllisome; 1.
DR PROSITE: PS00294; PRENYLATION; UNKNOWN.1.
FT NON_TER 101 101
SQ SEQUENCE 101 AA; 11067 MW; 3A71965F73F04498 CRC64;

Query Match 39.0%; Score 41; DB 2; Length 101;
Best Local Similarity 56.2%; Pred. No. 13;
Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

OY 4 ASSVGSKFSKTOTFOG 19
| : : | | | | |
DB 56 AQAAYNKFPYQTWOG 71

RESULT 10

RP MEDLINE-97121480; PubMed-8962146;
RX MEDLINE-97094384; PubMed-8939871;
RA Moore P.S., Bashhoff C., Weiss R.A., Chang Y.,
RT "Molecular mimicry of human cytokine and cytokine response pathway
genes by KSHV.";
RL Science 274:1739-1744(1996).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE-97296220; PubMed-9151804;
RA Neipel F., Albrecht J.C., Fleckenstein B.,
RT "Cell-homologous genes in the Kaposi's sarcoma-associated rhadinovirus
human herpesvirus 8: determinants of its pathogenicity?";
RL J. Virol. 71:4187-4192(1997).
RN EMBL: U75698; AAC57128.1; -
DR EMBL: U93872; AAB62651.1; -
DR HSPB; P12295; 3EUG.
DR InterPro: IPR003249; Urag_DNA_glycosyl.
DR InterPro: IPR002043; U_DNA_glycosylase.
DR Pfam: PF00315; UNG; 1.
DR ProDom: PD001588; Urag_DNA_glycosyl; 1.
DR PROSITE: PS00130; U_DNA_GLYCOSYLASE; 1.
SQ SEQUENCE 255 AA; 29008 MW; 3DF95D552DC97C5 CRC64;

Query Match 39.0%; Score 41; DB 12; Length 255;
Best Local Similarity 43.8%; Pred. No. 32;
Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

OY 5 SSVGSKFSKTOTFOGC 20
: : : | : | | | |
DB 215 ASLGGRHSRWRPFGC 230

RESULT 11
ID Q9U7F6 PRELIMINARY; PRT; 687 AA.
AC Q9U7F6;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DE 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DR ADHESIN.
GN ADH112.
OS Entamoeba histolytica.
OC Eukaryota; Entamoebidae; Entamoeba.
OX NCBI_TaxID=5759;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-HM1:IMSS;
RX MEDLINE-99348386; PubMed-10417646;
RA Garcia-Rivera G., Rodriguez M.A., Ocaiz R., Martinez-L.pez M.C.,
RT Entamoeba histolytica: a novel cysteine protease and an adhesin form
the 112 kDa surface protein.";
RL MOL. Microbiol. 33:556-568(1999).
DR EMBL: AF127375; AAF04256.1; -
SQ SEQUENCE 687 AA; 78128 MW; A57E592712DC7B50 CRC64;

Query Match 39.0%; Score 41; DB 5; Length 687;
Best Local Similarity 37.0%; Pred. No. 86;
Matches 10; Conservative 3; Mismatches 4; Indels 10; Gaps 1;

OY 2 CVASVGSKFSKT-----OTFO 18
| : : | | | | | | : | | |
DB 120 CCCMALGSSFSKTTDANSLSKSAVSFO 146

RESULT 12

ID Q9CHC7 PRELIMINARY; PRT; 722 AA.
AC Q9CHC7;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DE HYPOTHETICAL PROTEIN YIBC.
GN YIBC.
OS Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
OC Lactococcus.
OX NCBI_TaxID=1360;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-IL1403;
RA Bolotin A., Winkler P., Manger S., Jallion O., Malarme K.,
RT Weissbach J., Ehrlich S.D., Sorokin A.,
RT "The complete genome sequence of the lactic acid bacterium Lactococcus
lactis.";
RL Genome Res. 0:0-(2001).
DR EMBL: AE006314; AAK04903.1; -
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 722 AA; 82028 MW; 4B672DDB86903CD8 CRC64;

Query Match 39.0%; Score 41; DB 2; Length 722;
Best Local Similarity 53.3%; Pred. No. 91;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 4 ASSVGSKFSKTOTFO 18
| : : | | | | |
DB 335 AGSLPAKGTOTFO 349

RESULT 13
ID Q9M227 PRELIMINARY; PRT; 747 AA.
AC Q9M227;

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: December 19, 2001, 16:21:00 ; Search time 78.52 seconds
(without alignments)
5.732 Million cell updates/sec

Title: US-09-202-104a-6
Perfect score: 105
Sequence: 1 MCVASSVGSKFSKTFQGC 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/PTUS.COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	105	100.0	201	6 5171840-11	Patent No. 5171840
2	105	100.0	210	4 US-09-043-785-1	Sequence 1, Appl1
3	105	100.0	323	6 5171840-6	Patent No. 5171840
4	105	100.0	323	6 5480796-6	Patent No. 5480796
5	105	100.0	344	6 5171840-7	Patent No. 5171840
6	105	100.0	344	6 5480796-7	Patent No. 5480796
7	105	100.0	386	6 5171840-5	Patent No. 5171840
8	105	100.0	386	6 5480796-5	Patent No. 5480796
9	105	100.0	468	4 US-08-795-473B-5	Sequence 5, Appl1
10	105	100.0	468	6 5171840-2	Patent No. 5171840
11	105	100.0	468	6 5480796-2	Patent No. 5480796
12	39	37.1	201	1 US-07-929-580B-5	Sequence 5, Appl1
13	39	37.1	223	1 US-07-708-885B-3	Sequence 3, Appl1
14	39	37.1	223	1 US-07-714-386-3	Sequence 3, Appl1
15	39	37.1	223	1 US-07-708-888A-3	Sequence 3, Appl1
16	38	36.2	184	1 US-08-044-621D-30	Sequence 30, Appl1
17	38	36.2	184	1 US-08-044-621D-31	Sequence 31, Appl1
18	38	36.2	184	1 US-08-709-912-1	Sequence 1, Appl1
19	38	36.2	184	2 US-09-047-370-1	Sequence 1, Appl1
20	38	36.2	185	1 US-08-709-912-2	Sequence 2, Appl1
21	38	36.2	185	2 US-09-047-370-2	Sequence 2, Appl1
22	38	36.2	211	1 US-07-842-349-2	Sequence 2, Appl1
23	38	36.2	211	1 US-08-244-686-2	Sequence 2, Appl1
24	38	36.2	221	1 US-08-698-978-2	Sequence 2, Appl1
25	38	36.2	232	1 US-08-631-607-5	Sequence 5, Appl1
26	38	36.2	247	4 US-08-501-126-19	Sequence 19, Appl1
27	38	36.2	248	4 US-09-189-060B-2	Sequence 2, Appl1

28	38	36.2	248	4 US-09-189-060B-12	Sequence 12, Appl1
29	38	36.2	426	1 US-08-631-607-6	Sequence 6, Appl1
30	38	36.2	428	1 US-08-103-445-2	Sequence 2, Appl1
31	38	36.2	428	1 US-08-461-690B-2	Sequence 2, Appl1
32	38	36.2	430	1 US-08-631-607-7	Sequence 7, Appl1
33	38	36.2	432	1 US-08-631-607-2	Sequence 2, Appl1
34	38	36.2	441	4 US-09-625-188-4	Sequence 4, Appl1
35	37	35.2	253	3 US-08-581-148C-9	Sequence 9, Appl1
36	37	35.2	492	4 US-08-462-794-11	Sequence 11, Appl1
37	37	35.2	972	3 US-08-750-141A-2	Sequence 2, Appl1
38	37	35.2	2409	6 5180808-2	Patent No. 5180808
39	36.5	34.8	768	2 US-08-408-519-2	Sequence 2, Appl1
40	36.5	34.8	768	5 PCT-US95-03552-2	Sequence 2, Appl1
41	36	34.3	208	1 US-08-631-607-3	Sequence 3, Appl1
42	36	34.3	211	1 US-08-709-912-6	Sequence 6, Appl1
43	36	34.3	211	2 US-09-047-370-6	Sequence 6, Appl1
44	36	34.3	233	1 US-08-044-621D-24	Sequence 24, Appl1
45	36	34.3	1271	5 PCT-US94-08267-2	Sequence 2, Appl1

ALIGNMENTS

RESULT 1
5171840-11
Patent No. 5171840
APPLICANT: KISHIMOTO, TADAMITSU
TITLE OF INVENTION: RECEPTOR PROTEIN FOR HUMAN B CELL
STIMULATORY FACTOR-2
NUMBER OF SEQUENCES: 11
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/298,694
FILING DATE: 19-JAN-1989
SEQ ID NO:11:
LENGTH: 201
5171840-11

Query Match 100.0%; Score 105; DB 6; Length 201;
Best Local Similarity 100.0%; Pred. No. 2e+09; 0; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0;

QY 1 MCVASSVGSKFSKTFQGC 20
DB 70 MCVASSVGSKFSKTFQGC 89

RESULT 2
US-09-043-785-1
Sequence 1, Application US/09043785
Patent No. 6172042
GENERAL INFORMATION:
APPLICANT: CHEBATH, Judith
APPLICANT: HALIMI, Hubert
APPLICANT: REVEL, Michel
TITLE OF INVENTION: SYNTHETIC PEPTIDES THAT INHIBIT IL-6 ACTIVITY
FILE REFERENCE: Chebath-1
CURRENT APPLICATION NUMBER: US/09/043,785
CURRENT FILING DATE: 1998-09-02
EARLIER APPLICATION NUMBER: PCT/IL96/00119
EARLIER FILING DATE: 1996-09-26
EARLIER APPLICATION NUMBER: 115,453
EARLIER FILING DATE: 1995-09-26
EARLIER APPLICATION NUMBER: 118,097
EARLIER FILING DATE: 1996-05-01
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO: 1
LENGTH: 210
TYPE: PRT
ORGANISM: Human
US-09-043-785-1

Query Match 100.0%; Score 105; DB 4; Length 210;
Best Local Similarity 100.0%; Pred. No. 2.1e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MCVASSVSGSKFSKTOTFOGC 20
|||||
Db 80 MCVASSVSGSKFSKTOTFOGC 99

RESULT 3

5171840-6
; Patent No. 5171840
; APPLICANT: KISHIMOTO, TADAMITSU
; TITLE OF INVENTION: RECEPTOR PROTEIN FOR HUMAN B CELL
; STIMULATORY FACTOR-2
; NUMBER OF SEQUENCES: 11
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/298,694
; FILING DATE: 19-JAN-1989
; SEQ ID NO:6:
; LENGTH: 323
5171840-6

Query Match 100.0%; Score 105; DB 6; Length 323;
Best Local Similarity 100.0%; Pred. No. 3.3e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MCVASSVSGSKFSKTOTFOGC 20
|||||
Db 192 MCVASSVSGSKFSKTOTFOGC 211

RESULT 4

5480796-6
; Patent No. 5480796
; APPLICANT: KISHIMOTO, TADAMITSU
; TITLE OF INVENTION: ANTIBODIES AGAINST THE RECEPTOR PROTEIN
; FOR HUMAN B CELL STIMULATORY FACTOR-2
; NUMBER OF SEQUENCES: 8
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/907,650
; FILING DATE: 02-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 298,694
; FILING DATE: 19-JAN-1989
; SEQ ID NO:6:
; LENGTH: 323
5480796-6

Query Match 100.0%; Score 105; DB 6; Length 323;
Best Local Similarity 100.0%; Pred. No. 3.3e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MCVASSVSGSKFSKTOTFOGC 20
|||||
Db 192 MCVASSVSGSKFSKTOTFOGC 211

RESULT 5

5171840-7
; Patent No. 5171840
; APPLICANT: KISHIMOTO, TADAMITSU
; TITLE OF INVENTION: RECEPTOR PROTEIN FOR HUMAN B CELL
; STIMULATORY FACTOR-2
; NUMBER OF SEQUENCES: 11
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/298,694
; FILING DATE: 19-JAN-1989
; SEQ ID NO:7:
; LENGTH: 344

5171840-7
Query Match 100.0%; Score 105; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 3.5e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MCVASSVSGSKFSKTOTFOGC 20
|||||
Db 192 MCVASSVSGSKFSKTOTFOGC 211

RESULT 6

5480796-7
; Patent No. 5480796
; APPLICANT: KISHIMOTO, TADAMITSU
; TITLE OF INVENTION: ANTIBODIES AGAINST THE RECEPTOR PROTEIN
; FOR HUMAN B CELL STIMULATORY FACTOR-2
; NUMBER OF SEQUENCES: 8
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/907,650
; FILING DATE: 02-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 298,694
; FILING DATE: 19-JAN-1989
; SEQ ID NO:7:
; LENGTH: 344
5480796-7

Query Match 100.0%; Score 105; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 3.5e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MCVASSVSGSKFSKTOTFOGC 20
|||||
Db 192 MCVASSVSGSKFSKTOTFOGC 211

RESULT 7

5171840-5
; Patent No. 5171840
; APPLICANT: KISHIMOTO, TADAMITSU
; TITLE OF INVENTION: RECEPTOR PROTEIN FOR HUMAN B CELL
; STIMULATORY FACTOR-2
; NUMBER OF SEQUENCES: 11
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/298,694
; FILING DATE: 19-JAN-1989
; SEQ ID NO:5:
; LENGTH: 386
5171840-5

Query Match 100.0%; Score 105; DB 6; Length 386;
Best Local Similarity 100.0%; Pred. No. 4e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MCVASSVSGSKFSKTOTFOGC 20
|||||
Db 110 MCVASSVSGSKFSKTOTFOGC 129

RESULT 8

5480796-5
; Patent No. 5480796
; APPLICANT: KISHIMOTO, TADAMITSU
; TITLE OF INVENTION: ANTIBODIES AGAINST THE RECEPTOR PROTEIN
; FOR HUMAN B CELL STIMULATORY FACTOR-2
; NUMBER OF SEQUENCES: 8
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/907,650
; FILING DATE: 02-JUL-1992

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 298,694
; FILING DATE: 19-JAN-1989
; SEQ ID NO: 5
; LENGTH: 386
5480796-5

Query Match 100.0%; Score 105; DB 6; Length 386;
Best Local Similarity 100.0%; Pred. No. 4e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MCVASSVSGSKFSTQTFQGC 20
|||||
DB 110 MCVASSVSGSKFSTQTFQGC 129

RESULT 9
US-08-795-473B-5
; Sequence 5, Application US/08795473B
; Patent No. 6217858
; GENERAL INFORMATION:
; APPLICANT: Galun, Eithan
; APPLICANT: Nahot, Orit
; APPLICANT: Blum, Herbert E.
; TITLE OF INVENTION: A Pharmaceutical Composition for Treating
; TITLE OF INVENTION: Hepatitis B Virus (HBV) Infection
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Davidson, Davidson and Kappel, LLC
; STREET: 1140 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MS-DOS EDITOR
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/795,473B
; FILING DATE: 11-FEB-1997
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Davidson, Clifford M.
; REGISTRATION NUMBER: 32,728
; REFERENCE/DOCKET NUMBER: 963,1007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)-997-1028
; TELEFAX: (212)-997-1037
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 468 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
US-08-795-473B-5

Query Match 100.0%; Score 105; DB 4; Length 468;
Best Local Similarity 100.0%; Pred. No. 4.9e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MCVASSVSGSKFSTQTFQGC 20
|||||
DB 192 MCVASSVSGSKFSTQTFQGC 211

RESULT 10
5171840-2
; Patent No. 5171840
; APPLICANT: KISHIMOTO, TADAMITSU
; TITLE OF INVENTION: RECEPTOR PROTEIN FOR HUMAN B CELL

; STIMULATORY FACTOR-2
; NUMBER OF SEQUENCES: 11
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/298,694
; FILING DATE: 19-JAN-1989
; SEQ ID NO: 2
; LENGTH: 468
5171840-2

Query Match 100.0%; Score 105; DB 6; Length 468;
Best Local Similarity 100.0%; Pred. No. 4.9e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MCVASSVSGSKFSTQTFQGC 20
|||||
DB 192 MCVASSVSGSKFSTQTFQGC 211

RESULT 11
5480796-2
; Patent No. 5480796
; APPLICANT: KISHIMOTO, TADAMITSU
; TITLE OF INVENTION: ANTIBODIES AGAINST THE RECEPTOR PROTEIN
; FOR HUMAN B CELL STIMULATORY FACTOR-2
; NUMBER OF SEQUENCES: 8
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/907,650
; FILING DATE: 02-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 298,694
; FILING DATE: 19-JAN-1989
; SEQ ID NO: 2
; LENGTH: 468
5480796-2

Query Match 100.0%; Score 105; DB 6; Length 468;
Best Local Similarity 100.0%; Pred. No. 4.9e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MCVASSVSGSKFSTQTFQGC 20
|||||
DB 192 MCVASSVSGSKFSTQTFQGC 211

RESULT 12
US-07-929-580B-5
; Sequence 5, Application US/07929580B
; Patent No. 5426181
; GENERAL INFORMATION:
; APPLICANT: Lee, Tae Ho
; APPLICANT: Lee, Gene W.
; APPLICANT: Vilcek, Jan
; TITLE OF INVENTION: Cytokine-Induced Protein, TSG-14,
; TITLE OF INVENTION: DNA Coding Therefor and Uses Thereof
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Browdy and Neimark
; STREET: 419 Seventh Street, NW
; CITY: Washington
; STATE: DC
; COUNTRY: US
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/929,580B
; FILING DATE: 19920814
; CLASSIFICATION: 435

DATE: 25 OCT 1985
US-07-714-386-3

Query Match 37.1%; Score 39; DB 1: Length 223;
Best Local Similarity 50.0%; Pred. No. 62;
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 6 SVGSKFSTQTFQG 19
DB 158 SYGKFDROSFWG 171

RESULT 15

US-07-708-888A-3
Sequence 3, Application US/07708888A
Patent No. 5281697
GENERAL INFORMATION:
APPLICANT: Toth, Carol A.
APPLICANT: Thomas, Peter
APPLICANT: Maswoswe, Sibusisiwe M.
APPLICANT: Brigman, Joseph V.
TITLE OF INVENTION: CEA-Binding Protein
TITLE OF INVENTION: and Uses Thereof
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lahive & Cockfield
STREET: 60 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 720kb
COMPUTER: IBM XT
OPERATING SYSTEM: DOS 3.30
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07708,888A
FILING DATE: 19910531
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
APPLICATION NUMBER:
FILING DATE:
APPLICATION NUMBER:
FILING DATE:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 223 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: C-reactive protein
PUBLICATION INFORMATION:
AUTHORS: Lei, Ke-jian
AUTHORS: Liu, Teresa
AUTHORS: Zou, Gerald
AUTHORS: Soravia, Emilia
AUTHORS: Liu, Teh-Yung
AUTHORS: Goldman, Neil D.
TITLE: Genomic Sequence for Human
TITLE: C-reactive Protein
JOURNAL: Journal of Biological
JOURNAL: Chemistry
VOLUME: 260
ISSUE: 24
PAGES: 13377-83
DATE: 25 OCT 1985
US-07-708-888A-3

Query Match 37.1%; Score 39; DB 1; Length 223;

Best Local Similarity 50.0%; Pred. No. 62;
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 6 SVGSKFSTQTFQG 19
DB 158 SYGKFDROSFWG 171

Search completed: December 19, 2001, 16:21:00
Job time: 405 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: December 19, 2001, 16:19:35 ; Search time 170.68 seconds
(without alignments)
10.850 Million cell updates/sec

Title: US-09-202-104A-7

Perfect score: 145
Sequence: 1 PEKPKNLSCVINEGKKMKRCWMDGR 25

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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20: /SID8/gcgdata/geneseq/geneseq/AA2000.DAT.*
21: /SID8/gcgdata/geneseq/geneseq/AA2001.DAT.*
22: /SID8/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	145	100.0	25	19	AAW52207
2	145	100.0	180	17	AAW00404
3	145	100.0	329	18	AAW17859
4	145	100.0	332	20	AAW70799
5	145	100.0	332	21	AAV92188
6	145	100.0	658	17	AAV94576
7	145	100.0	708	14	AAV37804
8	145	100.0	708	17	AAV85911
9	145	100.0	727	21	AAV92192
10	145	100.0	738	21	AAV92194
11	145	100.0	859	20	AAW70796

12	145	100.0	859	21	AAV92184	Human gpi30-Fc-His
13	145	100.0	918	12	AAV10545	Recombinant human
14	145	100.0	918	15	AAV46233	Human soluble glyco
15	145	100.0	918	17	AAV73368	Human gpi30 protei
16	145	100.0	918	21	AAV44694	Human gpi30 protei
17	145	100.0	951	21	AAV70798	Human gpi30-C-gamm
18	145	100.0	951	21	AAV92186	Human gpi30-C-gamm
19	145	100.0	961	21	AAV92187	Human gpi30-J-C-ga
20	145	100.0	1158	21	AAV92205	Fusion polypeptide
21	145	100.0	1168	21	AAV92204	Fusion polypeptide
22	116	80.0	24	22	AAV88830	Human interleukin-
23	110	75.9	917	13	AAV26334	gpi30. Mus muscul
24	110	75.9	917	21	AAV55073	Mouse gpi30 protei
25	106	73.1	24	22	AAV88829	Human interleukin-
26	79	54.5	13	22	AAV84708	Human IL-6 recepto
27	67	46.2	252	22	AAV51243	Human haemopoietin
28	67	46.2	652	22	AAV51242	Human haemopoietin
29	67	46.2	662	22	AAV51244	Human haemopoietin
30	65.5	45.2	862	18	AAV12771	Human interleukin-
31	64	44.1	13	22	AAV48709	Mouse IL-6 recepto
32	63	43.4	24	22	AAV88831	Human interleukin-
33	63	43.4	303	20	AAV70843	Human Zcyto5 vari
34	63	43.4	303	20	AAV70845	Human Zcyto5 vari
35	63	43.4	350	19	AAV55015	Human Zcyto5 vari
36	63	43.4	350	22	AAE00824	Amino acid sequenc
37	63	43.4	385	20	AAV70842	Human NR6 haemopo
38	63	43.4	385	20	AAV70839	Human Zcyto5 vari
39	63	43.4	389	20	AAV70846	Human Zcyto5 vari
40	63	43.4	389	20	AAV70847	Human Zcyto5 vari
41	63	43.4	389	20	AAV70848	Human Zcyto5 vari
42	63	43.4	389	20	AAV70849	Human Zcyto5 vari
43	63	43.4	389	20	AAV70850	Human Zcyto5 vari
44	63	43.4	389	20	AAV70851	Human Zcyto5 vari
45	63	43.4	389	20	AAV70852	Human Zcyto5 vari

ALIGNMENTS

RESULT 1
ID AAW52207 standard; peptide: 25 AA.
XX AAW52207;
AC AAW52207;
XX 09-JUN-1998 (first entry)
XX Interleukin-6 antagonist peptide.
DE Interleukin-6; IL-6; antagonist; IL-6 related disease; multiple myeloma;
KW acquired immune deficiency syndrome-related lymphoma; immune response;
KW Rheumatoid arthritis; psoriasis; sepsis; osteoporosis; therapy;
XX Alzheimer's disease.
XX Synthetic.
OS Homo sapiens.
OS Homo sapiens.
XX WO9748728-A1.
XX 24-DEC-1997.
XX 19-JUN-1997; 97WO-NL00345.
XX 20-JUN-1996; 96EP-0201720.
XX (KOSTER) KOSTER H W.
XX Hoebe KHN, Van Leengoed LMG;
XX WPI: 1998-063080/06.
XX New peptide(s) with interleukin-6 agonist or antagonist activity -
XX useful for treatment, prevention and diagnosis of IL-6 associated

PT diseases
 XX
 PS Claim 6; Page 17; 28pp; English.
 XX
 CC This sequence represents a Interleukin-6 (IL-6) antagonist peptide. This
 CC sequence is a peptide of the invention, which are of 5-30 amino acids
 CC and have antagonistic activity against: (a) IL-6; (b) the alpha chain
 CC and/or beta chain of the IL-6 receptor (IL-6R); or (c) IL-6 activity. The
 CC antagonists are used to treat or prevent IL-6 related diseases (typical
 CC of many exemplified are multiple myeloma, acquired immune deficiency
 CC syndrome-related lymphoma, rheumatoid arthritis, psoriasis, sepsis,
 CC osteoporosis, Alzheimer's disease etc.), also to remove IL-6 or IL-6R
 CC from extracorporeal blood. They may also be used diagnostically for such
 CC diseases and IL-6 agonists are additives for cell cultures. Antibodies
 CC specific for the antagonists may be administered to subjects previously
 CC treated with the antagonists to counter their effects, also in
 CC extracorporeal dialysis and diagnosis. The antagonists are too small to
 CC induce an immune response and have minimal side effects (they are not
 CC lytic for erythrocytes nor toxic for polymorphonuclear cells or
 CC hepatocytes); contrast no-human anti-IL-6 antibodies. The mixtures, or
 CC multimers, have greater activity (acting on both IL-6 and its receptor)
 CC and the peptides can be engineered to increase half-life or to target
 CC organs by incorporating unnatural aa or altering the
 CC hydrophilic/lipophilic balance.
 CC
 XX Sequence 25 AA;
 SQ
 Query Match 100.0%; Score 145; DB 19; Length 25;
 Best Local Similarity 100.0%; Pred. No. 6.4e-14;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 PEKPNLSCTIVNEGKKMKRCMDGGR 25
 |||||
 Db 1 pekpnlsctivnegkkmkrcwdggr 25
 RESULT 2
 AAW00404
 ID AAW00404 standard; peptide: 180 AA.
 XX
 AC AAW00404;
 XX
 DT 29-AUG-1996 (first entry)
 XX
 DE Interleukin-6 antagonist peptide.
 XX
 KM IL-6; antagonist; autoimmune disease.
 XX
 OS Synthetic.
 XX
 PN JF07324097-A.
 XX
 PD 12-DEC-1995.
 XX
 PF 30-MAY-1994; 94JP-0117259.
 XX
 PR 30-MAY-1994; 94JP-0117259.
 XX
 PA (DAIL) DAICEL CHEM IND LTD.
 PA (FUJI) FUJISAWA PHARM CO LTD.
 XX
 DR WPI; 1996-065476/07.
 XX
 PT Interleukin 6 antagonist - useful for treating autoimmune diseases
 PS Claim 1; Page 2; 19pp; Japanese.
 XX
 CC New IL-6 antagonists are provided which are of formula X-W-Y, in
 CC which X is H or an amino-protecting group, Y is OH or a carboxy-
 CC protecting group, and W is a peptide containing all or part of the
 CC sequence as given in AAW00401, AAW00402, AAW00403 or AAW00404 (the
 CC present sequence), where any free mercapto groups in the sequence are

CC optionally protected. Specifically preferred partial peptides from
 CC the present sequence (AAW00436 - AAW00442) are claimed as new chemical
 CC compounds. The IL-6 antagonists are useful for treating autoimmune
 CC diseases.
 CC
 XX Sequence 180 AA;
 SQ
 Query Match 100.0%; Score 145; DB 17; Length 180;
 Best Local Similarity 100.0%; Pred. No. 5.2e-13;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 PEKPNLSCTIVNEGKKMKRCMDGGR 25
 |||||
 Db 4 pekpnlsctivnegkkmkrcwdggr 28
 RESULT 3
 AAW17859
 ID AAW17859 standard; Protein: 329 AA.
 XX
 AC AAW17859;
 XX
 DT 04-FEB-1998 (first entry)
 XX
 DE Rheumatoid arthritis auto-antigen clone A.
 XX
 KM Rheumatoid arthritis; auto-antigen; clone A; diagnosis;
 KM prediction; synovial cell.
 XX
 OS Homo sapiens.
 XX
 PN WO9717441-A1.
 XX
 PD 15-MAY-1997.
 XX
 PF 06-NOV-1996; 96WO-JP03250.
 XX
 PR 07-NOV-1995; 95JP-0288957.
 XX
 PA (KANF) KANEKA CORP.
 XX
 PI Kishimura M, Nakao K, Osakada F, Osaki S, Tanaka M;
 XX
 DR WPI; 1997-281030/25.
 DR N-PSDB; AAT68830.
 XX
 PT Auto-antigen from synovial cells of rheumatoid arthritis patients -
 PT binds to antibodies present in these patients, for diagnosis and
 PT prediction of the disease
 XX
 PS Claim 3; Pages 36-37; 61pp; Japanese.
 XX
 CC The present sequence is the rheumatoid arthritis (RA) auto-antigen
 CC clone A, which can be used to diagnose and predict the development
 CC of RA by reaction with antibodies in biological specimens, e.g.
 CC sera, from patients.
 CC RNA was isolated from synovial cells from a RA patient and used to
 CC construct a cDNA library. This was screened using IgG separated
 CC from the synovial fluid of a RA patient. Active clones were
 CC isolated in a cloning vector, and inserted into an expression
 CC vector for the transformation of E. coli NM522. Transformants on
 CC culture express clone A peptide and follistatin related protein
 CC into the culture medium.
 XX
 SQ Sequence 329 AA;
 Query Match 100.0%; Score 145; DB 18; Length 329;
 Best Local Similarity 100.0%; Pred. No. 9.9e-13;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 PEKPNLSCTIVNEGKKMKRCMDGGR 25

Db 126 pekpxnlscivnegkkmrcwcdggr 150

|||||

RESULT 4

AAW70799

ID AAW70799 standard; protein; 332 AA.

XX AAW70799;

DT 03-FEB-1999 (first entry)

XX Human gp130-delta-3fibro amino acid sequence.

DE gp130; cytokine antagonist; interleukin; gamma-interferon;
KW granulocyte macrophage colony-stimulating factor; J peptide;
XX transforming growth factor-beta.

OS Synthetic.

OS Homo sapiens.

XX Key Location/Qualifiers

FT 1..330

FT Protein /note="human gp130"

XX US5844099-A.

XX 01-DEC-1998.

XX 27-NOV-1995; 95US-0563105.

XX 27-NOV-1995; 95US-0563105.

XX 20-OCT-1993; 93US-0140222.

XX (REG-) REGENERON PHARM INC.

XX Economides A, Stahl N, Yancopoulos GD;

XX WPI; 1999-044669/04.

XX Cytokine antagonists - comprising extracellular domains of
PT specificity-determining and signal-transducing components of
PT cytokine receptor

XX Example 4; Fig 10; 46pp; English.

XX The present sequence represents the amino acid sequence of human
CC gp130-delta-3fibro. The protein is used in the course of the invention.
CC The specification describes cytokine antagonists comprising only the
CC extracellular domain of the specificity-determining component of

CC the cytokine receptor and the extracellular domain of a
CC signal-transducing component of the cytokine receptor. The cytokine

CC is an interleukin (IL-1, IL-2, IL-3, IL-4, IL-5 or IL-15),
CC granulocyte macrophage colony-stimulating factor (GM-CSF),

CC gamma-interferon or transforming growth factor-beta (TGF-beta). The
CC antagonist is capable of binding the cytokine to form a nonfunctional

CC complex. The compounds have therapeutic activity as cytokine antagonists
CC and can also be used in assays for identifying novel agonists and
CC antagonists of cytokines.

XX Sequence 332 AA;

Query Match 100.0%; Score 145; DB 20; Length 332;

Best Local Similarity 100.0%; Pred. No. 1e-12;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PEKPNLSCIVNEGKMKRCWCDGGR 25

DB 126 pekpxnlscivnegkkmrcwcdggr 150

RESULT 5

AAV92188
ID AAV92188 standard; protein; 332 AA.

XX AAV92188;

DT 01-AUG-2000 (first entry)

XX Human gp130-delta-3fibro.

DE gp130-delta-3fibro; cytokine; antagonist; CNTF; receptor; fusion protein;
KW cytosolic; immunomodulator; osteopathic.

OS Synthetic.

OS Homo sapiens.

XX Key Location/Qualifiers

FT 1..330

FT Protein /label="gp130

FT Peptide 331..332

FT /note="Ser-Gly bridge"

XX WO200018932-A2.

XX 06-APR-2000.

XX 22-SEP-1999; 99WO-US22045.

XX 25-SEP-1998; 98US-0101858.

XX 19-MAY-1999; 99US-0313942.

XX (REG-) REGENERON PHARM INC.

XX Stahl N, Yancopoulos GD;

XX WPI; 2000-293165/25.

XX Isolated nucleic acid molecule for treating cytokine-related diseases
PT or disorders encodes a fusion polypeptide capable of binding a cytokine
PT to form a nonfunctional complex

XX Example 4; Fig 10; 152pp; English.

XX The invention concerns production of antagonists to any cytokine that
CC utilizes an alpha specificity determining component, which when combined
CC with the cytokine, binds to a first beta signal transducing component to

CC form a non-functional intermediate which then binds to a second beta
CC signal transducing component causing beta-receptor dimerization, the

CC soluble alpha specificity determining component of the receptor
CC (SR-alpha) and the extracellular domain of the first beta signal

CC transducing component of the cytokine receptor (beta-1) are combined to
CC form heterodimers (SR-alpha:beta-1) that act as antagonist to the

CC cytokine by binding the cytokine to form a non-functional complex. The
CC receptor components are shared by cytokines such as the CNTF (ciliary

CC neurotrophic factor) family of cytokines. The invention provides the
CC basis for the development of IL-6 antagonists, as they show that if, in

CC the presence of a ligand, a non-functional intermediate complex,
CC consisting of the ligand, its alpha receptor and its beta-1 receptor

CC component, can be formed, it will effectively block the action of the
CC ligand. Effective antagonists of IL-6 or CNTF consist of heterodimers

CC of the extracellular domains of the alpha specificity determining
CC components of their receptors and the extracellular domain of gp130.

CC The resultant heterodimers, function as high-affinity traps, rendering
CC the cytokine inaccessible to form a signal transducing complex with the

CC native membrane-bound forms of their receptor. The nucleic acids and
CC polypeptides are useful for treating cytokine-related diseases or

CC disorders such as osteoporosis and primary and secondary effects of
CC cancer including multiple myeloma or cachexia.

XX Sequence 332 AA;

Query Match 100.0%; Score 145; DB 21; Length 332;

Best Local Similarity 100.0%; Pred. No. 1e-12;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PEKPRNLSCIYNEGKKMRCEWDGR 25
 |||||||||||||||||||
 Db 126 pekpknlscivnegkkmrcwdggr 150

RESULT 6

AAAR94576
 ID AAR94576 standard; Protein: 658 AA.

XX AAR94576;

XX 20-JUN-1996 (first entry)

XX Human gp130 splice variant.

XX GP130, transmembrane domain; growth factor antagonist;

XX embryo preimplantation; in vitro fertilisation.

XX Homo sapiens.

XX WO9609382-A1.

XX 28-MAR-1996.

XX 21-SEP-1995; 95WO-GB02243.

XX 21-SEP-1994; 94GB-0019021.

XX (ISTF) ARS APPLIED RES SYST HOLDING NV.

XX Dellow KA, Sharkey A, Smith SK;

XX WPI: 1996-188444/19.

XX N-PSDB; AAT14602.

XX New splice variant of gp130 lacking the trans-membrane domain
 useful as an antagonist for growth factors esp. for ensuring correct
 development of pre-implantation embryos

XX Example 2; Fig 1; 33pp; English.

XX A novel, soluble splice variant (AAR94576) of human gp130 corresponds
 CC to amino acids 1-613 of native gp130 (AAR75368) but has a novel
 CC C-terminal sequence (AAR94575) from amino acid 614 onwards.

XX The splice variant lacks a transmembrane region. It was initially
 CC detected during the morula to blastocyst transition of human
 CC embryos. The splice variant antagonises the action of growth
 CC factors, e.g. Interleukin-6, Leukaemia inhibitory factor,
 CC oncostatin M and Interleukin-11, and can be used to ensure correct
 CC development of preimplantation embryos, partic. for in vitro
 CC fertilisation.

XX Sequence 658 AA;

XX Query Match

Best Local Similarity 100.0%; Score 145; DB 17; Length 658;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PEKPRNLSCIYNEGKKMRCEWDGR 25
 |||||||||||||||||||

Db 126 pekpknlscivnegkkmrcwdggr 150

RESULT 7

AAAR37804
 ID AAR37804 standard; Protein: 708 AA.

XX AAR37804;

XX 01-OCT-1993 (first entry)

XX Human gp130 N-terminal fragment.

XX Oncostatin M; leukemia inhibitory factor; receptor; PCR; fusion;

XX LIF-R; gp130; linker.

XX Synthetic.

XX Key Location/Qualifiers

XX Peptide 1..22

XX Protein /label= sig-peptide

XX Domain /label= mat-protein

XX Region /label= extracellular_domain

XX Domain /label= transmembrane_region

XX Domain /note= "beginning with amino acid 620"

XX Domain /label= cytoplasmic_domain

XX Domain /note= "partial cytoplasmic domain"

XX Misc-difference 8

XX WO9310151-A.

XX 27-MAY-1993.

XX 20-NOV-1992; 92WO-US10272.

XX 22-NOV-1991; 91US-0797556.

XX (IMMV) IMMUNEX CORP.

XX Gearing DP;

XX WPI: 1993-182493/22.

XX N-PSDB; AAQ42588.

XX Receptor protein comprising gp130 covalently linked to LIF

XX Receptor - binds to oncostatin M and LIF useful for treating

XX Kaposi's sarcoma, atherosclerosis, obesity etc.

XX Disclosure; Page 48-53; 79pp; English.

XX A new receptor (R), able to bind oncostatin M and leukemia

XX inhibitory factor (LIF), comprises a gp130 polypeptide (AAQ42588)

XX covalently coupled to LIF-receptor (LIF-R) (AAQ42590); for example

XX via a FC region of an IgG1 antibody (AAQ42589).

XX Suitable gp130 polypeptides comprise amino acids 22-528, 22-320,

XX 120-320 etc., or lack all or part of the transmembrane region

XX and/or cytoplasmic domain.

XX Pref. both components of (R) are soluble proteins and are connected

XX by a polypeptide linker of 20-100 amino acids consisting of Gly, Asn,

XX Ser, Thr or Ala.

XX Sequence 708 AA;

Query Match

Best Local Similarity 100.0%; Score 145; DB 14; Length 708;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PEKPRNLSCIYNEGKKMRCEWDGR 25
 |||||||||||||||||||

Db 126 pekpknlscivnegkkmrcwdggr 150

RESULT 8

AAAR85911

ID	AA85911	standard; Protein; 708 AA.
XX	AA85911;	
AC		
XX	03-JUL-1996	(first entry)
DT		
XX	gp130 N-terminal fragment.	
DE		
XX		
KW	Human; gp130; inhibitor; oncostatin M; cytokine; antibody Fc region; oncostatin M receptor-beta chain; antibody; tumour; growth factor; therapy.	
KW		
XX		
OS	Homo sapiens.	
XX		
FH	Key	Location/Qualifiers
FT	Peptide	1..22
FT		/note="signal peptide"
FT	Peptide	23..708
FT		/note="N-terminal fragment of mature gp130"
FT	Modified-site	21..23
FT		/note="glycosylation site"
FT	Modified-site	61..63
FT		/note="glycosylation site"
FT	Modified-site	109..111
FT		/note="glycosylation site"
FT	Modified-site	135..137
FT		/note="glycosylation site"
FT	Cleavage-site	153..154
FT	Modified-site	155..207
FT		/note="glycosylation site"
FT	Modified-site	224..226
FT		/note="glycosylation site"
FT	Modified-site	357..359
FT		/note="glycosylation site"
FT	Modified-site	361..363
FT		/note="glycosylation site"
FT	Modified-site	368..370
FT		/note="glycosylation site"
FT	Modified-site	531..533
FT		/note="glycosylation site"
FT	Modified-site	542..544
FT		/note="glycosylation site"
FT	Cleavage-site	621..622
XX		
PN	W09533059-A2.	
PD		
XX	07-DEC-1995.	
XX		
PE	22-MAY-1995;	95WO-US06530.
XX		
PR	12-SEP-1994;	94US-0308881.
PR	26-MAY-1994;	94US-0249553.
XX		
PA	(IMGV) IMMUNEX CORP.	
XX		
PI	Cosman DJ, Mosley B;	
XX		
DR	WPI: 1996-030570/03.	
DR	N-PSDB: AAO74081.	
XX		
PT	Hetero:dimeric receptor proteins comprising OSM-R beta and gp 130	
PT	bind oncostatin M and are used in inhibiting biological activities	
PT	mediated by oncostatin M	
XX		
PS	Claim 1; Page 35-38; 60pp; English.	
XX		
CC	This sequence represents an N-terminal fragment of gp130 obtained from human placenta. gp130 binds to oncostatin M, which is a secreted single chain polypeptide cytokine. Oncostatin M regulates the growth of certain tumour derived and normal cell lines. This receptor protein, and the oncostatin M receptor-beta chain (see AA85912) sequence can be covalently joined, to give a heterodimeric receptor protein capable of binding to oncostatin M. The receptors can also comprise fusion	
CC		

CC	polypeptides, where an antibody Fc region is joined to the C-terminus of each of the soluble proteins. In this case, the two fusion polypeptides are joined by disulphide bonds between the two antibody Fc regions. The heterodimeric receptors can be used to inhibit biological activities mediated by oncostatin M. The advantage with using the heterodimeric receptors is that they bind to oncostatin M at greater levels than gp130 does alone.	CC
CC		CC
XX	Sequence 708 AA;	XX
SO		SO
Query Match	100.0%; Score 145; DB 17; Length 708;	
Best Local Similarity	100.0%; Pred. NO.2.2e-12;	
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 PEKPNLSCTIVEGKMKRCMDGGR 25 	
Db	126 pekphnlsctivnegkkmrcwdggr 150	
RESULT 9		
ID	AA92192	
XX	AA92192 standard; protein; 727 AA.	
AC	AA92192;	
XX		
DT	01-AUG-2000 (first entry)	
XX		
DE	Human gp130-kappa domain fusion protein.	
XX		
KW	gp130-kappa domain; cytokine; antagonist; CNTF; receptor; fusion protein;	
XX	cytostatic; immunomodulator; osteopathic.	
XX		
OS	Synthetic.	
XX	Homo sapiens.	
XX		
FA	Key	Location/Qualifiers
FT	protein	1..619
FT		/label= gp130
FT	Peptide	620..621
FT		/note= "Ser-Gly bridge"
FT	Protein	622..727
FT		/label= IgG1_kappa_domain
XX		
PN	WO200018932-A2.	
XX		
PD	06-APR-2000.	
XX		
PF	22-SEP-1999; 99WO-US22045.	
XX		
PR	25-SEP-1998; 98US-0101858.	
PR	19-MAY-1999; 99US-0313942.	
PA	(REGG-) REGENERON PHARM INC.	
XX		
PI	Stahl N, Yancopoulos GD;	
XX		
DR	WPI: 2000-293165/25.	
XX		
PT	Isolated nucleic acid molecule for treating cytokine-related diseases	
PT	or disorders encodes a fusion polypeptide capable of binding a cytokine	
PT	to form a nonfunctional complex	
XX		
XX		
PS	Example 4; Page -; 152pp; English.	
XX		
CC	The invention concerns production of antagonists to any cytokine that utilizes an alpha specificity determining component, which when combined with the cytokine, binds to a first beta signal transducing component to form a non-functional intermediate which then binds to a second beta signal transducing component causing beta-receptor dimerization, the soluble alpha specificity determining component of the receptor (sr-alpha) and the extracellular domain of the first beta signal transducing component of the cytokine receptor (beta-1) are combined to	

CC form heterodimers (sr-alpha:beta-1) that act as antagonist to the
 CC cytokine by binding the cytokien to form a non-functional complex. The
 CC receptor components are shared by cytokines such as the CNTF (clilary
 CC neurotrophic factor) family of cytokines. The invention provides the
 CC basis for the development of IL-6 antagonists, as they show that if, in
 CC the presence of a ligand, a non-functional intermediate complex,
 CC consisting of the ligand, its alpha receptor and its beta-1 receptor
 CC component, can be formed, it will effectively block the action of the
 CC ligand. Effective antagonists of IL-6 or CNTF consist of heterodimers
 CC of the extracellular domains of the alpha specificity determining
 CC components of their receptors and the extracellular domain of gp130.
 CC The resultant heterodimers, function as high-affinity traps, rendering
 CC the cytokine inaccessible to form a signal transducing complex with the
 CC native membrane-bound forms of their receptor. The nucleic acids and
 CC polypeptides are useful for treating cytokine-related diseases or
 CC disorders such as osteoporosis and primary and secondary effects of
 CC cancer including multiple myeloma or cachexia.
 CC NB. This sequence was constructed from the gp130 and kappa domain
 CC sequences given in figures 9 and 13 of the specification.

XX Sequence 727 AA;

Query Match 100.0%; Score 145; DB 21; Length 727;

Best Local Similarity 100.0%; Pred. No. 2,3e-12;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PEKPKNLSCIVNEGKKMKCEWDGGR 25

Db 126 pekpknlscivnegkkmcewdggr 150

RESULT 10

AAV92194 AAV92194 standard; protein; 738 AA.

AC AAV92194;

DT 01-AUG-2000 (first entry)

DE Human gp130-J-kappa fusion protein.

KW gp130-J-kappa; cytokine; antagonist; CNTF; receptor; fusion protein;

KW cytosolatic; immunomodulator; osteopathic.

OS Synthetic.

OS Homo sapiens.

FT Key Location/Qualifiers

FT Protein 1..619

FT Peptide /label= gp130

FT /note= "Ser-gly bridge"

FT Peptide 622..632

FT /note= "J-peptide"

FT Domain 633..738

FT /label= Kappa_domain

XX WO200018932-A2.

XX 06-APR-2000.

XX 22-SEP-1999; 99WO-US22045.

XX 25-SEP-1998; 98US-0101858.

XX 19-MAY-1999; 99US-0313942.

XX (REG-) REGENERON PHARM INC.

XX Stahl N, Yancopoulos GD;

XX WPI; 2000-293165/25.

PT Isolated nucleic acid molecule for treating cytokine-related diseases

PT or disorders encodes a fusion polypeptide capable of binding a cytokine

PT to form a nonfunctional complex.

XX Example 4; Page -; 152pp; English.

CC The invention concerns production of antagonists to any cytokine that
 CC utilizes an alpha specificity determining component, which when combined
 CC with the cytokine, binds to a first beta signal transducing component to
 CC form a non-functional intermediate which then binds to a second beta
 CC signal transducing component causing beta-receptor dimerization, the
 CC soluble alpha specificity determining component of the receptor
 CC (sr-alpha) and the extracellular domain of the first beta signal
 CC transducing component of the cytokine receptor (beta-1) are combined to
 CC form heterodimers (sr-alpha:beta-1) that act as antagonist to the
 CC cytokine by binding the cytokien to form a non-functional complex. The
 CC receptor components are shared by cytokines such as the CNTF (clilary
 CC neurotrophic factor) family of cytokines. The invention provides the
 CC basis for the development of IL-6 antagonists, as they show that if, in
 CC the presence of a ligand, a non-functional intermediate complex,
 CC consisting of the ligand, its alpha receptor and its beta-1 receptor
 CC component, can be formed, it will effectively block the action of the
 CC ligand. Effective antagonists of IL-6 or CNTF consist of heterodimers
 CC of the extracellular domains of the alpha specificity determining
 CC components of their receptors and the extracellular domain of gp130.
 CC The resultant heterodimers, function as high-affinity traps, rendering
 CC the cytokine inaccessible to form a signal transducing complex with the
 CC native membrane-bound forms of their receptor. The nucleic acids and
 CC polypeptides are useful for treating cytokine-related diseases or
 CC disorders such as osteoporosis and primary and secondary effects of
 CC cancer including multiple myeloma or cachexia.

XX Sequence 738 AA;

Query Match 100.0%; Score 145; DB 21; Length 738;

Best Local Similarity 100.0%; Pred. No. 2,4e-12;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PEKPKNLSCIVNEGKKMKCEWDGGR 25

Db 126 pekpknlscivnegkkmcewdggr 150

RESULT 11

AAW70796 AAW70796 standard; protein; 859 AA.

AC AAW70796;

DT 03-FEB-1999 (first entry)

DE Human gp130-FC-Hls6 amino acid sequence.

KW gp130; cytokine antagonist; interleukin; gamma-interferon;

KW granulocyte macrophage colony-stimulating factor; J peptide;

KW transforming growth factor-beta.

OS Synthetic.

OS Homo sapiens.

FT Key Location/Qualifiers

FT Protein 1..619

FT MISC-difference 2 /note= "human gp130"

FT /label= L2V

FT /note= "amino acid changed to accomodate a Kozak

FT Peptide 1..22

FT MISC-difference 620..621 /note= "signal peptide"

FT Protein 662..853 /note= "Ser-gly bridge"

```

FT Disulfide-bond 632..635 /note="from the Fc domain of human IgG1"
FT Peptide 854..859
FT /note="hexahistidine tag"
XX
XX US5844099-A.
XX
XX 01-DEC-1998.
XX
XX 27-NOV-1995; 95US-0563105.
XX
XX 27-NOV-1995; 95US-0563105.
XX
XX 20-OCT-1993; 93US-0140222.
XX
XX (REGG-) REGENERON PHARM INC.
XX
XX Economides A, Stahl N, Yancopoulos GD;
XX WPI, 1999-044669/04.
XX
XX Cytokine antagonists - comprising extracellular domains of
XX specificity-determining and signal-transducing components of
XX cytokine receptor
XX
XX Example 3; Fig 4; 46pp; English.
XX
XX The present sequence represents the amino acid sequence of human
XX gp130-Fc-His6. The protein is used in the course of the invention. The
XX specification describes cytokine antagonists comprising only the
XX extracellular domain of the specificity-determining component of
XX the cytokine receptor and the extracellular domain of a
XX signal-transducing component of the cytokine receptor. The cytokine
XX is an interleukin (IL-1, IL-2, IL-3, IL-4, IL-5 or IL-15).
XX granulocyte macrophage colony-stimulating factor (GM-CSF),
XX gamma-interferon or transforming growth factor-beta (TGF-beta). The
XX antagonist is capable of binding the cytokine to form a nonfunctional
XX complex. The compounds have therapeutic activity as cytokine antagonists
XX and can also be used in assays for identifying novel agonists and
XX antagonists of cytokines.
XX
XX Sequence 859 AA;
XX
XX
XX Query Match 100.0%; Score 145; DB 20; Length 859;
XX Best Local Similarity 100.0%; Pred. No. 2.8e-12;
XX Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 PEKPNLSCTIVNEGKMKRCWMDGR 25
XX ||||||||||||||||||||
XX Db 126 pekpnlsctivnegkkmrcwmdgr 150
XX
XX RESULT 12
XX AAY92184
XX ID AAY92184 standard; protein; 859 AA.
XX
XX AAY92184;
XX
XX 01-AUG-2000 (first entry)
XX
XX Human gp130-Fc-His6.
XX
XX gp130-Fc-His6; cytokine; antagonist; CNTF; receptor; fusion protein;
XX cytostatic; immunomodulator; osteopathic.
XX
XX Synthetic.
XX
XX Homo sapiens.
XX
XX key Location/Qualifiers
XX Protein 1..619
XX /label= gp130
XX Peptide 1..22
XX /label= signal_peptide

```

```

FT Peptide 620..621
FT /note="Ser-Gly bridge"
FT Disulfide-bond 632
FT /note="forms inter-chain disulfide bridge that
FT link two Fc domains"
XX
XX Disulfide-bond 635
XX /note="forms inter-chain disulfide bridge that
XX link two Fc domains"
XX
XX Protein 662..853
XX /label= IgG1_Fc-domain
XX Peptide 854..859
XX /label= histidine_tag
XX
XX MO200018932-A2.
XX
XX 06-APR-2000.
XX
XX 22-SEP-1999; 99WO-US22045.
XX
XX 25-SEP-1998; 98US-0101858.
XX 19-MAY-1999; 99US-0313942.
XX
XX (REGG-) REGENERON PHARM INC.
XX
XX Stahl N, Yancopoulos GD;
XX WPI, 2000-293165/25.
XX
XX Isolated nucleic acid molecule for treating cytokine-related diseases
XX or disorders encodes a fusion polypeptide capable of binding a cytokine
XX to form a nonfunctional complex
XX
XX Example 3; Fig 4; 152pp; English.
XX
XX The invention concerns production of antagonists to any cytokine that
XX utilizes an alpha specificity determining component, which when combined
XX with the cytokine, binds to a first beta signal transducing component to
XX form a non-functional intermediate which then binds to a second beta
XX signal transducing component causing beta-receptor dimerization, the
XX soluble alpha specificity determining component of the receptor
XX (SR-alpha) and the extracellular domain of the first beta signal
XX transducing component of the cytokine receptor (beta-1) are combined to
XX form heterodimers (SR-alpha:beta-1) that act as antagonist to the
XX cytokine by binding the cytokine to form a non-functional complex. The
XX receptor components are shared by cytokines such as the CNTF (ciliary
XX neurotrophic factor) family of cytokines. The invention provides the
XX basis for the development of IL-6 antagonists, as they show that if, in
XX the presence of a ligand, a non-functional intermediate complex,
XX consisting of the ligand, its alpha receptor and its beta-1 receptor
XX component, can be formed, it will effectively block the action of the
XX ligand. Effective antagonists of IL-6 or CNTF consist of heterodimers
XX of the extracellular domains of the alpha specificity determining
XX components of their receptors and the extracellular domain of gp130.
XX The resultant heterodimers, function as high-affinity traps, rendering
XX the cytokine inaccessible to form a signal transducing complex with the
XX native membrane-bound forms of their receptor. The nucleic acids and
XX polypeptides are useful for treating cytokine-related diseases or
XX disorders such as osteoporosis and primary and secondary effects of
XX cancer including multiple myeloma or cachexia.
XX
XX Sequence 859 AA;
XX
XX
XX Query Match 100.0%; Score 145; DB 21; Length 859;
XX Best Local Similarity 100.0%; Pred. No. 2.8e-12;
XX Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 PEKPNLSCTIVNEGKMKRCWMDGR 25
XX ||||||||||||||||||||
XX Db 126 pekpnlsctivnegkkmrcwmdgr 150
XX
XX RESULT 13

```

AA010545
ID AA010545 standard; Protein: 918 AA.
AC AA010545;
XX
DT 12-APR-1991 (first entry)
DE Recombinant human gp130 protein.
XX
KM Recombinant human gp130; interleukin-6; interleukin-6 receptor;
KM immunity; haematopoiesis; inflammation; therapy.
XX
OS Homo sapiens.
XX
PN EP411946-A.
PD 06-FEB-1991.
XX
PF 02-AUG-1990; 90EP-0308530.
XX
PR 31-MAY-1990; 90JP-0140069.
PR 03-AUG-1989; 89JP-0200230.
XX
PA (KISH/) KISHIMOTO T.
XX
PI Kishimoto T;
XX
DR WPI: 1991-038820/06.
DR N-PSDB; AA010402.
XX
PT Recombinant human gp130 protein - acts in the transmission of
PT Interleukin-6 signal for defence mechanisms
XX
PS Disclosure; fig 7; 32pp; English.
XX
CC This gp130 protein is produced using standard recombinant DNA
CC methods (see AA010402); free from any other human protein. It
CC participates in the transmission of the interleukin (IL)-6 sig-
CC nal, and therefore the proliferation and differentiation of an
CC organism. It is important in an animals defence mechanisms, e.g.
CC immunity, haematopoiesis and inflammation.
XX
SQ Sequence 918 AA;

Query Match 100.0%; Score 145; DB 12; Length 918;
Best Local Similarity 100.0%; Pred. No. 3e-12;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PEKPKNLSCIVNEGKMKRCWDGGR 25
DB 126 pekpknlscivnegkkmrcwdggr 150
|||||

RESULT 14
AA046233
ID AA046233 standard; Protein: 918 AA.
XX
AC AA046233;
XX
DT 15-SEP-1994 (first entry)
XX
DE Human soluble glycoprotein (GP) 130.
XX
KM Glycoprotein; soluble; gp; gp130; antibody production; assay;
KM immunochemical assay; detection; immunogen; transmembrane domain.
XX
OS Homo sapiens.
XX
PN JP06022786-A.
PD 01-FEB-1994.
XX

PF 02-AUG-1991; 91JP-0217924.
XX
PR 02-AUG-1991; 91JP-0217924.
XX
PA (KISH/) KISHIMOTO C.
PA (TOYT) TOSOH CORP.
XX
DR WPI: 1994-071006/09.
DR N-PSDB; AA056931.
XX
PT Preparation of recombinant soluble human gp 130 deriv - for use
PT in the production of anti-gp 130 antibody for immunochemical
PT assay
XX
PS Claim 1; Figure 7; 13pp; Japanese.
XX
CC The soluble glycoprotein (gp) 130 can be used as an immunogen for
CC the preparation of anti-gp130 antibody and as the standard substance
CC for immunochemical assay of gp130. Soluble gp130 cDNA was prepared
CC by inserting a termination codon prior to the extracellular domain
CC or transmembrane domain of the gp130 coding sequence or simply by
CC eliminating the transmembrane domain.
XX
SQ Sequence 918 AA;

Query Match 100.0%; Score 145; DB 15; Length 918;
Best Local Similarity 100.0%; Pred. No. 3e-12;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PEKPKNLSCIVNEGKMKRCWDGGR 25
DB 126 pekpknlscivnegkkmrcwdggr 150
|||||

RESULT 15
AA075368
ID AA075368 standard; Protein: 918 AA.
XX
AC AA075368;
XX
DT 20-JUN-1996 (first entry)
XX
DE Human gp130 protein.
XX
KM Gp130; transmembrane domain; growth factor antagonist;
KM embryo pre-implantation; in vitro fertilisation.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Region 620..641
FT /label= Transmembrane_region
XX
XX MO9609382-A1.
XX
XX 28-MAR-1996.
XX
XX 21-SEP-1995; 95WO-G802243.
XX
XX 21-SEP-1994; 94GB-0019021.
XX
PA (ISTF) ARS APPLIED RES SYST HOLDING NV.
XX
PI Dellow KA, Sharkey A, Smith SK;
XX
XX WPI: 1996-188444/19.
XX
DR N-PSDB; AAT14603.
XX
PT New splice variant of gp130 lacking the trans-membrane domain
PT useful as an antagonist for growth factors esp. for ensuring correct
PT development of pre-implantation embryos
XX

PS Disclosure: Fig 2: 33pp; English.
XX
CC A DNA sequence (AAT14603) codes for native human gp130 (AAR75368).
CC A novel splice variant (see AAT14602) that lacks the transmembrane
CC region was identified in the morula to blastocyst transition stage
CC of the human embryo. The splice variant antagonises the action
CC of certain growth factors and can be used to ensure correct
CC development of preimplantation embryos.
XX
SQ Sequence 918 AA;

Query Match 100.0%; Score 145; DB 17; Length 918;
Best Local Similarity 100.0%; Pred. No. 3e-12;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 PEKPKNLSCIVNEGKKMKRCWDGGR 25
|||||
Db 126 pekpknlscivnegkkmkrcwdggr 150

Search completed: December 19, 2001, 16:19:35
Job time: 360 sec

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OM protein - protein search, using sw model

Run on: December 19, 2001, 16:22:39 ; Search time 88.82 seconds

21.441 Million cell updates/sec

Title: US-09-202-104A-7

Sequence: 1 PEKPKNLSCIVNEGKKMRCEWDGGR 25

Scoring table: BLOSUM62

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

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Minimum DB seq length: 0
Maximum DB seq length: 20000000000

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Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

```
1: p1r1: *
2: p1r2: *
3: p1r3: *
4: p1r4: *
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query Match	Length	DB	ID	Description
	1	145	100.0	918	2	A36337	membrane glycoprotein
	2	110	75.9	917	2	I49699	glycoprotein 130 -
	3	92	63.4	918	2	A44257	interleukin-6 signal
	4	62	42.8	1092	2	JX0312	differentiation-stimulating factor
	5	60	41.4	1097	2	S17308	leukemia inhibitor
	6	54.5	37.6	771	2	B38252	granulocyte colony-stimulating factor
	7	54.5	37.6	783	2	JH0329	granulocyte colony-stimulating factor
	8	54.5	37.6	863	2	C38252	granulocyte colony-stimulating factor
	9	54	37.2	1639	2	T50119	probable sensory transducer
	10	53.5	36.9	471	2	PS0154	125k surface antigen
	11	53.5	36.9	837	2	A34698	granulocyte colony-stimulating factor
	12	49	33.8	830	2	I50455	prolactin receptor
	13	49	33.8	831	2	JQ1655	prolactin receptor
	14	49	33.8	990	2	S23416	antibiotic resistance protein
	15	49	33.8	2302	2	T14328	protein-tyrosine phosphatase
	16	49	33.8	2395	1	S50820	surface protein tyrosine phosphatase
	17	48.5	33.4	952	2	T47145	hypothetical protein
	18	48.5	33.4	1253	2	T46248	hypothetical protein
	19	48.5	33.4	1212	2	T28157	erythrocyte membrane protein
	20	48.5	33.4	2647	2	T28161	hypothetical protein
	21	48	33.1	196	1	I40053	anthranilate synthase
	22	48	33.1	250	2	T33879	hypothetical protein
	23	48	33.1	382	1	G01589	ionizing radiation-inducible protein
	24	48	33.1	684	2	S60266	novel antigen receptor
	25	48	33.1	896	2	I56563	interleukin-3 receptor
	26	48	33.1	1757	2	T14318	ubiquitin-protein ligase
	27	47.5	32.8	537	2	B33485	spore coat protein
	28	47.5	32.8	640	2	B32935	hypothetical protein
	29	47	32.4	155	2	G72249	ribosomal protein

30	47	32.4	401	2	S55793	ornithine--oxo-ac
31	47	32.4	451	2	T49011	hypothetical prote
32	47	32.4	519	2	D70695	hypothetical prote
33	47	32.4	581	2	I45971	prolactin receptor
34	47	32.4	878	1	A40091	interleukin-3 rece
35	47	32.4	896	1	A35782	cytokine receptor
36	47	32.4	899	2	C71608	origin recognition
37	47	32.4	1043	2	A56037	DNA-binding protei
38	47	32.4	1117	2	JC4934	delta-crystallin/E
39	47	32.4	1124	2	JX0293	zinc finger protei
40	46.5	32.1	396	2	S22909	interleukin-3 rece
41	46.5	32.1	596	2	T01237	hypothetical prote
42	46	31.7	260	2	JC4850	trypsin-like prote
43	46	31.7	324	2	G64463	hypothetical prote
44	46	31.7	391	2	T49115	pectate lyase like
45	46	31.7	451	2	F75083	phospho-sugar muta

ALIGNMENTS

RESULT 1

membrane glycoprotein gp130 precursor - human

```
C;Date: 12-Apr-1991 #sequence_revision 12-Apr-1991 #text_change 28-Jul-2000
```

R; Hibl, M.; Murakami, M.; Salto, M.; Hirano, T.; Taga, T.; Kishimoto, T

A; Title: Molecular cloning and expression of an IL-6 signal transducer, gp130

A; Accession: A36337

A;Molecule type: mRNA

A; Cross-references: GB:M57230; NID:g186353; PIDN:AAA59155.1; PID:g186354

A;Gene: GDB:IL6ST; GP130
A;Cross: r6f0r00000; GDB:126735; OMTM:600604

A;Map position: 5q11-5q11
C:Superfamily: cytokine receptor homolog

Keywords: glycoprotein; membrane protein

Query Match	100.0%;	Score 145;	DB 2;	Length 918
Post Topic Similarity	100.0%;	Prod No 5	00-13;	

Matches	25;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
---------	-----	--------------	----	------------	----	--------	----	------	----

QY 1 PEKPNLSIIVNEGKKMRCEWDGGR 25

Db 126 PEKPNLSCTVNEGKKMRCEWDGGR 150

RESULT 2

149699
130 - mouse

C:Species: Mus musculus (house mouse)
C:Date: 03-Aug-1996 #sequence revision 03-Aug-1996 #text change 28-Jul-2000

C/Accession: I49699; I48370
R-Salto, M.; Yoshida, K.; Hibi, M.; Taga, T.; Kishimoto, T.

J. Immunol. 148, 4066-4071, 1992

A;Accession: T49699
A;Reference number: 148370; MUID:92291532

A:Status: translated from GB/EMBL/DB

A;Residues: 1-91/ <RE

A;Accession: I483/0
A;Status: translated from GR/EMBL/DBJ

A: Molecule type: mRNA
A: Residues: 1-917 <REF2>

C>Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 05-Nov-1999
C/Accession: JH0329; S21608
R:Larsen, A.; Davis, T.; Curtis, B.M.; Gimpel, S.; Sims, J.E.; Cosman, D.; Park, L.; Sor
J. Exp. Med. 172, 1559-1570, 1990
A>Title: Expression cloning of a human granulocyte colony-stimulating factor receptor: a
A/Reference number: JH0329; MUID:91079757
A/Accession: JH0329
A/Molecule type: mRNA
A/Residues: 1-783 <LAR>
A/Cross-references: GB:X55720; NID:931698; PIDN:CAA93252.1; PID:g31699
A/Experimental source: placenta
C/Keywords: glycoprotein; transmembrane protein
F/1-24/Domain: signal sequence #status predicted <Sig>
F/25-783/Product: granulocyte colony-stimulating factor receptor D7 #status predicted <M
F/25-627/Domain: extracellular #status predicted <EXT>
F/628-653/Domain: transmembrane #status predicted <TM>
F/654-783/Domain: intracellular #status predicted <INT>
F/93,128,134,389,474,579,610/Binding site: carbohydrate (Asn) (covalent) #status predict

Query Match 37.6%; Score 54.5; DB 2; Length 783;
Best Local Similarity 40.0%; Pred. No. 6.1;
Matches 10; Conservative 5; Mismatches 9; Indels 1; Gaps 1;

Qy 1 PERKMLSCIVN-EGKKRCEWDG 24
| | | | | : | : | : |
Db 123 PAIPHNLSCIMNLTSSLICQWEPG 147

RESULT 8
C38252
granulocyte colony-stimulating factor receptor precursor, long form - human
N/Contains: granulocyte colony-stimulating factor, long form; granulocyte colony-stimula
C/Species: Homo sapiens (man)
C/Date: 14-Jun-1991 #sequence_revision 30-Jan-1993 #text_change 05-Nov-1999
C/Accession: C38252; A38252; JH0330; A46486; S68332; S21607
R:Fukunaga, R.; Seto, Y.; Mizushima, S.; Nagata, S.
Proc. Natl. Acad. Sci. U.S.A. 87, 8702-8706, 1990
A>Title: Three different mRNAs encoding human granulocyte colony-stimulating factor rece
A/Reference number: A38252; MUID:91062348
A/Accession: C38252
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-863 <FRU>
A/Cross-references: GB:M59820; GB:M38027; NID:g183046; PIDN:AAA63178.1; PID:g183049
A/Note: clones PHG1 and PHG5
A/Accession: A38252
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-680,708-863 <FUD>
A/Cross-references: GB:M59818; GB:M38025; NID:g183046; PIDN:AAA63176.1; PID:g183047
A/Note: clone PH03
R:Larsen, A.; Davis, T.; Curtis, B.M.; Gimpel, S.; Sims, J.E.; Cosman, D.; Park, L.; Sor
J. Exp. Med. 172, 1559-1570, 1990
A>Title: Expression cloning of a human granulocyte colony-stimulating factor receptor: a
A/Reference number: JH0329; MUID:91079757
A/Accession: JH0330
A/Molecule type: mRNA
A/Residues: 1-680,708-863 <LAR>
A/Cross-references: GB:X55721; NID:g31696; PIDN:CAA93253.1; PID:g31697
A/Note: clone 25-1; placenta
R:Seto, Y.; Fukunaga, R.; Nagata, S.
J. Immunol. 148, 259-266, 1992
A>Title: Chromosomal gene organization of the human granulocyte colony-stimulating facto
A/Reference number: A46486; MUID:92091782
A/Accession: A46486
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 855-863 <SET>
A/Cross-references: GB:S71484; NID:g240883; PIDN:AAB20660.1; PID:g240884
A/Experimental source: granulocyte
A/Note: sequence extracted from NCBI backbone (NCBIN:71484, NCBI:P:71485)
R:Hanlu, M.; Horan, T.; Arakawa, T.; Le, J.; Katta, V.; Rohde, M.F.

Arch. Biochem. Biophys. 324, 344-356, 1995
A>Title: Extracellular domain of granulocyte-colony stimulating factor receptor.
A/Reference number: S68331; MUID:96132662
A/Accession: S68332
A/Molecule type: protein
A/Residues: 234-269 <HAN>
C/Genetics:
A/Gene: GDB:CSF3R
A/Cross-references: GDB:126430; OMIM:138971
A/Map position: 1p35-1p34.3
C/Keywords: alternative splicing; glycoprotein; transmembrane protein
F/1-24/Domain: signal sequence #status predicted <Sig>
F/25-863/Product: granulocyte colony-stimulating factor receptor, long form #status p
F/25-680,708-863/Product: granulocyte colony-stimulating factor receptor, short form
F/25-627/Domain: extracellular #status predicted <EXT>
F/628-653/Domain: transmembrane #status predicted <TM>
F/654-863/Domain: intracellular #status predicted <INT>
F/93,128,134,389,474,579,610/Binding site: carbohydrate (Asn) (covalent) #status pred

Query Match 37.6%; Score 54.5; DB 2; Length 863;
Best Local Similarity 40.0%; Pred. No. 6.8;
Matches 10; Conservative 5; Mismatches 9; Indels 1; Gaps 1;

Qy 1 PERKMLSCIVN-EGKKRCEWDG 24
| | | | | : | : | : |
Db 123 PAIPHNLSCIMNLTSSLICQWEPG 147

RESULT 9
T50119
probable sensory transduction histidine kinase [imported] - fission yeast (Schizosac
C/Species: Schizosaccharomyces pombe
C/Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 09-Jun-2000
C/Accession: T50119
R:Seeger, K.; Harris, D.; Wood, V.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, February 2000
A/Reference number: Z25039
A/Accession: T50119
A/Status: preliminary; translated from GB/EMBL/DDBJ
A/Molecule type: DNA
A/Residues: 1-1639 <SEE>
A/Cross-references: EMBL:AL157734; PIDN:CA875776.1; GSPDB:GN00066; SPDB:SPAC1834.08
C/Experimental source: strain 972h(-); cosmid c1834
C/Genetics:
A/Gene: SPDB:SPAC1834.08
A/Map position: 1
A/Introns: 23/3

Query Match 37.2%; Score 54; DB 2; Length 1639;
Best Local Similarity 45.5%; Pred. No. 15;
Matches 10; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

Qy 3 KPKMLSCIVN-EGKKRCEWDG 24
: | | | | | : | : | | |
Db 219 EPRDLSDIYNTPMOLRCYDGG 240

RESULT 10
PS0154
125k surface antigen M17 - Entamoeba histolytica (fragment)
C/Species: Entamoeba histolytica
C/Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
R:Edman, U.; Meraz, M.A.; Rausser, S.; Agabian, N.; Meza, I.
J. Exp. Med. 172, 879-888, 1990
A>Title: Characterization of an immuno-dominant variable surface antigen from pathoge
A/Reference number: JH0284; MUID:90354788
A/Accession: PS0154
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-471 <EDM>

A:Experimental source: strain Wistar

C:Genetics:

A:Note: PTPRO

C:Keywords: phosphoric monoester hydrolase

F:1-18/Domain: signal sequence #status predicted <SIG>

F:19-2302/Product: protein-tyrosine phosphatase receptor type, GMCI #status predicted <M

Query Match 33.8%; Score 49; DB 2; Length 2302;

Best Local Similarity 28.0%; Pred. No. 1.1e+02;

Matches 7; Conservative 6; Mismatches 12; Indels 0; Gaps 0;

OY 1 PEKPKNLSCIVNEGKKMRCEMDGCR 25

DB 1343 PEAVRNIECVARDMQSVSVRMDDPR 1367

Search completed: December 19, 2001, 16:22:39
Job time: 459 sec

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OM protein - protein search, using sw model

Run on: December 19, 2001, 16:26:16 ; Search time 48.45 Seconds
(without alignments)
18.919 Million cell updates/sec

Title: US-09-202-104a-7
Perfect score: 145
Sequence: 1 PEKPKNLSCIVNEGKKMKRCWDCGR 25

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 3664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	145	100.0	918	1 IL6B_HUMAN	P40189 homo sapien
2	110	75.9	917	1 IL6B_MOUSE	Q00560 mus musculi
3	92	63.4	918	1 IL6B_RAT	P40190 rattus norv
4	65.5	45.2	862	1 IL2S_HUMAN	O99665 homo sapien
5	63.5	43.8	874	1 IL2S_MOUSE	P97378 mus musculi
6	62	42.8	1092	1 ILIR_MOUSE	P42703 mus musculi
7	60	41.4	1097	1 ILIR_HUMAN	P42702 homo sapien
8	54.5	37.6	836	1 GCSR_HUMAN	O99602 homo sapien
9	53.5	36.9	837	1 GCSR_MOUSE	P40223 mus musculi
10	49	33.8	830	1 PRUR_COLLI	O90374 columba liv
11	49	33.8	831	1 PRUR_CHICK	O04594 gallus gall
12	49	33.8	986	1 EPRB_STARP	P30195 staphylococ
13	48	33.1	196	1 TRPG_BUCAP	P42388 buchnera ap
14	48	33.1	398	1 DAP3_HUMAN	P51398 homo sapien
15	47.5	32.8	537	1 SP70_DICDI	P15692 dicyostell
16	47.5	32.8	640	1 APRN_ENTHI	P20301 entamoeba h
17	47	32.4	159	1 RL22_THEMA	P38511 thermotoga
18	47	32.4	401	1 ORT_BACSU	P38821 bacillus su
19	47	32.4	581	1 PRUR_BOVIN	Q28172 bos taurus
20	47	32.4	878	1 IL3B_MOUSE	P26554 mus musculi
21	47	32.4	896	1 CYRB_MOUSE	P26555 mus musculi
22	47	32.4	1043	1 TCF8_MESAU	O60542 mesocricetu
23	47	32.4	1109	1 TCF8_RAT	O62947 rattus norv
24	47	32.4	1117	1 TCF8_MOUSE	O64318 mus musculi
25	47	32.4	1124	1 TCF8_HUMAN	P37775 homo sapien
26	46.5	32.1	396	1 IL3A_MOUSE	P37775 mus musculi
27	46	31.7	321	1 YD12_METJA	O58108 methanococ
28	46	31.7	548	1 HR3_MANSE	O08882 manduca sex
29	46	31.7	557	1 HR3_GALME	P49668 gallieria me
30	46	31.7	831	1 PRUR_MEIGA	O91094 metacaris g
31	46	31.7	844	1 SAK_RANCA	P31226 rana catesb
32	46	31.7	897	1 CYRB_HUMAN	P32927 homo sapien
33	46	31.7	2704	1 G168_PAPPR	P17053 paramacium

ALIGNMENTS

RESULT 1	ID	IL6B_HUMAN	STANDARD:	PRT:	918 AA.
AC	P40189	Q9U041	31, Created		
DT	01-FEB-1995	(Rel. 31, Last sequence update)			
DT	20-AUG-2001	(Rel. 40, Last annotation update)			
DE	INTERLEUKIN-6 RECEPTOR BETA CHAIN PRECURSOR (IL-6R-BETA) (INTERLEUKIN 6 SIGNAL TRANSDUCER) (MEMBRANE GLYCOPROTEIN 130) (GP130) (ONCOSTATIN M RECEPTOR) (CDW130) (CD130 ANTIGEN).				
GN	IL6ST.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]	SEQUENCE FROM N.A. (ISOFORM 1).			
RP	TISSUE=Myeloma, and Placenta;				
RC	MEDLINE=91084844; PubMed=2261637;				
RA	Hibi M., Murakami M., Saito M., Hirano T., Taga T., Kishimoto T.;				
RT	"Molecular cloning and expression of an IL-6 signal transducer, gp130".				
RL	Cell 63:1149-1157(1990).				
RN	[2]	SEQUENCE FROM N.A. (ISOFORM 2).			
RP	TISSUE=Synovium;				
RC	PubMed=10880057;				
RX	Tanaka M., Kishimura M., Ozaki S., Osakada F., Hashimoto H., Okubo M., Murakami M., Nakao K.;				
RA	"Cloning of novel soluble gp130 and detection of its neutralizing autoantibodies in rheumatoid arthritis."				
RT	J. Clin. Invest. 106:137-144(2000).				
RL	[3]	PARTIAL SEQUENCE, DISULFIDE BONDS, AND CARBOHYDRATE-LINKAGE SITES. PubMed=11098061;			
RX	Moritz R.L., Hall N.E., Connolly L.M., Simpson R.J.;				
RA	"Determination of the disulfide structure and N-glycosylation sites of the extracellular domain of the human signal transducer gp130."				
RT	J. Biol. Chem. 276:8244-8253(2001).				
RL	[4]	X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 122-325. MEDLINE=98169383; PubMed=9501088;			
RX	Bravo J., Staunton D., Heath J.K., Jones E.Y.;				
RA	"Crystal structure of a cytokine-binding region of gp130."				
RT	EMBO J. 17:1665-1674(1998).				
RL	EMBO J. 17:1665-1674(1998).				
CC	-1- FUNCTION: SIGNAL-TRANSDUCING MOLECULE. THE RECEPTOR SYSTEMS FOR IL-6, ILF, OSM, CNTF, IL-11 AND CT-1 CAN UTILIZE GP130 FOR INITIATING SIGNAL TRANSMISSION. BINDS TO IL-6/IL-6-R (ALPHA CHAIN) COMPLEX, RESULTING IN THE FORMATION OF HIGH-AFFINITY IL-6 BINDING SITES, AND TRANSDUCES THE SIGNAL. DOES NOT BIND IL-6. MAY HAVE A ROLE IN EMBRYONIC DEVELOPMENT (BY SIMILARITY).				
CC	-1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.				
CC	-1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (ISOFORM 1) AND SECRETED (ISOFORM 2).				
CC	-1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 (SHOWN HERE) AND 2/GP130-RAPS; ARE PRODUCED BY ALTERNATIVE SPLICING.				

34	46	31.7	2715	1	G156_PAPPR	P13837 paramacium
35	45.5	31.4	504	1	IRF5_HUMAN	Q13568 homo sapien
36	45	31.0	214	1	IPR_ORYSA	O22537 oryza sativ
37	45	31.0	390	1	VGIL_HSV1	P06487 herpes simp
38	45	31.0	487	1	HR3_DROME	P31396 drosophila
39	45	31.0	630	1	PRUR_ORENI	O91313 oreochromis
40	45	31.0	761	1	METE_VIBCH	O9krd8 vibrio chol
41	45	31.0	2715	1	TRX2_HUMAN	O9unm6 homo sapien
42	44	30.3	142	1	GLB1_LUMTE	P08924 lumbricus t
43	44	30.3	258	1	VSP3_TRICE	Q9dfe6 timaresuru
44	44	30.3	400	1	GMCR_HUMAN	P15509 homo sapien
45	44	30.3	459	1	CBIA_SALTY	P29946 salmonella

CC -1- TISSUE SPECIFICITY: FOUND IN ALL THE TISSUES AND CELL LINES
CC EXAMINED. EXPRESSION NOT RESTRICTED TO IL-6 RESPONSIVE CELLS.
CC -1- DISEASE: GP130-RAPS IS AN AUTOANTIGEN FOUND IN RHEUMATOID
CC ARTHRITIS (RA) BUT IT IS NOT SPECIFIC TO PATIENTS WITH RA.
CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC -1- SIMILARITY: CONTAINS 5 FIBRONECTIN TYPE-III-LIKE DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -1- DATABASE: NAME-PROV; NOTE-CD guide CD130 entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd130.htm".
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: M57230; AAA59155.1; -.
CC EMBL: AB015706; BAA78112.1; -.
CC PIR: A36337; A36337.
CC PDB: 1BOU; 26-AUG-98.
CC MIM: 600694; -.
CC DR InterPro: IPR002996; CRA1.
CC DR InterPro: IPR001777; FN_III.
CC DR InterPro: IPR003529; Hematopo_receptor_L_F2.
CC DR Pfam: PF00041; fn3; 3.
CC DR PRINTS: PR00014; FNTYPEIII.
CC DR SMART: SM00060; FN3; 3.
CC DR PROSITE: PS01353; HEMATOPO_REC_L_F2; 1.
CC KW Receptor; Transmembrane; Glycoprotein; Immunoglobulin domain; Signal;
KW Repeat; 3d-structure; Alternative splicing.
FT SIGNAL 1 22
FT DOMAIN 23 918 INTERLEUKIN-6 RECEPTOR BETA CHAIN.
FT TRANSSEM 23 641 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 642 918 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 26 120 IG-LIKE C2-TYPE DOMAIN.
FT DOMAIN 124 222 FIBRONECTIN TYPE-III 1.
FT DOMAIN 323 324 FIBRONECTIN TYPE-III 2.
FT DOMAIN 423 423 FIBRONECTIN TYPE-III 3.
FT DOMAIN 424 517 FIBRONECTIN TYPE-III 4.
FT DOMAIN 518 613 FIBRONECTIN TYPE-III 5.
FT DOMAIN 725 753 SER-RICH.
FT DISULFID 28 54
FT DISULFID 48 103
FT DISULFID 134 144
FT DISULFID 172 182
FT DISULFID 458 466
FT CARBOHYD 43 43 N-LINKED (GLCNAC. . .).
FT CARBOHYD 83 83 N-LINKED (GLCNAC. . .).
FT CARBOHYD 131 131 N-LINKED (GLCNAC. . .).
FT CARBOHYD 157 157 N-LINKED (GLCNAC. . .).
FT CARBOHYD 227 227 N-LINKED (GLCNAC. . .).
FT CARBOHYD 379 379 N-LINKED (GLCNAC. . .).
FT CARBOHYD 383 383 N-LINKED (GLCNAC. . .).
FT CARBOHYD 553 553 N-LINKED (GLCNAC. . .).
FT CARBOHYD 564 564 N-LINKED (GLCNAC. . .).
FT VPSPLIC 325 329 RPSKA -> NIASF (IN GP130-RAPS).
FT VARSPLIC 330 918
FT SEQUENCE 918 AA; 103522 MW; D813F3672DD10D53 CRC64;
Query Match 100.0%; Score 145; DB 1; Length 918;
Best Local Similarity 100.0%; Pred. No. 4, 7e-14;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

IL6B_MOUSE
ID IL6B_MOUSE STANDARD: PRT; 917 AA.
AC Q00560;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE INTERLEUKIN-6 RECEPTOR BETA CHAIN PRECURSOR (IL-6R-BETA) (INTERLEUKIN
DE 6 SIGNAL TRANSDUCER) (MEMBRANE GLYCOPROTEIN 130) (GP130).
GN IL6ST.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ICR; TISSUE=Macrophage;
RX MEDLINE=92291532; PubMed=1602143;
RA Saito M., Yoshida K., Hibi M., Taga T., Kishimoto T.;
RT Molecular cloning of a murine il-6 receptor-associated signal
RT transducer, gp130, and its regulated expression in vivo. *;
RL J. Immunol. 148:4066-4071(1992).
CC -1- FUNCTION: SIGNAL-TRANSDUCING MOLECULE. THE RECEPTOR SYSTEMS FOR
CC IL-6, LIF, OSM, CNTF, AND IL-11 CAN UTILIZE GP130 FOR INITIATING
CC SIGNAL TRANSMISSION. BINDS TO IL-6/IL-6-R (ALPHA CHAIN) COMPLEX,
CC RESULTING IN THE FORMATION OF HIGH-AFFINITY IL-6 BINDING SITES.
CC AND TRANSDUCES THE SIGNAL. DOES NOT BIND IL-6. MAY HAVE A ROLE IN
CC EMBRYONIC DEVELOPMENT.
CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: FOUND IN TISSUES SUCH AS BRAIN, HEART, THYMUS,
CC SPLEEN, KIDNEY, LUNG AND LIVER. FOUND IN ALL THE CELL LINES TESTED
CC EXCEPT BAF-B03. EXPRESSION NOT RESTRICTED TO IL-6-RESPONSIVE
CC CELLS.
CC -1- DEVELOPMENTAL STAGE: IN EMBRYONIC STEM CELLS IT IS FOUND FROM DAY
CC 6 OF GESTATION. IT REACHES A PEAK ON DAY 8 AND GRADUALLY DECLINES
CC DURING THE REST OF EMBRYOGENESIS.
CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC -1- SIMILARITY: CONTAINS 5 FIBRONECTIN TYPE-III-LIKE DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: X62646; CAA44515.1; -.
CC EMBL: M83336; AAA37723.1; -.
CC HSSP: P40189; 1BOU.
CC MCD: MGI:96560; 1l6st.
CC DR InterPro: IPR002996; CRA1.
CC DR InterPro: IPR001777; FN_III.
CC DR InterPro: IPR003529; Hematopo_receptor_L_F2.
CC DR Pfam: PF00041; fn3; 4.
CC DR PRINTS: PR00014; FNTYPEIII.
CC DR SMART: SM00060; FN3; 2.
CC DR PROSITE: PS01353; HEMATOPO_REC_L_F2; 1.
CC KW Receptor; Transmembrane; Glycoprotein; Immunoglobulin domain; Signal;
KW Repeat.
FT SIGNAL 1 22
FT CHAIN 23 917 INTERLEUKIN-6 RECEPTOR BETA CHAIN.
FT DOMAIN 23 617 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 618 639
FT DOMAIN 640 917 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 26 120 IG-LIKE C2-TYPE DOMAIN.
FT DOMAIN 124 220 FIBRONECTIN TYPE-III 1.
FT DOMAIN 321 322 FIBRONECTIN TYPE-III 2.
FT DOMAIN 421 420 FIBRONECTIN TYPE-III 3.
FT DOMAIN 422 515 FIBRONECTIN TYPE-III 4.
FT DOMAIN 516 611 FIBRONECTIN TYPE-III 5.
FT DOMAIN 723 741 SER-RICH.

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FT DISULFID 28 54 BY SIMILARITY.
FT DISULFID 48 103 BY SIMILARITY.
FT DISULFID 134 144 BY SIMILARITY.
FT DISULFID 172 180 BY SIMILARITY.
FT DISULFID 456 464 BY SIMILARITY.
FT CARBOHYD 43 43 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 61 61 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 83 83 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 131 131 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 157 157 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 225 225 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 388 388 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 476 476 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 551 551 N-LINKED (GLCNAC. . .) (POTENTIAL).
SO SEQUENCE 917 AA; 102452 MW; FCFPD220BC2466F4 CRC64;

Query Match 75.9%; Score 110; DB 1; Length 917;
Best Local Similarity 72.0%; Pred. No. 8.5e-09;
Matches 18; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 1 PEKPNLSCTVNEGKMKCEMDGCR 25
DB 126 PDKPTNLSCTVNEGKMKCEMDGCR 150

RESULT 3
IL6B_RAT 3 STANDARD; PRT: 918 AA.
AC P40190;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE INTERLEUKIN-6 RECEPTOR BETA CHAIN PRECURSOR (IL-6R-BETA) (INTERLEUKIN
DE 6 SIGNAL TRANSDUCER) (MEMBRANE GLYCOPROTEIN 130) (GP130).
GN IL6ST.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Rattus.
OX NCBI_Taxid=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=93052397; PubMed=1427893;
RA Wang Y., Nesbitt J.E., Fuentes N.L., Fuller G.M.;
RT "Molecular cloning and characterization of the rat liver IL-6 signal
RT transducing molecule, gp130."
RL Genomics 14:666-672(1992).
CC -1- FUNCTION: SIGNAL-TRANSDUCING MOLECULE. THE RECEPTOR SYSTEMS FOR
CC IL-6, LIF, OSM, CNTP, AND IL-11 CAN UTILIZE GP130 FOR INITIATING
CC SIGNAL TRANSMISSION. BINDS TO IL-6/IL-6R (ALPHA CHAIN) COMPLEX,
CC RESULTING IN THE FORMATION OF HIGH-AFFINITY IL-6 BINDING SITES,
CC AND TRANSDUCES THE SIGNAL. DOES NOT BIND IL-6. MAY HAVE A ROLE IN
CC EMBRYONIC DEVELOPMENT (BY SIMILARITY).
CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: FOUND IN HEPATOCYTES, ASTROCYTES, FIBROBLASTS
CC AND ENDOTHELIAL CELLS.
CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC -1- SIMILARITY: CONTAINS 5 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC .....
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CC or send an email to license@isb-sib.ch).
CC .....
CC EMBL; M92340; ?; NOT_ANNOTATED_CDS.
CC PIR; A44257; A44257.
CC HSSP; P40189; 1BQU.

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DR InterPro; IPR002996; CRIA.
DR InterPro; IPR001777; FN_IL1L.
DR InterPro; IPR003529; Hematopo_receptor_L_F2.
DR Pfam; PF00041; fn3; 3.
DR SMART; SM00060; FN3; 3.
DR PROSITE; PS01353; HEMATOPO_REC_L_F2; 1.
KW Receptor; Transmembrane; Glycoprotein; Immunoglobulin domain; Signal;
KW Repeat.
FT SIGNAL 1 22
FT CHAIN 23 918
FT DOMAIN 23 618
FT TRANSMEM 619 640
FT DOMAIN 641 918
FT DOMAIN 26 120
FT DOMAIN 124 221
FT DOMAIN 222 323
FT DOMAIN 324 422
FT DOMAIN 423 516
FT DOMAIN 517 612
FT DOMAIN 724 754
FT DISULFID 28 54
FT DISULFID 48 103
FT DISULFID 134 144
FT DISULFID 172 181
FT DISULFID 457 465
FT CARBOHYD 43 43
FT CARBOHYD 61 61
FT CARBOHYD 83 83
FT CARBOHYD 131 131
FT CARBOHYD 157 157
FT CARBOHYD 205 205
FT CARBOHYD 226 226
FT CARBOHYD 382 382
FT CARBOHYD 389 389
FT CARBOHYD 477 477
FT CARBOHYD 552 552
SO SEQUENCE 918 AA; 102450 MW; 9E18B6ECEF087F7 CRC64;

Query Match 63.4%; Score 92; DB 1; Length 918;
Best Local Similarity 68.0%; Pred. No. 4.3e-06;
Matches 17; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

OY 1 PEKPNLSCTVNEGKMKCEMDGCR 25
DB 126 PDKPTNLSCTVNEGKMKCEMDGCR 150

RESULT 4
IL12S_HUMAN 4 STANDARD; PRT: 862 AA.
AC Q99665;
DT 20-AUG-2001 (Rel. 40, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE INTERLEUKIN-12 RECEPTOR BETA-2 CHAIN PRECURSOR (IL-12 RECEPTOR BETA-
DE 2) (IL-12R-BETA2).
GN IL12RB2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=97098510; PubMed=8943050;
RX Presek D.H., Yang H., Minetti L.J., Chua A.O., Nabavi N., Wu C.-Y.,
RA Gately M.K., Gubler U.;
RT "A functional interleukin-12 receptor complex is composed of two
RT beta-type cytokine receptor subunits."
RL Proc. Natl. Acad. Sci. U.S.A. 93:14002-14007(1996).
CC -1- FUNCTION: INVOLVED IN IL-12 TRANSDUCTION. BINDS TO IL-12 WITH A
CC LOW AFFINITY.
CC -1- SUBUNIT: DIMER/OLIGOMER. DISULFIDE-LINKED. THE FUNCTIONAL HIGH

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CC AFFINITY IL-12 RECEPTOR IS COMPOSED OF AT LEAST IL12RB1 AND
CC IL12RB2.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
CC -1- SIMILARITY: CONTAINS 3 FIBRONECTIN TYPE III-LIKE DOMAINS.

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CC EMBL: U64198; AAB36675.1; -
CC HSSP: P40189; 1BQV.
CC MIM: 601642; -
DR InterPro: IPR002996; CRLA.
DR InterPro: IPR001777; FN.III.
DR InterPro: IPR003529; Hematopo_receptor_L_F2.
DR Pfam: PF00041; FN3; 3.
DR SMART: SM00060; FN3; 3.
DR PROSITE: PS01353; HEMATOPO_REC_L_F2; 1.
KM Receptor; Transmembrane; Glycoprotein; Signal; Repeat.
FT SIGNAL 1 21
FT CHAIN 1 21
FT DOMAIN 22 624
FT TRANSSEM 625 641
FT DOMAIN 642 862
FT DOMAIN 224 306
FT DOMAIN 421 508
FT DOMAIN 519 607
FT CARBOHYD 48 48
FT CARBOHYD 129 129
FT CARBOHYD 166 166
FT CARBOHYD 195 195
FT CARBOHYD 271 271
FT CARBOHYD 347 347
FT CARBOHYD 376 376
FT CARBOHYD 480 480
SQ SEQUENCE 862 AA; 97134 MW; 67C0E0D946B8D58 CRC64;

Query Match 45.2%; Score 65.5; DB 1; Length 862;
Best Local Similarity 50.0%; Pred. No. 0.039;
Matches 13; Conservative 4; Mismatches 8; Indels 1; Gaps 1;

OY 1 PEKPNLSCI-VNEGKKRCMDGR 25
DB 124 PEOPNLSCIOGEGYACTWGR 149

RESULT 5
ID 1125_MOUSE STANDARD: PRT: 874 AA.
AC P97378;
DT 20-AUG-2001 (Rel. 40, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE INTERLEUKIN-12 RECEPTOR BETA-2 CHAIN PRECURSOR (IL-12 RECEPTOR BETA-
DE 2) (IL-12R-BETA).
GN IL12RB2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97098510; Pubmed=8943050;
RA Presky D.H., Yang H., Minetti L.J., Chua A.O., Nabavi N., Wu C.-Y.,
RT Gately M.K., Gubler U.;
RT "A functional interleukin 12 receptor complex is composed of two
RT beta-type cytokine receptor subunits.";

RL Proc. Natl. Acad. Sci. U.S.A. 93:14002-14007(1996).
CC -1- FUNCTION: INVOLVED IN IL-12 TRANSDUCTION. BINDS TO IL-12 WITH A
CC LOW AFFINITY.
CC -1- SUBUNIT: DISULFIDE-LINKED HOMODIMER/OLIGOMER. THE FUNCTIONAL HIGH
CC AFFINITY IL-12 RECEPTOR IS COMPOSED OF AT LEAST IL12RB1 AND
CC IL12RB2.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
CC -1- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.

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CC EMBL: U64199; AAB36676.1; -
CC HSSP: P40189; 1BQV.
CC MCD: MGI:1270861; IL12RB2.
DR InterPro: IPR002996; CRLA.
DR InterPro: IPR001777; FN.III.
DR InterPro: IPR003529; Hematopo_receptor_L_F2.
DR Pfam: PF00041; FN3; 4.
DR PRINTS: PR00014; FNTYPEIIT.
DR SMART: SM00060; FN3; 3.
DR PROSITE: PS01353; HEMATOPO_REC_L_F2; 1.
KM Receptor; Transmembrane; Glycoprotein; Signal; Repeat.
FT SIGNAL 1 20
FT CHAIN 1 20
FT DOMAIN 21 639
FT DOMAIN 640 874
FT TRANSSEM 657 874
FT DOMAIN 137 230
FT DOMAIN 240 322
FT DOMAIN 436 523
FT DOMAIN 534 622
FT CARBOHYD 48 48
FT CARBOHYD 101 101
FT CARBOHYD 114 114
FT CARBOHYD 142 142
FT CARBOHYD 151 151
FT CARBOHYD 169 169
FT CARBOHYD 179 179
FT CARBOHYD 224 224
FT CARBOHYD 252 252
FT CARBOHYD 279 279
FT CARBOHYD 287 287
FT CARBOHYD 323 323
FT CARBOHYD 391 391
FT CARBOHYD 495 495
SQ SEQUENCE 874 AA; 98196 MW; 582E4D21BFBD67 CRC64;

Query Match 43.8%; Score 63.5; DB 1; Length 874;
Best Local Similarity 44.4%; Pred. No. 0.079;
Matches 12; Conservative 6; Mismatches 6; Indels 3; Gaps 2;

OY 1 PEKPNLSCIYNEGKK-MRCMDGR 25
DB 137 PEOPNLSC-VQEGNGTVACSWNSGK 162

RESULT 6
ID LIFR_MOUSE STANDARD: PRT: 1092 AA.
AC P42703;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE LEUKEMIA INHIBITORY FACTOR RECEPTOR PRECURSOR (LIF-R) (D-FACTOR/LIF
DE RECEPTOR).

FT CARBOHYD 112 112 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 132 132 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 303 303 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 315 315 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 335 335 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 831 AA; 94102 MW; 1C4E75791DCADBE9 CRC64;

Query Match 33.8%; Score 49; DB 1; Length 831;
 Best Local Similarity 39.3%; Pred. No. 11;

Matches 11; Conservative 2; Mismatches 11; Indels 4; Gaps 1;

OY 1 PEKPNLSCTVNEGKRCM-----DGG 24
 DB 231 PEKPNLSCTVNEGKRCM-----DGG 258

RESULT 12

EPIT_STAP STANDARD; PRT; 986 AA.
 AC P30195;
 DT 01-APR-1993 (rel. 25, Created)
 DT 01-APR-1993 (rel. 25, Last sequence update)
 DT 20-AUG-2001 (rel. 40, Last annotation update)
 DE EPIDERMIN BIOSYNTHESIS PROTEIN EPIT.
 GN EPIT.
 OS Staphylococcus epidermidis.
 OG Plasmid ptn 32.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group;
 OC Bacillus/Staphylococcus group; Staphylococcus.
 OX NCBI_TaxID=1282;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=TV 3298 / DSM 3095;
 RX MEDLINE=92155237; PubMed=1740156;
 RA Schnell N., Engelke G., Augustin J., Rosenstein R., Ungermann V.,
 RA Goetz F., Entian K.-D.;
 RT Analysis of genes involved in the biosynthesis of lanthibiotic
 RT epidermin.";
 RL Eur. J. Biochem. 204:57-68(1992).
 CC -1- FUNCTION: INVOLVED IN THE POSTTRANSLATIONAL MODIFICATION OF THE
 CC LANTHIBIOTIC EPIDERMIN.
 CC -1- SUBCELLULAR LOCATION: POSSIBLY ASSOCIATED WITH, AND ANCHORED TO,
 CC THE CYTOPLASMIC SIDE OF THE MEMBRANE.
 CC -1- SIMILARITY: TO B.SUBTILIS SPAB AND L.LACTIS NISB.
 CC -----
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 CC -----
 CC EMBL; X62386; CAA44253.1; -.
 KW Plasmid.
 DR EMBL; X62386; CAA44253.1; -.
 SQ SEQUENCE 986 AA; 116708 MW; 343CE98526847850 CRC64;

Query Match 33.8%; Score 49; DB 1; Length 986;
 Best Local Similarity 47.8%; Pred. No. 13;

Matches 11; Conservative 2; Mismatches 10; Indels 0; Gaps 0;

OY 1 PEKPNLSCTVNEGKRCM-----DGG 23
 DB 962 PEKPNLSCTVNEGKRCM-----DGG 984

RESULT 13
 TRPG_BUCAP STANDARD; PRT; 196 AA.
 ID TRPG_BUCAP
 AC P42388;

DT 01-NOV-1995 (rel. 32, Created)
 DT 01-NOV-1995 (rel. 32, Last sequence update)
 DT 30-MAY-2000 (rel. 39, Last annotation update)
 DE ANTHRANILATE SYNTHASE COMPONENT II (EC 4.1.3.27) (GLUTAMINE AMIDO-
 DE TRANSFERASE).
 GN TRPG.
 OS Buchnera aphidicola (subsp. Schizaphis graminum).
 OC Bacteria; Proteobacteria; gamma subdivision; Buchnera.

NCBI_TaxID=98794;

RP SEQUENCE FROM N.A.

RX MEDLINE=94224833; PubMed=8170994;

RA Lai C.-Y., Baumann L., Baumann P.;

RT Amplification of trpg: adaptation of Buchnera aphidicola to an

RT endosymbiotic association with aphids.";

RL Proc. Natl. Acad. Sci. U.S.A. 91:3819-3823(1994).

CC -1- CATALYTIC ACTIVITY: CHORISMATE + L-GLUTAMINE = ANTHRANILATE +
 CC PYRUVATE + L-GLUTAMATE.

CC -1- PATHWAY: FIRST STEP IN BIOSYNTHESIS OF TRYPTOPHAN.

CC -1- SUBUNIT: TETRAMER OF TWO COMPONENTS I AND TWO COMPONENTS II.

CC -1- MISCELLANEOUS: COMPONENT I CATALYZES THE FORMATION OF ANTHRANILATE
 CC USING AMMONIA RATHER THAN GLUTAMINE, WHEREAS COMPONENT II PROVIDES
 CC GLUTAMINE AMIDOTRANSFERASE ACTIVITY.

CC -1- SIMILARITY: TO OTHER TYPE-1 GLUTAMINE AMIDOTRANSFERASE DOMAINS.

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 CC -----

DR EMBL; Z21938; CAA79932.1; -.
 DR InterPro: IPR002385; Antc_synthI.
 DR InterPro: IPR000991; GATase_1.
 DR Pfam: PF00117; GATase_1.
 DR PRINTS: PR00096; GATASE.
 DR PRINTS: PR00097; ANTSYNTHASEII.
 DR PROSITE: PS00442; GATASE_TYPE_I.1.
 KW tryptophan biosynthesis; lysase; glutamine amidotransferase.
 FT ACT_SITE 84 BY SIMILARITY.
 FT ACT_SITE 170 BY SIMILARITY.
 FT ACT_SITE 172 BY SIMILARITY.
 SQ SEQUENCE 196 AA; 21866 MW; 2FB23F9DAB441F3E CRC64;

Query Match 33.1%; Score 48; DB 1; Length 196;
 Best Local Similarity 45.0%; Pred. No. 3.9;
 Matches 9; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

OY 1 PEKPNLSCTVNEGKRCM-----DGG 20
 DB 58 PEKPNLSCTVNEGKRCM-----DGG 77

RESULT 14

DAP3_HUMAN STANDARD; PRT; 398 AA.
 ID DAP3_HUMAN
 AC P51398;
 DT 01-OCT-1996 (rel. 34, Created)
 DT 01-OCT-1996 (rel. 34, Last sequence update)
 DT 20-AUG-2001 (rel. 40, Last annotation update)
 DE MITOCHONDRIAL 28S RIBOSOMAL PROTEIN S29 (MRP-S29) (DEATH-ASSOCIATED
 DE PROTEIN 3) (DAP-3).
 GN DAP3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96070931; PubMed=7499268;

RA Kimsil J.L., Deiss L.P., Bayewitch M., Ravesh T., Khaspekov G.,
RA Kimchi A.;
RT *Isolation of DAP3, a novel mediator of interferon-gamma-induced cell
RT death.";
RL J. Biol. Chem. 270:27932-27936(1995).
RN [2]
RP IDENTIFICATION.
RA Koc E.C., Burkhardt W., Blackburn K., Koc H., Moseley A.,
RA Spremull L.L.;
RT "A proteomic approach to the identification of mammalian
RT mitochondrial small subunit ribosomal proteins.";
RL Submitted (DEC-2000) to the SWISS-PROT data bank.
CC -I- FUNCTION: INVOLVED IN MEDIATING INTERFERON-GAMMA-INDUCED CELL
CC DEATH.
CC -I- SUBCELLULAR LOCATION: MITOCHONDRIAL.
CC -I- TISSUE SPECIFICITY: DBIDUTIONS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X83544; CAA58535.1; .
DR MIM: 602074; .
KW Apoptosis; ATP-Binding; Ribosomal protein; Mitochondrion.
FT NP_BIND 128 135 ATP (POTENTIAL).
SQ SEQUENCE 398 AA; 4556 MW; 778AF183FA04DEC8 CRC64;

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: December 19, 2001, 16:25:23 ; Search time 157.32 Seconds
(without alignments)
23.244 Million cell updates/sec

Title: US-09-202-104A-7
Perfect score: 145
Sequence: 1 PEKPKNLSCTVNEGKKRCEWDGGR 25

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 473505 seqs, 146272329 residues
Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: SP:archaea:*
2: SP:bacteria:*
3: SP:fungi:*
4: SP:human:*
5: SP_invertebrate:*
6: SP_mammal:*
7: SP_mhc:*
8: SP_organelle:*
9: SP_phage:*
10: SP_plant:*
11: SP_rodent:*
12: SP_virus:*
13: SP_vertebrate:*
14: SP_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	145	100.0	329	4	Q9U041	Q9u041 homo sapien
2	81	55.9	918	13	Q9W6U9	Q9w6u9 gallus galli
3	78	53.8	881	13	Q57519	Q57519 xenopus lae
4	64.5	44.5	861	6	Q9BEG2	Q9begt bos taurus
5	64	44.1	970	11	Q88821	Q88821 mus musculus
6	64	44.1	971	11	Q70458	Q70458 mus musculus
7	63	43.4	422	4	Q75462	Q75462 homo sapien
8	63	43.4	422	4	Q9U0H5	Q9uhh5 homo sapien
9	63	43.4	422	4	Q9G6U9	Q9g6u9 homo sapien
10	62	42.8	425	11	Q9U0M58	Q9um58 mus musculus
11	62	42.8	1093	11	Q70535	Q70535 rattus norv
12	57	39.3	463	6	Q9GMB5	Q9gmb5 bos indicus
13	54	37.2	465	6	Q9GMB1	Q9gmb1 syncerus ca
14	54	37.2	1639	3	Q9P707	Q9p7q7 schizosacch
15	53	36.6	1015	11	Q9D4G5	Q9d4g5 mus musculus
16	51	35.2	453	6	Q9GMB6	Q9gmb6 bos indicus
17	51	35.2	461	6	Q9GMB4	Q9gmb4 bos taurus
18	51	35.2	638	13	Q9DE08	Q9de08 oncorhynch
19	50	34.5	381	10	Q9L7W6	Q9l7w6 arabidopsis

20	50	34.5	890	11 Q921A0	Q921A0 cavia porce
21	50	34.5	2478	13 Q93406	Q93406 brachydanio
22	49	33.8	638	5 Q9YU08	Q9YU08 drosophila
23	49	33.8	2302	11 Q88488	Q88488 rattus norv
24	49	33.8	2395	5 Q27167	Q27167 paramacium
25	48.5	33.4	952	4 Q9NSN1	Q9NSN1 homo sapien
26	48.5	33.4	1253	4 Q9UN29	Q9UN29 homo sapien
27	48.5	33.4	1253	4 Q9UN29	Q9UN29 homo sapien
28	48.5	33.4	1281	4 Q9ULQ2	Q9ULQ2 homo sapien
29	48.5	33.4	2212	5 Q94657	Q94657 plasmodium
30	48.5	33.4	2647	5 P90580	P90580 plasmodium
31	48	33.1	250	5 Q9TYP7	Q9TYP7 caenorhabdi
32	48	33.1	382	4 Q13044	Q13044 homo sapien
33	48	33.1	478	13 Q98T93	Q98T93 xenopus lae
34	48	33.1	581	6 Q46561	Q46561 ovis aries
35	48	33.1	638	13 Q42372	Q42372 brachydanio
36	48	33.1	684	13 Q90544	Q90544 ginglymosto
37	48	33.1	896	11 Q64146	Q64146 rattus norv
38	48	33.1	1757	11 Q70481	Q70481 mus musculus
39	47.5	32.8	470	5 Q05351	Q05351 entamoeba h
40	47.5	32.8	528	10 Q9LW16	Q9LW16 oryza sativ
41	47	32.4	290	5 Q24111	Q24111 drosophila
42	47	32.4	296	6 Q18880	Q18880 bos taurus
43	47	32.4	347	5 P91779	P91779 polyandroca
44	47	32.4	410	5 Q9N374	Q9N374 caenorhabdi
45	47	32.4	434	5 P91780	P91780 polyandroca

ALIGNMENTS

```

RESULT 1
ID Q9U041 PRELIMINARY; PRT; 329 AA.
AC Q9U041;
DT 01-MAY-2000 (TREMBLrel, 13, Created)
DT 01-MAY-2000 (TREMBLrel, 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel, 17, Last annotation update)
DE GP130 OF THE RHEUMATOID ARTHRITIS ANTIGENIC PEPTIDE-BEARING SOLUBLE
DE FORM (GP130-RAPS).
GN GP130.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=SYNOVIAL;
RA Tanaka M., Kishimura M., Ozaki S., Hashimoto H., Osakada F., Okubo M.,
RA Morakami M., Nakao K.;
RT "Cloning of novel soluble gp130 and detection of its neutralizing
RT autoantibodies in rheumatoid arthritis.";
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB015706; BAA78112.1; -
DR HSSP; P40189; 1BOU.
DR InterPro; IPR002996; CRIA.
DR InterPro; IPR003962; FNIII_repeat.
DR InterPro; IPR003961; FN_III.
DR Pfam; PF00041; fn3; 1.
DR PRINTS; PR00014; FNTYPEIII.
DR SMART; SM00060; FN3; 1.
KW Repeat.
SQ
SEQUENCE 329 AA; 37484 MW; D9776576E34FC596 CRC64;

```

Query Match 100.0%; Score 145; DB 4; Length 329;
Best Local Similarity 100.0%; Pred. No. 6.5e-14;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PEKPKNLSCTVNEGKKRCEWDGGR 25
DB 126 PEKPKNLSCTVNEGKKRCEWDGGR 150

```

RESULT 2
Q9M6U9 PRELIMINARY; PRT; 918 AA.
ID 09M6U9
AC 09M6U9
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE GLYCOPROTEIN 130 PRECURSOR.
GN GPI30.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_Taxid=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-EMBRYONIC HEART PRIMARY CULTURE (E7, E8);
RX MEDLINE=99026068; PubMed=9806927;
RA Geiselen M., Heller S., Pennica D., Ernberger U., Rohrer H.;
RT "The specification of sympathetic neurotransmitter phenotype depends
on gp130 cytokine receptor signaling."
RL Development 125:4791-4801(1998).
DR EMBL: AJ011688; CAB42084.1; -.
DR HSSP: P40189; 180U
DR InterPro: IPR002996; CRIA.
DR InterPro: IPR003961; FN_III.
DR InterPro: IPR003529; Hematopo_receptor_L_F2.
DR Pfam: PF00041; fn3; 4.
DR SMART: SM00060; FN3; 3.
DR PROSITE: PS01353; HEMATOPO_REC_L_F2; UNKNOWN_1.
KW Signal.
FT SIGNAL 1 26 POTENTIAL.
FT CHAIN 1 264 POTENTIAL.
SQ SEQUENCE 918 AA; 102495 MW; FE7625FE3E3613EF CRC64;

Query Match 55.9%; Score 81; DB 13; Length 918;
Best Local Similarity 58.6%; Pred. No. 0.00077;
Matches 17; Conservative 1; Mismatches 7; Indels 4; Gaps 1;

QY 1 PEKPNLSICIVNEGK---MRCEWDGR 25
|||:|||||:|:|:|
Db 129 PEKPNLSICIVLSPKVMYMCITWNGR 157

RESULT 3
057519 PRELIMINARY; PRT; 881 AA.
ID 057519
AC 057519
DT 01-JUN-1998 (TREMBlrel. 06, Created)
DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE GPI30P1.
GN XGP130.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodidae; Xenopus.
OX NCBI_Taxid=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Chen J., Grace A., Chien K.R.;
RT Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
RL EMBL: AF041845; AAC03531.1; -.
DR HSSP: P40189; 180U
DR InterPro: IPR002996; CRIA.
DR InterPro: IPR003961; FN_III.
DR InterPro: IPR003529; Hematopo_receptor_L_F2.
DR Pfam: PF00041; fn3; 4.
DR SMART: SM00060; FN3; 1.
DR PROSITE: PS01353; HEMATOPO_REC_L_F2; UNKNOWN_1.
SQ SEQUENCE 881 AA; 99003 MW; 7DE7942D211138A0 CRC64;

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Query Match 53.8%; Score 78; DB 13; Length 881;
Best Local Similarity 52.0%; Pred. No. 0.0021;
Matches 13; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 1 PEKPNLSICIVNEGKKMKRCEWDGR 25
|:|:|:|:|:|:|:|:|
Db 122 PDKPPTLCTIVYNDNLCTCTWDPGR 146

RESULT 4
Q9BEG2 PRELIMINARY; PRT; 861 AA.
ID Q9BEG2
AC Q9BEG2
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE IL-12 RECEPTOR BETA2 PRECURSOR.
GN IL-12R BETA2.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_Taxid=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-LYMPH NODE;
RA Waldvogel A.S., Zakher A., Heussler V.T.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ308426; CAC28320.1; -.
KW Signal; Receptor.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 1 24 IL-12 RECEPTOR BETA2.
FT CHAIN 1 24 861 IL-12 RECEPTOR BETA2.
SQ SEQUENCE 861 AA; 96208 MW; 4B7B1E5D1E358E5B CRC64;

Query Match 44.5%; Score 64.5; DB 6; Length 861;
Best Local Similarity 48.1%; Pred. No. 0.022;
Matches 13; Conservative 6; Mismatches 5; Indels 3; Gaps 2;

QY 1 PEKPNLSICIVNEGK---MRCEWDGR 25
|||:|||||:|:|:|
Db 124 PEKPNLSICIVNGKRGVCTWNGR 149

RESULT 5
088821 PRELIMINARY; PRT; 970 AA.
ID 088821
AC 088821
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE ONCOSTATIN M RECEPTOR BETA.
GN OSMR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Tanaka M., Hara T., Copeland N.G., Gilbert D.J., Jenkins N.A.,
RA Miyajima A.;
RT "Structure of the mouse oncostatin M (OSM) receptor: molecular cloning
of the OSM receptor beta subunit."
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB015978; BAA33725.1; -.
DR HSSP: P40189; 180U.
DR HSSP: MG1:1330819; Osmr.
DR InterPro: IPR002996; CRIA.
DR InterPro: IPR003961; FN_III.
DR InterPro: IPR003529; Hematopo_receptor_L_F2.
DR Pfam: PF00041; fn3; 3.
DR SMART: SM00060; FN3; 3.

```


DT 01-JUN-2001 (TREMBlrel. 17, last annotation update)
 DE ONCOSATIN-M SPECIFIC RECEPTOR BETA SUBUNIT.
 GN OSMB.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97115791; PubMed=8999038;
 RA Mosley B., De Imus C., Friend D., Bolani N., Thoma B., Park L.,
 RA Cosman D.;
 RL J. Biol. Chem. 271:32635-32643(1996).
 DR EMBL; U60805; AAC50946.1; -.
 DR InterPro: IPR001005; MYD_DNA_bind.
 DR InterPro: IPR002996; CRIA.
 DR InterPro: IPR003529; Hematopo_receptor_L_F2.
 DR InterPro: IPR003961; FN_III.
 DR Pfam: PF00041; fn3; 4.
 DR PROSITE: PS01353; HEMATOPO_REC_L_F2; UNKNOWN_1.
 DR PROSITE: PS00037; MYB_1; UNKNOWN_1.
 DR SMART: SM00060; FN3; 2.
 SQ SEQUENCE 979 AA; 110508 MW; 179852CA3D90D9EF CRC64;

Query Match 43.4%; Score 63; DB 4; Length 979;
 Best Local Similarity 43.5%; Pred. No. 0.42;
 Matches 10; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

OY 2 EKPKNLSCTIVEGKKMKRCMDG 24

DB 238 EEPKDFSCETDEFKTHCTWDPG 260

RESULT 10

O9JMS8 PRELIMINARY: PRT: 425 AA.

DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, last annotation update)
 DE CYTOKINE RECEPTOR LIKE MOLECULE 3 PRECURSOR.
 GN CRLF1 OR CRLF3.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Hiroyama T., Iwama A., Nakamura Y., Nakachi H.;
 RT "cytokine receptor like molecule 3."
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB040038; BAA92777.1; -.
 DR MGI:1340030; Crlf1.
 DR InterPro: IPR002996; CRIA.
 DR InterPro: IPR003961; FN_III.
 DR Pfam: PF00041; fn3; 2.
 DR SMART: SM00060; FN3; 1.
 KM Signal; Receptor.
 FT SIGNAL 1 34 POTENTIAL.
 SQ SEQUENCE 425 AA; 46662 MW; 910535C629CA7056 CRC64;

Query Match 42.8%; Score 62; DB 11; Length 425;
 Best Local Similarity 45.8%; Pred. No. 0.26;
 Matches 11; Conservative 2; Mismatches 11; Indels 0; Gaps 0;

OY 1 PEKPNLSCTIVEGKKMKRCMDG 24

DB 138 PEKPNLSCTIVEGKKMKRCMDG 161

RESULT 11

O70535 PRELIMINARY: PRT: 1093 AA.
 ID O70535;
 DT 01-AUG-1998 (TREMBlrel. 07, Created)
 DT 01-AUG-1998 (TREMBlrel. 07, last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, last annotation update)
 DE LEUKEMIA INHIBITOR FACTOR RECEPTOR ALPHA-CHAIN.
 OS Rattus norvegicus (Rat).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MISTER-ITAMICHI; TISSUE=LIVER;
 RX MEDLINE=98007878; PubMed=9349722;
 RA Aikawa J., Ikeda-Naiki S., Ohgane J., Min K.S., Imanura T., Sasai K.,
 RA Shikata K., Ogawa T.;
 RT "Molecular cloning of rat leukemia inhibitory factor receptor alpha-chain gene and its expression during pregnancy."
 RL Biochim. Biophys. Acta 1353:265-276(1997).
 DR EMBL; D86345; BAA25907.1; -.
 DR HSSP; P40189; IBQU.
 DR InterPro: IPR002996; CRIA.
 DR InterPro: IPR003961; FN_III.
 DR InterPro: IPR003529; Hematopo_receptor_L_F2.
 DR Pfam: PF00041; fn3; 4.
 DR SMART: SM00060; FN3; 3.
 DR PROSITE: PS01353; HEMATOPO_REC_L_F2; UNKNOWN_1.
 SQ SEQUENCE 1093 AA; 122393 MW; 08D43DEAF8F5E3F6 CRC64;

Query Match 42.8%; Score 62; DB 11; Length 1093;
 Best Local Similarity 40.0%; Pred. No. 0.66;
 Matches 10; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

OY 1 PEKPNLSCTIVEGKKMKRCMDG 25

DB 329 PDVPOKLSCTETHDEKETICSNMPCR 353

RESULT 12

O9GMB5 PRELIMINARY: PRT: 463 AA.

DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, last annotation update)
 DE MEMBRANE TYROSINE PHOSPHATASE (FRAGMENT).
 GN CD45.
 OS Bos indicus (Zebu).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 CC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9915;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BOBAN; TISSUE=PERIPHERAL BLOOD;
 RA Bailligall K.T.;
 RT "The CD45 locus in cattle: allelic polymorphism and evidence for.
 RT exceptional positive natural selection."
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ400866; CAC05416.1; -.
 DR InterPro: IPR003961; FN_III.
 DR Pfam: PF00041; fn3; 2.
 DR SMART: SM00060; FN3; 2.
 FT NON-TER 463
 SQ SEQUENCE 463 AA; 52236 MW; EABF7F83F387596F CRC64;

Query Match 39.3%; Score 57; DB 6; Length 463;
 Best Local Similarity 38.1%; Pred. No. 1.6;
 Matches 8; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

```

OY      1 PEKPNLSCTVNEGKKRCEM 21
      |||||
Db      231 PEARONFTCSAKNGTSGCTW 251

RESULT  13
O9GMB1  PRELIMINARY;      PRT;      465 AA.
AC      09GMB1;
DT      01-MAR-2001 (TREMBlrel. 16, Created)
DT      01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT      01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE      MEMBRANE TYROSINE PHOSPHATASE (FRAGMENT).
GN      CD45.
OS      Syncerus caffer (cape buffalo).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC      Bovidae; Bovinae; Syncerus.
OX      NCBI_TaxID=9970;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=PERIPHERAL BLOOD;
RA      Ballingall K.T.;
RT      "The CD45 locus in cattle: allelic polymorphism and evidence for
RT      exceptional positive natural selection.";
RL      Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR      EMBL; AA400867; CAC05420.1;
DR      InterPro: IPR003961; FN_111.
DR      Pfam; PF00041; fn3; 2.
DR      SMART; SM00060; FN3; 3.
FT      NON_TER
SQ      SEQUENCE      465 AA; 52290 MW; 9415673F219A368A CRC64;

Query Match      37.28; Score 54; DB 6; Length 465;
Best Local Similarity 38.18; Pred. No. 4.6;
Matches 8; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

OY      1 PEKPNLSCTVNEGKKRCEM 21
      |||||
Db      233 PEARONFTCSAKNGTSGCTW 253

RESULT  14
O9P707  PRELIMINARY;      PRT;      1639 AA.
AC      09P707;
DT      01-OCT-2000 (TREMBlrel. 15, Created)
DT      01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT      01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE      PUTATIVE SENSOR TRANSDUCTION HISTIDINE KINASE.
GN      SPAC1834.08.
OS      Schizosaccharomyces pombe (fission yeast).
OC      Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC      Schizosaccharomycetales; Schizosaccharomycetaceae;
OC      Schizosaccharomyces.
OX      NCBI_TaxID=4896;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=972H-;
RA      Seeger K., Harris D., Wood V., Rajandream M.A., Barrell B.G.;
RL      Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
CC      -1- SIMILARITY: THE N-TERMINAL REGION IS SIMILAR TO THAT OF OTHER
CC      REGULATORY COMPONENTS OF SENSOR TRANSDUCTION SYSTEMS.
DR      EMBL; AL157734; CAB75776.1;
DR      InterPro: IPR000410; Bcrl_sensor.
DR      InterPro: IPR003594; HATPase_C.
DR      InterPro: IPR003661; His_kinA.
DR      InterPro: IPR001610; PAC.
DR      InterPro: IPR000014; PAS.
DR      InterPro: IPR000700; PAS-assoc_C.
DR      InterPro: IPR001789; Response_reg.
DR      Pfam; PF02518; HATPase_c; 1.

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DR      Pfam; PF00785; PAC; 1.
DR      Pfam; PF00989; PAS; 2.
DR      Pfam; PF00072; response_reg; 1.
DR      Pfam; PF00512; signal; 1.
DR      PRINTS; PR00344; BCTRLSENSOR.
DR      SMART; SM00387; HATPase_c; 1.
DR      SMART; SM00388; HSKA; 1.
DR      SMART; SM00086; PAC; 2.
DR      SMART; SM00091; PAS; 1.
DR      SMART; SM00448; REC; 1.
KW      Kinase; Phosphorylation; Sensory transduction.
SQ      SEQUENCE      1639 AA; 184578 MW; 6A653BA0F3B357B5 CRC64;

Query Match      37.28; Score 54; DB 3; Length 1639;
Best Local Similarity 45.58; Pred. No. 16;
Matches 10; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

OY      3 KPNLSCTVNEGKKRCEMDG 24
      |||||
Db      219 EPRDSDIYTPMOLRCYDGG 240

RESULT  15
O9D4G5  PRELIMINARY;      PRT;      1015 AA.
AC      09D4G5;
DT      01-JUN-2001 (TREMBlrel. 17, Created)
DT      01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT      01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE      4932434G09RIK PROTEIN.
GN      4932434G09RIK.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=C57BL/6J; TISSUE=TESTIS;
RX      MEDLINE=21085860; PubMed=11217851;
RA      Kawai T., Shingawa A., Shibata K., Yoshio M., Itoh M., Ishii Y.,
RA      Araiwa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA      Alizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,
RA      Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA      Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA      Fieischmann W., Gaasterland T., Glissl C., King B., Kochiwa H.,
RA      Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA      Schirral L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA      Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA      Blake J., Boffelli D., Bojunga N., Carrinci P., de Bonaldo M.F.,
RA      Brownstein M.J., Bull C., Fletcher C., Fujita M., Gariboldi M.,
RA      Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA      Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA      Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA      Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA      Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilmink L.,
RA      Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohzuki S.,
RA      Hayashizaki Y.;
RT      "Functional annotation of a full-length mouse cDNA collection.";
RL      Nature 409:685-690(2001).
DR      EMBL; AK016547; BAB30296.1;
DR      MGI; MGI:1914974; 4932434G09RIK.
SQ      SEQUENCE      1015 AA; 114028 MW; 964D1F9392FADF36 CRC64;

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Query Match      36.68; Score 53; DB 11; Length 1015;
Best Local Similarity 40.98; Pred. No. 14;
Matches 9; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

OY      1 PEKPNLSCTVNEGKKRCEMD 22
      |||||
Db      764 PRKPEVTGCGAQOEGCTVAMEWN 785

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Search completed: December 19, 2001, 16:25:24
Job time: 549 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: December 19, 2001, 16:21:00 ; Search time 78.52 Seconds
(without alignments)
7.165 Million cell updates/sec

Title: US-09-202-104A-7

Perfect score: 145
Sequence: 1 PEKKNLSCTVNEGKMKRCWGDGR 25

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_AA:*
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2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/PTUS.COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	145	100.0	488	2	US-08-599-455B-5
2	145	100.0	488	4	US-09-069-781B-5
3	145	100.0	572	2	US-08-419-652-5
4	145	100.0	658	2	US-08-825-558-4
5	145	100.0	708	1	US-07-797-556-2
6	145	100.0	708	1	US-08-308-881-2
7	145	100.0	708	2	US-09-058-263-2
8	145	100.0	708	2	US-09-059-099-2
9	145	100.0	708	3	US-09-058-264-2
10	145	100.0	708	5	PCT-US95-06530-2
11	145	100.0	918	2	US-08-825-558-6
12	65.5	45.2	862	2	US-08-685-118-2
13	65.5	45.2	862	2	US-08-915-495-2
14	65.5	45.2	862	2	US-08-914-520-2
15	63	43.4	303	4	US-09-071-224-21
16	63	43.4	303	4	US-09-071-224-23
17	63	43.4	385	4	US-09-071-224-20
18	63	43.4	388	4	US-09-071-224-17
19	63	43.4	389	4	US-09-071-224-22
20	63	43.4	389	4	US-09-071-224-24
21	63	43.4	389	4	US-09-071-224-25
22	63	43.4	389	4	US-09-071-224-26
23	63	43.4	389	4	US-09-071-224-27
24	63	43.4	389	4	US-09-071-224-28
25	63	43.4	389	4	US-09-071-224-29
26	63	43.4	389	4	US-09-071-224-30
27	63	43.4	389	4	US-09-071-224-31

28	63	43.4	392	4	US-09-071-224-18	Sequence 18, Appl
29	63	43.4	422	4	US-09-071-224-2	Sequence 2, Appl
30	63	43.4	425	4	US-09-071-224-4	Sequence 4, Appl
31	63	43.4	434	3	US-09-012-072-4	Sequence 4, Appl
32	63	43.4	434	4	US-09-120-601-4	Sequence 4, Appl
33	63	43.4	448	4	US-09-120-601-6	Sequence 6, Appl
34	63	43.4	979	1	US-08-308-881-6	Sequence 6, Appl
35	63	43.4	979	2	US-09-058-263-6	Sequence 6, Appl
36	63	43.4	979	2	US-09-059-099-6	Sequence 6, Appl
37	63	43.4	979	3	US-09-058-264-6	Sequence 6, Appl
38	63	43.4	979	5	PCT-US95-06530-6	Sequence 6, Appl
39	62	42.8	385	4	US-09-071-224-19	Sequence 19, Appl
40	62	42.8	405	3	US-09-012-072-2	Sequence 2, Appl
41	62	42.8	405	4	US-09-120-601-2	Sequence 2, Appl
42	62	42.8	425	4	US-09-071-224-6	Sequence 6, Appl
43	62	42.8	719	1	US-07-943-843-4	Sequence 4, Appl
44	62	42.8	719	1	US-08-347-003-4	Sequence 4, Appl
45	60	41.4	620	2	US-08-419-652-7	Sequence 7, Appl

ALIGNMENTS

RESULT 1
US-08-599-455B-5
; Sequence 5, Application US/08599455B
; Patent No. 5972621
; GENERAL INFORMATION:
; APPLICANT: Tartaglia, Louis A.
; APPLICANT: Tepper, Robert I.
; APPLICANT: Culpepper, Janice A.
; TITLE OF INVENTION: METHODS OF IDENTIFYING COMPOUNDS THAT
; TITLE OF INVENTION: MODULATE BODY WEIGHT USING THE OB RECEPTOR
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/599,455B
; FILING DATE: 22-JAN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/583,153
; FILING DATE: 28-DEC-1995
; APPLICATION NUMBER: 08/570,142
; FILING DATE: 11-DEC-1995
; APPLICATION NUMBER: 08/569,485
; FILING DATE: 08-DEC-1995
; APPLICATION NUMBER: 08/566,622
; FILING DATE: 04-DEC-1995
; APPLICATION NUMBER: 08/562,663
; FILING DATE: 27-NOV-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Melkielejohn, Ph.D., Anita L.
; REGISTRATION NUMBER: 35,283
; REFERENCE/DOCKET NUMBER: 07334/017001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 488 amino acids
; TYPE: amino acid
; TOPOLOGY: Linear

MOLECULE TYPE: protein
US-08-599-455B-5

Query Match 100.0%; Score 145; DB 2; Length 488;
Best Local Similarity 100.0%; Pred. No. 1.5e-13;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PEKPNLSCTVNEGKMKRCMDGGR 25
Db 97 PEKPNLSCTVNEGKMKRCMDGGR 121

RESULT 2

US-09-069-781B-5
Sequence 5, Application US/09069781B
Patent No. 6287782
GENERAL INFORMATION:
APPLICANT: Tartaglia, Louis A.
APPLICANT: Tepper, Robert I.
APPLICANT: Culpepper, Janice A.
APPLICANT: White, David W.
TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR
TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR
TITLE OF INVENTION: INCLUDING OBESITY AND CACHEXIA
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/069,781B
FILING DATE: 29-APRIL-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/864,564
FILING DATE: 28-MAY-1997
APPLICATION NUMBER: US 08/708,123
FILING DATE: 03-SEP-1996
APPLICATION NUMBER: US 08/638,524
FILING DATE: 26-APR-1996
APPLICATION NUMBER: US 08/599,455
FILING DATE: 22-JAN-1996
APPLICATION NUMBER: US 08/583,153
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: US 08/570,142
FILING DATE: 11-DEC-1995
APPLICATION NUMBER: US 08/569,485
FILING DATE: 08-DEC-1995
APPLICATION NUMBER: US 08/566,622
FILING DATE: 04-DEC-1995
APPLICATION NUMBER: US 08/562,663
FILING DATE: 27-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: Melkiojohn, P.D., Anita L.
REGISTRATION/DOCKET NUMBER: 35,283
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 488 amino acids
TYPE: amino acid
TOPOLOGY: unknown

MOLECULE TYPE: protein
US-09-069-781B-5

Query Match 100.0%; Score 145; DB 4; Length 488;
Best Local Similarity 100.0%; Pred. No. 1.5e-13;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PEKPNLSCTVNEGKMKRCMDGGR 25
Db 97 PEKPNLSCTVNEGKMKRCMDGGR 121

RESULT 3

US-08-419-652-5
Sequence 5, Application US/08419652
Patent No. 5831007
GENERAL INFORMATION:
APPLICANT: Chua, Anne O
APPLICANT: Gubler, Ulrich A
TITLE OF INVENTION: INTERLEUKIN-12 RECEPTOR
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
CITY: Nutley
STATE: New Jersey
COUNTRY: United States of America
ZIP: 07110-1199
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: PC compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/419,652
FILING DATE: 11-APR-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/248,532
FILING DATE: 31-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/094,713
FILING DATE: 19-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Kass, Alan P
REGISTRATION/DOCKET NUMBER: 32142
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201) 235-4205
TELEFAX: (201) 235-3500
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 572 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Region
LOCATION: 1..572
OTHER INFORMATION: /note- "Represents residues 124 to
US-08-419-652-5"

Query Match 100.0%; Score 145; DB 2; Length 572;
Best Local Similarity 100.0%; Pred. No. 1.7e-13;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PEKPNLSCTVNEGKMKRCMDGGR 25
Db 3 PEKPNLSCTVNEGKMKRCMDGGR 27

RESULT 4
US-08-825-558-4
; Sequence 4, Application US/08825558
; Patent No. 5965724
; GENERAL INFORMATION:
; APPLICANT: SHARKEY, ANDREW
; APPLICANT: SMITH, STEPHEN K.
; APPLICANT: DELLOW, KIMBERLEY A.
; TITLE OF INVENTION: GP 130 Lacking the Transmembrane Domain
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX
; STREET: 1100 NEW YORK AVENUE
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/825,558
; FILING DATE: 19-MAR-1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: ESMOND, ROBERT W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 0623, 0530001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)371-2600
; TELEFAX: (202)371-2540
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 658 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-825-558-4

Query Match 100.0%; Score 145; DB 2; Length 658;
Best Local Similarity 100.0%; Pred. No. 2e-13;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PEKPNLSCIVNGKKRMCEWDCGR 25
DB 126 PEKPNLSCIVNGKKRMCEWDCGR 150

RESULT 5
US-07-797-556-2
; Sequence 2, Application US/07797556
; Patent No. 5262522
; GENERAL INFORMATION:
; APPLICANT: Gearing, David P.
; TITLE OF INVENTION: Receptor for Oncostatin M and Leukemia
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/797,556
; FILING DATE: 19911122
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Seese, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2607
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-587-0430
; TELEFAX: 206-587-0606
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 708 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-797-556-2

Query Match 100.0%; Score 145; DB 1; Length 708;
Best Local Similarity 100.0%; Pred. No. 2.2e-13;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PEKPNLSCIVNGKKRMCEWDCGR 25
DB 126 PEKPNLSCIVNGKKRMCEWDCGR 150

RESULT 6
US-08-308-881-2
; Sequence 2, Application US/08308881
; Patent No. 5783672
; GENERAL INFORMATION:
; APPLICANT: Mosley, Bruce
; APPLICANT: Cosman, David J.
; TITLE OF INVENTION: Receptor for Oncostatin M
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple 7.1
; SOFTWARE: Microsoft Word, Version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/308,881
; FILING DATE: 12-SEP-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/249,553
; FILING DATE: 26-MAY-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Seese, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2614-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 708 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-308-881-2

Query Match 100.0%; Score 145; DB 1; Length 708;
Best Local Similarity 100.0%; Pred. No. 2, 2e-13;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PEKPNLSICIYNEGKMKRCMDGGR 25
|||||
Db 126 PEKPNLSICIYNEGKMKRCMDGGR 150

RESULT 7
US-09-058-263-2
Sequence 2, Application US/09058263
Patent No. 5891997
GENERAL INFORMATION:
APPLICANT: Mosley, Bruce
APPLICANT: Cosman, David J.
TITLE OF INVENTION: Receptor for Oncostatin M
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.1
SOFTWARE: Microsoft Word, Version 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/058, 263
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/308, 881
FILING DATE: 12-SEP-1994
APPLICATION NUMBER: US 08/249, 553
FILING DATE: 26-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Seese, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2614-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 708 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-058-263-2

Query Match 100.0%; Score 145; DB 2; Length 708;
Best Local Similarity 100.0%; Pred. No. 2, 2e-13;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PEKPNLSICIYNEGKMKRCMDGGR 25
|||||
Db 126 PEKPNLSICIYNEGKMKRCMDGGR 150

RESULT 8
US-09-059-099-2
Sequence 2, Application US/09059099
Patent No. 5925740
GENERAL INFORMATION:
APPLICANT: Mosley, Bruce
APPLICANT: Cosman, David J.

TITLE OF INVENTION: Receptor for Oncostatin M
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.1
SOFTWARE: Microsoft Word, Version 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/059, 099
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/308, 881
FILING DATE: 12-SEP-1994
APPLICATION NUMBER: US 08/249, 553
FILING DATE: 26-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Seese, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2614-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 708 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-059-099-2

Query Match 100.0%; Score 145; DB 2; Length 708;
Best Local Similarity 100.0%; Pred. No. 2, 2e-13;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PEKPNLSICIYNEGKMKRCMDGGR 25
|||||
Db 126 PEKPNLSICIYNEGKMKRCMDGGR 150

RESULT 9
US-09-058-264-2
Sequence 2, Application US/09058264
Patent No. 6010886
GENERAL INFORMATION:
APPLICANT: Mosley, Bruce
APPLICANT: Cosman, David J.
TITLE OF INVENTION: Receptor for Oncostatin M
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.1
SOFTWARE: Microsoft Word, Version 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/058, 264
FILING DATE:

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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/308,881
FILING DATE: 12-SEP-1994
APPLICATION NUMBER: US 08/249,553
FILING DATE: 26-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Seese, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2614-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 708 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-058-264-2

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```

Query Match          100.0%; Score 145; DB 3; Length 708;
Best Local Similarity 100.0%; Pred. No. 2.2e-13;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 PEKPNLSCIVNEGKKMKRCWMDGR 25
DB 126 PEKPNLSCIVNEGKKMKRCWMDGR 150

```

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RESULT 10
PCT-US95-06530-2

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```

Sequence 2, Application PC/TUS9506530
GENERAL INFORMATION:
APPLICANT: Mosley, Bruce
APPLICANT: Cosman, David J.
TITLE OF INVENTION: Receptor for Oncostatin M
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSER: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT-US95/06530
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/308,881
FILING DATE: 09-SEP-1994
APPLICATION NUMBER: US 08/249,553
FILING DATE: 26-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Anderson, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2614-WO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 708 amino acids
TYPE: amino acid

```

```

TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-06530-2

```

```

Query Match          100.0%; Score 145; DB 5; Length 708;
Best Local Similarity 100.0%; Pred. No. 2.2e-13;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 PEKPNLSCIVNEGKKMKRCWMDGR 25
DB 126 PEKPNLSCIVNEGKKMKRCWMDGR 150

```

```

RESULT 11
US-08-825-558-6

```

```

Sequence 6, Application US/08825558
Patent No. 5965724
GENERAL INFORMATION:
APPLICANT: SHARKEY, ANDREW
APPLICANT: SMITH, STEPHEN R.
APPLICANT: DELLOW, KIMBERLEY A.
TITLE OF INVENTION: Gp 130 Lacking the Transmembrane Domain
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSER: STERN, KESSLER, GOLDSTEIN & FOX
STREET: 1100 NEW YORK AVENUE
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/825,558
FILING DATE: 19-MAR-1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: ESMOND, ROBERT W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 0623.0530001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)371-2600
TELEFAX: (202)371-2540
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 918 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-825-558-6

```

```

Query Match          100.0%; Score 145; DB 2; Length 918;
Best Local Similarity 100.0%; Pred. No. 2.9e-13;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 PEKPNLSCIVNEGKKMKRCWMDGR 25
DB 126 PEKPNLSCIVNEGKKMKRCWMDGR 150

```

```

RESULT 12
US-08-685-118-2

```

```

Sequence 2, Application US/08685118
Patent No. 5840530
GENERAL INFORMATION:
APPLICANT: Gubler, Ulrich A
APPLICANT: Presky, David H
TITLE OF INVENTION: RECEPTORS FOR HUMAN IL-12

```

NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
CITY: Nutley
STATE: NJ
COUNTRY: USA
ZIP: 07110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/685,118
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Silverman, Robert A.
REGISTRATION NUMBER: 35,682
REFERENCE/DOCKET NUMBER: CD 9195
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201) 235-2863
TELEFAX: (201) 235-2363
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 862 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-685-118-2

Query Match 45.2%; Score 65.5; DB 2; Length 862;
Best Local Similarity 50.0%; Pred. No. 0.13;
Matches 13; Conservative 4; Mismatches 8; Indels 1; Gaps 1;

OY 1 PEKPNLSCT-VNEGKMKRCMDGR 25
||:||||| :|:|
Db 124 PEOPNLSCTKGEGTACTWGR 149

RESULT 13
US-08-915-495-2
Sequence 2, Application US/08915495
Patent No. 5852176
GENERAL INFORMATION:
APPLICANT: Gubler, Ulrich A
APPLICANT: Presky, David H
TITLE OF INVENTION: RECEPTORS FOR HUMAN IL-12
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
CITY: Nutley
STATE: NJ
COUNTRY: USA
ZIP: 07110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/915,495
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/685,118
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Silverman, Robert A.
REGISTRATION NUMBER: 35,682

REFERENCE/DOCKET NUMBER: CD 9195
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201) 235-2863
TELEFAX: (201) 235-2363
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 862 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-915-495-2

Query Match 45.2%; Score 65.5; DB 2; Length 862;
Best Local Similarity 50.0%; Pred. No. 0.13;
Matches 13; Conservative 4; Mismatches 8; Indels 1; Gaps 1;

OY 1 PEKPNLSCT-VNEGKMKRCMDGR 25
||:||||| :|:|
Db 124 PEOPNLSCTKGEGTACTWGR 149

RESULT 14
US-08-914-520-2
Sequence 2, Application US/08914520
Patent No. 5919903
GENERAL INFORMATION:
APPLICANT: Gubler, Ulrich A
APPLICANT: Presky, David H
TITLE OF INVENTION: RECEPTORS FOR HUMAN IL-12
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
CITY: Nutley
STATE: NJ
COUNTRY: USA
ZIP: 07110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/914,520
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/685,118
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Silverman, Robert A.
REGISTRATION NUMBER: 35,682
REFERENCE/DOCKET NUMBER: CD 9135
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201) 235-2863
TELEFAX: (201) 235-2363
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 862 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-914-520-2

Query Match 45.2%; Score 65.5; DB 2; Length 862;
Best Local Similarity 50.0%; Pred. No. 0.13;
Matches 13; Conservative 4; Mismatches 8; Indels 1; Gaps 1;

OY 1 PEKPNLSCT-VNEGKMKRCMDGR 25
||:||||| :|:|
Db 124 PEOPNLSCTKGEGTACTWGR 149

RESULT 15
US-09-071-224-21

; Sequence 21, Application US/09071224
; Patent No. 6271343

; GENERAL INFORMATION:

; APPLICANT: Lok, S1

; APPLICANT: Presnell, Scott R.

; APPLICANT: Jelmeberg, Anna C.

; APPLICANT: Gilbert, Teresa

; APPLICANT: Foster, Donald C.

; APPLICANT: Adams, Robyn L.

; APPLICANT: Lehner, Joyce M.

; TITLE OF INVENTION: MAMMALIAN ZCYTORS

; NUMBER OF SEQUENCES: 37

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Zymogenetics

; STREET: 1201 Eastlake Ave East

; CITY: Seattle

; STATE: WA

; COUNTRY: USA

; ZIP: 98102

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FASTSEQ for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/071,224

; FILING DATE:

; CLASSIFICATION:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Lunn, Paul G

; REGISTRATION NUMBER: 32,743

; REFERENCE/DOCKET NUMBER: 96-22

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 206-442-6627

; TELEFAX: 206-442-6678

; TELEX:

; INFORMATION FOR SEQ ID NO: 21:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 303 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-09-071-224-21

Query Match 43.4%; Score 63; DB 4; Length 303;

Best Local Similarity 45.8%; Pred. No. 0.094;

Matches 11; Conservative 2; Mismatches 11; Indels 0; Gaps 0;

OY 1 PEKPKMLSCIVNEGKMKRCBWDG 24

DB 98 PEKPVNISCSKSKMKDLCRWTPG 121

Search completed: December 19, 2001, 16:21:01
Job time: 406 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 19, 2001, 16:19:35 ; Search time 170.68 Seconds
(without alignments)
10.850 Million cell updates/sec

Title: US-09-202-104a-8
139
Perfect score: 1 NFKLSEWATHKFKADCKAKKRDPTPS 25
Sequence:

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues
Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

A.Geneseq_1101.*
1: /SID8/gcgdata/geneseq/geneseq/AA1980.DAT.*
2: /SID8/gcgdata/geneseq/geneseq/AA1981.DAT.*
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22: /SID8/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	139	100.0	25	19	AAW52208
2	139	100.0	180	17	AAW00404
3	139	100.0	329	18	AAW17859
4	139	100.0	332	20	AAW70799
5	139	100.0	332	21	AAV92188
6	139	100.0	658	17	AAK94576
7	139	100.0	708	14	AAK37804
8	139	100.0	708	17	AAK85911
9	139	100.0	727	21	AAV92192
10	139	100.0	738	21	AAV92194
11	139	100.0	859	20	AAW70796

12	139	100.0	859	21	AAV92184
13	139	100.0	918	15	AAK10545
14	139	100.0	918	12	AAK46233
15	139	100.0	918	17	AAK75368
16	139	100.0	918	20	AAV44694
17	139	100.0	951	21	AAW70798
18	139	100.0	951	21	AAV92186
19	139	100.0	961	21	AAV92187
20	139	100.0	1158	21	AAV92205
21	139	100.0	1168	21	AAV92204
22	118	84.9	24	22	AAK88833
23	102	73.4	24	22	AAK88832
24	88	63.3	917	13	AAK26334
25	88	63.3	917	21	AAV55073
26	61	43.9	24	22	AAK88834
27	50	36.0	2799	19	AAK81867
28	46	33.1	24	22	AAK88831
29	46	33.1	592	12	AAK86914
30	45.5	32.7	436	20	AAV37223
31	45.5	32.7	563	21	AAK45223
32	45.5	32.7	571	21	AAK45222
33	45.5	32.7	585	21	AAK45221
34	45	32.4	286	21	AAK39945
35	45	32.4	292	21	AAK39944
36	45	32.4	369	22	AAK91613
37	44	31.7	2410	18	AAK19723
38	44	31.7	2480	18	AAK19724
39	44	31.7	2644	18	AAK13152
40	44	31.7	2644	20	AAK84271
41	43	30.9	10	22	AAK49032
42	43	30.9	328	21	AAK18899
43	43	30.9	339	21	AAK19406
44	43	30.9	341	22	AAK40059
45	43	30.9	369	22	AAK41845

ALIGNMENTS

RESULT 1
ID AAW52208 standard; peptide; 25 AA.
XX AAW52208;
AC AAW52208;
XX 09-JUN-1998 (first entry)
DT
XX
DE Interleukin-6 antagonist peptide.
XX
KW Interleukin-6; IL-6; antagonist; IL-6 related disease; multiple myeloma;
KW acquired immune deficiency syndrome-related lymphoma; immune response;
KW rheumatoid arthritis; psoriasis; sepsis; osteoporosis; therapy;
KW Alzheimer's disease.
XX
OS Synthetic.
OS Homo sapiens.
XX
XX WO9748728-A1.
XX
XX 24-DEC-1997.
XX
XX 19-JUN-1997; 97MO-NU0345.
XX
XX 20-JUN-1996; 96EP-0201720.
XX
XX (KOSTR/) KOSTER H W.
XX
XX Hoebe KHN, Van Leengoed LAMG;
XX
XX WPI; 1998-063080/06.
XX
XX New peptide(s) with interleukin-6 agonist or antagonist activity -
XX useful for treatment, prevention and diagnosis of IL-6 associated

PT diseases
 XX
 PS Claim 6; Page 17; 28pp; English.
 XX
 CC This sequence represents a Interleukin-6 (IL-6) antagonist peptide. This
 CC sequence is a peptide of the invention, which are of 5-30 amino acids
 CC and have antagonistic activity against: (a) IL-6; (b) the alpha chain
 CC and/or beta chain of the IL-6 receptor (IL-6R); or (c) IL-6 activity. The
 CC antagonists are used to treat or prevent IL-6 related diseases (typical
 CC of many exemplified are multiple myeloma, acquired immune deficiency
 CC syndrome-related lymphoma, rheumatoid arthritis, psoriasis, sepsis,
 CC osteoporosis, Alzheimer's disease etc.), also to remove IL-6 or IL-6R
 CC from extracorporeal blood. They may also be used diagnostically for such
 CC diseases and IL-6 agonists are additives for cell cultures. Antibodies
 CC specific for the antagonists may be administered to subjects previously
 CC treated with the antagonists to counter their effects, also in
 CC extracorporeal dialysis and diagnosis. The antagonists are too small to
 CC induce an immune response and have minimal side effects (they are not
 CC lytic for erythrocytes nor toxic for polymorphonuclear cells or
 CC hepatocytes); contrast no-human anti-IL-6 antibodies. The mixtures, or
 CC multimers, have greater activity (acting on both IL-6 and its receptor)
 CC and the peptides can be engineered to increase half-life or to target
 CC organs by incorporating unnatural aa or altering the
 CC hydrophilic/lipophilic balance.
 CC
 XX Sequence 25 AA:
 SQ
 Query Match 100.0%; Score 139; DB 19; Length 25;
 Best Local Similarity 100.0%; Pred. No. 1.2e-14;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 NPTLSEWATHKFDCKAKRDPTPS 25
 ||||||||||||||||||
 Db 1 nftlksewathkfdckakrdtpstps 25
 RESULT 2
 AAW00404
 ID AAW00404 standard; peptide; 180 AA.
 XX
 AC AAW00404;
 XX
 DT 29-AUG-1996 (first entry)
 XX
 DE Interleukin-6 antagonist peptide.
 XX
 KW IL-6; antagonist; autoimmune disease.
 XX
 OS Synthetic.
 PS JP07324097-A.
 XX
 PD 12-DEC-1995.
 XX
 PF 30-MAY-1994; 94JP-0117259.
 XX
 PR 30-MAY-1994; 94JP-0117259.
 XX
 RA (DAIIL) DAICEL CHEM IND LTD.
 PA (FUJII) FUJISAWA PHARM CO LTD.
 XX
 DR WPI; 1996-065476/07.
 XX
 PT Interleukin 6 antagonist - useful for treating autoimmune diseases
 XX
 PS Claim 1; Page 2; 19pp; Japanese.
 XX
 CC New-IL-6 antagonists are provided which are of formula X-W-Y, in
 CC which X is H or an amino-protecting group, Y is OH or a carboxy-
 CC protecting group, and W is a peptide containing all or part of the
 CC sequence as given in AAW00401, AAW00402, AAW00403 or AAW00404 (the
 CC present sequence), where any free mercapto groups in the sequence are

CC optionally protected. Specifically preferred partial peptides from
 CC the present sequence (AAW00436 - AAW00442) are claimed as new chemical
 CC compounds. The IL-6 antagonists are useful for treating autoimmune
 CC diseases.
 CC
 XX
 SQ Sequence 180 AA;
 Query Match 100.0%; Score 139; DB 17; Length 180;
 Best Local Similarity 100.0%; Pred. No. 9.5e-14;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 NPTLSEWATHKFDCKAKRDPTPS 25
 ||||||||||||||||||
 Db 35 nftlksewathkfdckakrdtpstps 59
 RESULT 3
 AAW17859
 ID AAW17859 standard; Protein; 329 AA.
 XX
 AC AAW17859;
 XX
 DT 04-FEB-1998 (first entry)
 XX
 DE Rheumatoid arthritis auto-antigen clone A.
 XX
 DE Rheumatoid arthritis; auto-antigen; clone A; diagnosis;
 KW Rheumatoid arthritis; synovial cell.
 XX
 OS Homo sapiens.
 XX
 PN WO9717441-A1.
 XX
 PD 15-MAY-1997.
 XX
 PF 06-NOV-1996; 96WO-JP03250.
 XX
 PR 07-NOV-1995; 95JP-0288957.
 XX
 PA (KANF) KANEKA CORP.
 XX
 PI Kishimura M, Nakao K, Osakada F, Osaki S, Tanaka M;
 DR WPI; 1997-281030/25.
 DR N-PSDB; AAT68830.
 XX
 PT Auto-antigen from synovial cells of rheumatoid arthritis patients -
 PT binds to antibodies present in these patients, for diagnosis and
 PT prediction of the disease
 XX
 PS Claim 3; Pages 36-37; 61pp; Japanese.
 XX
 CC The present sequence is the rheumatoid arthritis (RA) auto-antigen
 CC clone A, which can be used to diagnose and predict the development
 CC of RA by reaction with antibodies in biological specimens, e.g.
 CC sera, from patients.
 CC RNA was isolated from synovial cells from a RA patient and used to
 CC construct a cDNA library. This was screened using IgG separated
 CC from the synovial fluid of a RA patient. Active clones were
 CC isolated in a cloning vector, and inserted into an expression
 CC vector for the transformation of E. coli NM522. Transformants on
 CC culture express clone A peptide and follistatin related protein
 CC into the culture medium.
 XX
 SQ Sequence 329 AA;
 Query Match 100.0%; Score 139; DB 18; Length 329;
 Best Local Similarity 100.0%; Pred. No. 1.8e-13;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 NPTLSEWATHKFDCKAKRDPTPS 25

Db 157 nftlksewathkfadckakrtdpts 181

RESULT 4

AAW70799 standard; protein; 332 AA.

AAW70799;

03-FEB-1999 (first entry)

Human gp130-delta-3fibro amino acid sequence.

gp130; cytokine antagonist; interleukin; gamma-interferon;

granulocyte macrophage colony-stimulating factor; J peptide;

transforming growth factor-beta.

Synthetic.

Homo sapiens.

Key Location/Qualifiers

FT Protein 1..330 /note="human gp130"

US5844099-A.

01-DEC-1998.

27-NOV-1995; 95US-0563105.

27-NOV-1995; 95US-0563105.

20-OCT-1993; 93US-0140222.

(REG-) REGENERON PHARM INC.

Economides A, Stahl N, Yancopoulos GD;

WPI; 1999-044669/04.

Cytokine antagonists - comprising extracellular domains of

specificity-determining and signal-transducing components of

cytokine receptor

Example 4; Fig 10; 46pp; English.

The present sequence represents the amino acid sequence of human

gp130-delta-3fibro. The protein is used in the course of the invention.

The specification describes cytokine antagonists comprising only the

extracellular domain of the specificity-determining component of

the cytokine receptor and the extracellular domain of a

signal-transducing component of the cytokine receptor. The cytokine

is an interleukin (IL-1, IL-2, IL-3, IL-4, IL-5 or IL-15),

granulocyte macrophage colony-stimulating factor (GM-CSF),

gamma-interferon or transforming growth factor-beta (TGF-beta). The

antagonist is capable of binding the cytokine to form a nonfunctional

complex. The compounds have therapeutic activity as cytokine antagonists

and can also be used in assays for identifying novel agonists and

antagonists of cytokines.

Sequence 332 AA;

Query Match 100.0%; Score 139; DB 20; Length 332;

Best Local Similarity 100.0%; Pred. No. 1.8e-13;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 NFKSEMATHKFAADCKAKRDPPTS 25

157 nftlksewathkfadckakrtdpts 181

RESULT 5

AAV92188 standard; protein; 332 AA.

AAV92188;

01-AUG-2000 (first entry)

Human gp130-delta-3fibro.

gp130-delta-3fibro; cytokine; antagonist; CNTF; receptor; fusion protein;

cytostatic; immunomodulator; osteopathic.

Synthetic.

Homo sapiens.

Key Location/Qualifiers

FT Protein 1..330 /label="gp130"

Peptide 331..332 /note="Ser-Gly bridge"

WO200018932-A2.

06-APR-2000.

22-SEP-1999; 99WO-US22045.

25-SEP-1998; 98US-0101858.

19-MAY-1999; 99US-0313942.

(REG-) REGENERON PHARM INC.

Stahl N, Yancopoulos GD;

WPI; 2000-293165/25.

Isolated nucleic acid molecule for treating cytokine-related diseases

or disorders encodes a fusion polypeptide capable of binding a cytokine

to form a nonfunctional complex

Example 4; Fig 10; 152pp; English.

The invention concerns production of antagonists to any cytokine that

utilizes an alpha specificity determining component, which when combined

with the cytokine, binds to a first beta signal transducing component to

form a non-functional intermediate which then binds to a second beta

signal transducing component causing beta-receptor dimerization, the

soluble alpha specificity determining component of the receptor

(SR-alpha) and the extracellular domain of the first beta signal

transducing component of the cytokine receptor (beta-1) are combined to

form heterodimers (SR-alpha:beta-1) that act as antagonist to the

cytokine by binding the cytokine to form a non-functional complex. The

receptor components are shared by cytokines such as the CNTF (ciliary

neurotrophic factor) family of cytokines. The invention provides the

basis for the development of IL-6 antagonists, as they show that IL-6

the presence of a ligand, a non-functional intermediate complex,

consisting of the ligand, its alpha receptor and its beta-1 receptor

component, can be formed. It will effectively block the action of the

ligand. Effective antagonists of IL-6 or CNTF consist of heterodimers

of the extracellular domains of the alpha specificity determining

components of their receptors and the extracellular domain of gp130.

The resultant heterodimers, function as high-affinity traps, rendering

the cytokine inaccessible to form a signal transducing complex with the

native membrane-bound forms of their receptor. The nucleic acids and

polypeptides are useful for treating cytokine-related diseases or

cancer including multiple myeloma or cachexia.

Sequence 332 AA;

Query Match 100.0%; Score 139; DB 21; Length 332;

Best Local Similarity 100.0%; Pred. No. 1.8e-13;

ID	AA85911	standard; Protein; 708 AA.
XX		
AC	AA85911;	
XX		
DT	03-JUL-1996	(first entry)
XX		
DE	gpi30 N-terminal fragment.	
XX		
KW	Human; gpi30; inhibitor; oncostatin M; cytokine; antibody Fc region;	
KW	oncostatin M receptor-beta chain; antibody; tumour; growth factor;	
XX	therapy.	
XX		
OS	Homo sapiens.	
XX		
FH	Key	Location/Qualifiers
FT	Peptide	1..22
FT		/note= "signal peptide"
FT	Peptide	23..708
FT		/note= "N-terminal fragment of mature gpi30"
FT	Modified-site	21..23
FT		/note= "glycosylation site"
FT	Modified-site	61..63
FT		/note= "glycosylation site"
FT	Modified-site	109..111
FT		/note= "glycosylation site"
FT	Modified-site	135..137
FT		/note= "glycosylation site"
FT	Cleavage-site	153..154
FT	Modified-site	205..207
FT		/note= "glycosylation site"
FT	Modified-site	224..226
FT		/note= "glycosylation site"
FT	Modified-site	357..359
FT		/note= "glycosylation site"
FT	Modified-site	361..363
FT		/note= "glycosylation site"
FT	Modified-site	368..370
FT		/note= "glycosylation site"
FT	Modified-site	531..533
FT		/note= "glycosylation site"
FT	Modified-site	542..544
FT		/note= "glycosylation site"
FT	Cleavage-site	621..622
XX		
PN	W09533059-A2.	
PD		
XX	07-DEC-1995.	
XX		
PF	22-MAY-1995;	95WO-US06530.
XX		
PR	12-SEP-1994;	94US-0308881.
PR	26-MAY-1994;	94US-0249553.
XX		
PA	(IMMV) IMMUNEX CORP.	
XX		
PI	Cosman DJ, Mosley B;	
XX		
DR	WPI: 1996-030570/03.	
DR	N-PSDB; AA074081.	
XX		
XX		
PT	Hetero:dimeric receptor proteins comprising OSM-R beta and gp 130	-
PT	bind oncostatin M and are used in inhibiting biological activities	
PT	mediated by oncostatin M	
XX		
PS	Claim 1; Page 35-38; 60pp; English.	
XX		
CC	This sequence represents an N-terminal fragment of gpi30 obtained from	
CC	human placenta. gpi30 binds to oncostatin M, which is a secreted single	
CC	chain polypeptide cytokine. Oncostatin M regulates the growth of	
CC	certain tumour derived and normal cell lines. This receptor protein, and	
CC	the oncostatin M receptor-beta chain (see AA85912) sequence can be	
CC	covalently joined, to give a heterodimeric receptor protein capable of	
CC	binding to oncostatin M. The receptors can also comprise fusion	

CC	polypeptides, where an antibody Fc region is joined to the C-terminus of each of the soluble proteins. In this case, the two fusion polypeptides are joined by disulfide bonds between the two antibody Fc regions. The heterodimeric receptors can be used to inhibit biological activities mediated by oncostatin M. The advantage with using the heterodimeric receptors is that they bind to oncostatin M at greater levels than gp130 does alone.
CC	
XX	Sequence 708 AA;
SQ	
OY	1 NPTLKESEWATHKFAADCKRAKRDPPTS 25
Dd	157 nftlksewathkfadckrakrdtpsts 181
RESULT 9	
ID	AAY92192 standard; protein: 727 AA.
XX	
AC	AAY92192;
XX	
DT	01-AUG-2000 (first entry)
XX	
DE	Human gp130-kappa domain fusion protein.
XX	
KM	gp130-kappa domain; cytokine; antagonist; CNTF; receptor; fusion protein;
RW	cytostatic; immunomodulator; osteopathic.
XX	
OS	Synthetic.
OS	Homo sapiens.
XX	
FH	Key Location/Qualifiers
FT	1..619
FT	/label= gp130
FT	Peptide 620..621
FT	/note= "Ser-Gly bridge"
FT	Protein 622..727
FT	/label= IgG1_kappa_domain
XX	
PN	MO200018932-A2.
XX	
PD	06-APR-2000.
XX	
PF	22-SEP-1999; 99WO-US22045.
XX	
PR	25-SEP-1998; 98US-O101858.
PR	19-MAY-1999; 99US-O313942.
XX	
PA	(REG-) REGENERON PHARM INC.
XX	
PI	Stahl N, Yancopoulos GD;
XX	
DR	WPI: 2000-293165/25.
XX	
PT	Isolated nucleic acid molecule for treating cytokine-related diseases or disorders encodes a fusion polypeptide capable of binding a cytokine to form a nonfunctional complex
XX	
PS	Example 4; Page -: 152pp; English.
XX	
CC	The invention concerns production of antagonists to any cytokine that utilizes an alpha specificity determining component, which when combined with the cytokine, binds to a first beta signal transducing component to form a non-functional intermediate which then binds to a second beta signal transducing component causing beta-receptor dimerization. the soluble alpha specificity determining component of the receptor (sr-alpha) and the extracellular domain of the first beta signal transducing component of the cytokine receptor (beta-1) are combined to
CC	

CC form heterodimers (SR-alpha:beta-1) that act as antagonist to the
CC cytokine by binding the cytokine to form a non-functional complex. The
CC receptor components are shared by cytokines such as the CNTF (iliary
CC neurotrophic factor) family of cytokines. The invention provides the
CC basis for the development of IL-6 antagonists, as they show that if, in
CC the presence of a ligand, a non-functional intermediate complex,
CC consisting of the ligand, its alpha receptor and its beta-1 receptor
CC component, can be formed, it will effectively block the action of the
CC ligand. Effective antagonists of IL-6 or CNTF consist of heterodimers
CC of the extracellular domains of the alpha specificity determining
CC components of their receptors and the extracellular domain of gp130.
CC The resultant heterodimers, function as high-affinity traps, rendering
CC the cytokine inaccessible to form a signal transducing complex with the
CC native membrane-bound forms of their receptor. The nucleic acids and
CC polypeptides are useful for treating cytokine-related diseases or
CC disorders such as osteoporosis and primary and secondary effects of
CC cancer including multiple myeloma or cachexia.
CC NB. This sequence was constructed from the gp130 and kappa domain
CC sequences given in Figures 9 and 13 of the specification.
XX
SQ Sequence 727 AA;

Query Match 100.0%; Score 139; DB 21; Length 727;
Best Local Similarity 100.0%; Pred. No. 4.1e-13;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NPTLSEWATHKFPADCKAKRDTPTS 25
Db 157 nftlksewathkfpadckakrtdpts 181
|||||

RESULT 10
ID AAY92194 standard; protein: 738 AA.
XX
AC AAY92194;
XX
DT 01-AUG-2000 (first entry)
XX
DE Human gp130-J-kappa fusion protein.
XX
KW gp130-J-kappa: cytokine; antagonist; CNTF; receptor; fusion protein;
KW cytosstatic; immunomodulator; osteopathic.
XX
OS Synthetic.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FH Protein 1..619
FT /label= gp130
FT 620..621
FT /note= "Ser-Gly bridge"
FT Peptide 622..632
FT /note= "J-peptide"
FT Domain 633..738
FT /label= kappa_domain
XX
PN WO200018932-A2.
XX
PD 06-APR-2000.
XX
PP 22-SEP-1999; 99WO-US22045.
XX
PR 25-SEP-1998; 98US-0101858.
PR 19-MAY-1999; 99US-0313942.
XX
PA (REG-) REGENERON PHARM INC.
XX
PI Stahl N, Yancopoulos GD;
XX
DR WPI; 2000-293165/25.
XX

PT Isolated nucleic acid molecule for treating cytokine-related diseases
PT or disorders encodes a fusion polypeptide capable of binding a cytokine
PT to form a nonfunctional complex
XX
PS Example 4; Page -: 152pp; English.
XX
CC The invention concerns production of antagonists to any cytokine that
CC utilizes an alpha specificity determining component, which when combined
CC with the cytokine, binds to a first beta signal transducing component to
CC form a non-functional intermediate which then binds to a second beta
CC signal transducing component causing beta-receptor dimerization, the
CC soluble alpha specificity determining component of the receptor
CC (SR-alpha) and the extracellular domain of the first beta signal
CC transducing component of the cytokine receptor (beta-1) are combined to
CC form heterodimers (SR-alpha:beta-1) that act as antagonist to the
CC cytokine by binding the cytokine to form a non-functional complex. The
CC receptor components are shared by cytokines such as the CNTF (iliary
CC neurotrophic factor) family of cytokines. The invention provides the
CC basis for the development of IL-6 antagonists, as they show that if, in
CC the presence of a ligand, a non-functional intermediate complex,
CC consisting of the ligand, its alpha receptor and its beta-1 receptor
CC component, can be formed, it will effectively block the action of the
CC ligand. Effective antagonists of IL-6 or CNTF consist of heterodimers
CC of the extracellular domains of the alpha specificity determining
CC components of their receptors and the extracellular domain of gp130.
CC The resultant heterodimers, function as high-affinity traps, rendering
CC the cytokine inaccessible to form a signal transducing complex with the
CC native membrane-bound forms of their receptor. The nucleic acids and
CC polypeptides are useful for treating cytokine-related diseases or
CC disorders such as osteoporosis and primary and secondary effects of
CC cancer including multiple myeloma or cachexia.
XX
SQ Sequence 738 AA;

Query Match 100.0%; Score 139; DB 21; Length 738;
Best Local Similarity 100.0%; Pred. No. 4.2e-13;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NPTLSEWATHKFPADCKAKRDTPTS 25
Db 157 nftlksewathkfpadckakrtdpts 181
|||||

RESULT 11
ID AAW70796 standard; protein: 859 AA.
XX
AC AAW70796;
XX
DT 03-FEB-1999 (first entry)
XX
DE Human gp130-FC-His6 amino acid sequence.
XX
KW gp130; cytokine antagonist; interleukin; gamma-interferon;
KW granulocyte macrophage colony-stimulating factor; J peptide;
KW transforming growth factor-beta.
XX
OS Synthetic.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FH Protein 1..619
FT /note= "human gp130"
FT MISC-difference 2
FT /label= L2Y
FT /note= "amino acid changed to accomodate a kozak
FT Peptide 1..22
FT /note= "signal peptide"
FT MISC-difference 620..621
FT /note= "Ser-Gly bridge"
FT Protein 662..853

```

FT Disulfide-bond 632..635 /note="from the Fc domain of human IgG1"
FT Peptide 854..859
FT /note="hexahistidine tag"
XX US5844099-A.
XX PN
XX PD 01-DEC-1998.
XX PF 27-NOV-1995; 95US-0563105.
XX PR 27-NOV-1995; 95US-0563105.
XX PR 20-OCT-1993; 93US-0140222.
XX PA (REGG-) REGENERON PHARM INC.
XX PI Economides A, Stahl N, Yancopoulos GD;
XX DR WPI; 1999-044669/04.
XX PT Cytokine antagonists - comprising extracellular domains of
XX PT specificity-determining and signal-transducing components of
XX PT cytokine receptor
XX PS Example 3; Fig 4; 46pp; English.
XX CC The present sequence represents the amino acid sequence of human
XX CC gp130-Fc-His6. The protein is used in the course of the invention. The
XX CC specification describes cytokine antagonists comprising only the
XX CC extracellular domain of the specificity-determining component of
XX CC the cytokine receptor and the extracellular domain of a
XX CC signal-transducing component of the cytokine receptor. The cytokine
XX CC is an interleukin (IL-1, IL-2, IL-3, IL-4, IL-5 or IL-15),
XX CC granulocyte macrophage colony-stimulating factor (GM-CSF),
XX CC gamma-interferon or transforming growth factor beta (TGF-beta). The
XX CC antagonist is capable of binding the cytokine to form a nonfunctional
XX CC complex. The compounds have therapeutic activity as cytokine antagonists
XX CC and can also be used in assays for identifying novel agonists and
XX CC antagonists of cytokines.
XX SQ Sequence 859 AA;

Query Match 100.0%; Score 139; DB 20; Length 859;
Best Local Similarity 100.0%; Pred. No. 4.9e-13;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NPTLKSEMAHKRPADCKAKRDPT 25
Db 157 nftlksewathkftadckakrdpts 181

RESULT 12
AA92184
ID AA92184 standard; protein; 859 AA.
XX
AC AA92184;
XX
XX 01-AUG-2000 (first entry)
XX DE Human gp130-Fc-His6.
XX
XX gp130-Fc-His6: cytokine; antagonist; CNTF; receptor; fusion protein;
XX cytosolic; immunomodulator; osteopathic.
XX OS Synthetic.
XX OS Homo sapiens.
XX
XX Key Location/Qualifiers
XX Protein 1..619
XX Peptide 1..22
XX /label= gp130
XX /label= signal_peptide

```

```

FT Peptide 620..621
FT Disulfide-bond 632..635 /note="Ser-Gly bridge"
FT Disulfide-bond 632 /note="forms inter-chain disulfide bridge that
FT /note="link two Fc domains"
FT Disulfide-bond 635 /note="forms inter-chain disulfide bridge that
FT /note="link two Fc domains"
XX
XX FT Protein 662..853
XX FT /label= IgG1_Fc-domain
XX FT Peptide 854..859
XX FT /label= histidine_tag
XX PN WO200018932-A2.
XX PD 06-APR-2000.
XX PF 22-SEP-1999; 99WO-US22045.
XX PR 25-SEP-1998; 98US-0101858.
XX PR 19-MAY-1999; 99US-0313942.
XX PA (REGG-) REGENERON PHARM INC.
XX PI Stahl N, Yancopoulos GD;
XX DR WPI; 2000-293165/25.
XX CC Isolated nucleic acid molecule for treating cytokine-related diseases
XX CC or disorders encodes a fusion polypeptide capable of binding a cytokine
XX CC to form a nonfunctional complex
XX PS Example 3; Fig 4; 152pp; English.
XX
XX CC The invention concerns production of antagonists to any cytokine that
XX CC utilizes an alpha specificity determining component, which when combined
XX CC with the cytokine, binds to a first beta signal transducing component to
XX CC form a non-functional intermediate which then binds to a second beta
XX CC signal transducing component causing beta-receptor dimerization, the
XX CC soluble alpha specificity determining component of the receptor
XX CC (SR-alpha) and the extracellular domain of the first beta signal
XX CC transducing component of the cytokine receptor (beta-1) are combined to
XX CC form heterodimers (SR-alpha:beta-1) that act as antagonist to the
XX CC cytokine by binding the cytokine to form a non-functional complex. The
XX CC receptor components are shared by cytokines such as the CNTF (ciliary
XX CC neurotrophic factor) family of cytokines. The invention provides the
XX CC basis for the development of IL-6 antagonists, as they show that if, in
XX CC the presence of a ligand, a non-functional intermediate complex,
XX CC consisting of the ligand, its alpha receptor and its beta-1 receptor
XX CC component, can be formed, it will effectively block the action of the
XX CC ligand. Effective antagonists of IL-6 or CNTF consist of heterodimers
XX CC of the extracellular domains of the alpha specificity determining
XX CC components of their receptors and the extracellular domain of gp130.
XX CC The resultant heterodimers, function as high-affinity traps, rendering
XX CC the cytokine inaccessible to form a signal transducing complex with the
XX CC native membrane-bound forms of their receptor. The nucleic acids and
XX CC polypeptides are useful for treating cytokine-related diseases or
XX CC disorders such as osteoporosis and primary and secondary effects of
XX CC cancer including multiple myeloma or cachexia.
XX SQ Sequence 859 AA;

Query Match 100.0%; Score 139; DB 21; Length 859;
Best Local Similarity 100.0%; Pred. No. 4.9e-13;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NPTLKSEMAHKRPADCKAKRDPT 25
Db 157 nftlksewathkftadckakrdpts 181

RESULT 13

```

```

AAR10545
ID AAR10545 standard; Protein; 918 AA.
XX
AC AAR10545;
XX
DT 12-APR-1991 (first entry)
XX
DE Recombinant human gp130 protein.
XX
KW Recombinant human gp130; interleukin-6; interleukin-6 receptor;
XX immunity; haematopoiesis; inflammation; therapy.
XX
OS Homo sapiens.
XX
EP411946-A.
XX
PD 06-FEB-1991.
XX
PF 02-AUG-1990; 90EP-0308530.
XX
PR 31-MAY-1990; 90JP-0140069.
XX
PR 03-AUG-1989; 89JP-0200230.
XX
PA (KISH/) KISHIMOTO T.
XX
PI Kishimoto T;
XX
DR WPI: 1991-038820/06.
XX
DR N-PSDB; AAQ10402.
XX
PT Recombinant human gp130 protein - acts in the transmission of
XX interleukin-6 signal for defence mechanisms
XX
PS Disclosure; fig 7; 32pp; English.
XX
CC This gp130 protein is produced using standard recombinant DNA
XX methods (see AAQ10402). Free from any other human protein. It
XX participates in the transmission of the interleukin (IL)-6 sig-
XX nal, and therefore the proliferation and differentiation of an
XX organism. It is important in an animals defence mechanisms, e.g.
XX immunity, haematopoiesis and inflammation.
XX
SQ Sequence 918 AA;

Query Match 100.0%; Score 139; DB 12; Length 918;
Best Local Similarity 100.0%; Pred. No. 5.3e-13;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NFTLKSEWATHKPADCKAKKRDPTPS 25
Db 157 nftlksewathkfadckakrtdpts 181

RESULT 14
AAR46233
ID AAR46233 standard; Protein; 918 AA.
XX
AC AAR46233;
XX
DT 15-SEP-1994 (first entry)
XX
DE Human soluble glycoprotein (gp) 130.
XX
KW Glycoprotein; soluble; gp; gp130; antibody production; assay;
XX immunochemical assay; detection; immunogen; transmembrane domain.
XX
OS Homo sapiens.
XX
PN JP06022786-A.
XX
PN 01-FEB-1994.
XX

```

```

PF 02-AUG-1991; 91JP-0217924.
XX
XX 02-AUG-1991; 91JP-0217924.
XX
PA (KISH/) KISHIMOTO C.
XX (TOYO ) TOSOH CORP.
XX
DR WPI: 1994-071006/09.
XX
DR N-PSDB; AAQ56931.
XX
PT Preparation of recombinant soluble human gp 130 deriv - for use
XX in the production of anti-gp 130 antibody for immunochemical
XX assay
XX
PS Claim 1; Figure 7; 13pp; Japanese.
XX
CC The soluble glycoprotein (gp) 130 can be used as an immunogen for
XX the preparation of anti-gp130 antibody and as the standard substance
XX for immunochemical assay of gp130. Soluble gp130 cDNA was prepared
XX by inserting a termination codon prior to the extracellular domain
XX or transmembrane domain of the gp130 coding sequence or simply by
XX eliminating the transmembrane domain.
XX
SQ Sequence 918 AA;

Query Match 100.0%; Score 139; DB 15; Length 918;
Best Local Similarity 100.0%; Pred. No. 5.3e-13;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NFTLKSEWATHKPADCKAKKRDPTPS 25
Db 157 nftlksewathkfadckakrtdpts 181

RESULT 15
AAR75368
ID AAR75368 standard; Protein; 918 AA.
XX
AC AAR75368;
XX
DT 20-JUN-1996 (first entry)
XX
DE Human gp130 protein.
XX
KW Gp130; transmembrane domain; growth factor antagonist;
XX embryo pre-implantation; in vitro fertilisation.
XX
OS Homo sapiens.
XX
XX
FH Key Location/Qualifiers
FT Region 620..641
FT /label= transmembrane_region
XX
PN W09609382-A1.
XX
XX 28-MAR-1996.
XX
XX 21-SEP-1995; 95WO-G802243.
XX
XX 21-SEP-1994; 94GB-0019021.
XX
XX (ISTF ) ARS APPLIED RES SYST HOLDING NV.
XX
XX Dellow KA, Sharkey A, Smith SK.
XX WPI: 1996-186444/19.
XX
XX N-PSDB; AAT14603.
XX
XX New splice variant of gp130 lacking the trans-membrane domain
XX PT useful as an antagonist for growth factors esp. for ensuring correct
XX PT development of pre-implantation embryos
XX

```

PS Disclosure; Fig 2; 33pp; English.
XX
CC A DNA sequence (AA114603) codes for native human gp130 (AA075368).
CC A novel splice variant (see AA114602) that lacks the transmembrane
CC region was identified in the morula to blastocyst transition stage
CC of the human embryo. The splice variant antagonises the action
CC of certain growth factors and can be used to ensure correct
CC development of preimplantation embryos.
XX
SQ Sequence 918 AA;

Query Match 100.0%; Score 139; DB 17; Length 918;
Best Local Similarity 100.0%; Pred. No. 5.3e-13;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NPTLKSEWATHKFPADCKAKRDPTPS 25
|||||
Db 157 nftlksewathkfpadckakrdtpts 181

Search completed: December 19, 2001, 16:19:36
Job time: 361 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: December 19, 2001, 16:22:39 ; Search time 88.82 seconds
(without alignments)
21.441 Million cell updates/sec

Title: US-09-202-104a-8
Perfect score: 139
Sequence: 1 NFKLSEWATHKFKADCKAKRDPTPS 25

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	139	100.0	918	2	A36337
2	88	63.3	917	2	I49699
3	88	63.3	918	2	A44257
4	50	36.0	266	2	I49059
5	49	35.3	2895	2	T08437
6	46.5	33.5	717	2	T27066
7	46.5	33.5	717	2	T27067
8	46	33.1	294	2	S74853
9	46	33.1	343	2	T15253
10	46	33.1	571	2	S13392
11	46	33.1	583	2	S36781
12	46	33.1	592	1	S13391
13	46	33.1	991	2	E83137
14	45.5	32.7	533	2	T48403
15	45	32.4	67	2	PL0186
16	45	32.4	78	2	D34509
17	45	32.4	106	2	I50741
18	45	32.4	266	2	I49363
19	45	32.4	286	2	T04268
20	45	32.4	381	2	T29826
21	44.5	32.0	1657	2	T25421
22	44	31.7	266	2	I49114
23	44	31.7	2899	2	T21546
24	43.5	31.3	415	2	S35760
25	43	30.9	139	2	T27577
26	43	30.9	209	2	D86758
27	43	30.9	361	2	G70862
28	43	30.9	2301	1	GNNYTN
29	43	30.9	2303	1	GNNYTP

30	43	30.9	2303	2	S13554	genome polypeptide
31	42.5	30.6	488	2	G71568	probable (peli12)
32	42.5	30.6	569	2	S52350	thiamin pyrophosph
33	42	30.2	78	2	C34509	Ig light chain C r
34	42	30.2	170	2	T36230	hypothetical prote
35	42	30.2	240	2	A41797	Ig light chain - s
36	42	30.2	36	2	C83537	hypothetical prote
37	42	30.2	336	2	I40826	beta-toxin - Clost
38	42	30.2	381	2	S14132	protease-5'-phosp
39	42	30.2	422	2	H69979	protease homolog
40	42	30.2	437	1	S22655	translational elonga
41	42	30.2	437	1	S26649	translational elonga
42	42	30.2	444	2	S40980	hypothetical prote
43	42	30.2	447	2	T00834	probable SET-domain
44	42	30.2	680	2	T29204	hypothetical prote
45	42	30.2	996	2	T47518	nonphototropic hyp

ALIGNMENTS

RESULT 1
A36337
membrane glycoprotein gp130 precursor - human
C:Species: Homo sapiens (man)
C:Date: 12-Apr-1991 #sequence_revision 12-Apr-1991 #text_change 28-Jul-2000
C:Accession: A36337
R:Hit1, M.; Murakami, M.; Salto, M.; Hirano, T.; Tago, T.; Kishimoto, T.
Cell 63, 1149-1157, 1990
A:Title: Molecular cloning and expression of an IL-6 signal transducer, gp130.
A:Reference number: A36337; MUID:91084844
A:Accession: A36337
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-918 <HIB>
A:Cross-references: GB:M57230; NID:9186353; PIDN:AAA59155.1; PID:9186354
C:Genetics:
A:Gene: GDB:IL6ST; GP130
A:Cross-references: GDB:126725; OMIM:600694
A:Map position: 5q11-5q11
C:Superfamily: cytokine receptor homology
C:Keywords: glycoprotein; membrane protein
F:134-316/Domain: cytokine receptor homology <CRS>

Query Match 100.0%; Score 139; DB 2; Length 918;
Best Local Similarity 100.0%; Pred. No. 1e-13;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NFKLSEWATHKFKADCKAKRDPTPS 25
DB 157 NFKLSEWATHKFKADCKAKRDPTPS 181
RESULT 2
I49699
glycoprotein 130 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 28-Jul-2000
C:Accession: I49699; I48370
R:Salto, M.; Yoshida, K.; Hibi, M.; Tago, T.; Kishimoto, T.
J. Immunol. 148, 4066-4071, 1992
A:Title: Molecular cloning of a murine IL-6 receptor-associated signal transducer, gp
A:Reference number: I48370; MUID:92291532
A:Accession: I49699
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-917 <RES>
A:Cross-references: GB:M83336; NID:9193591; PIDN:AAA37723.1; PID:9193592
A:Accession: I48370
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-917 <RES>

A:Cross-references: EMBL:X62646; NID:g840816; PIDN:CAA44515.1; PID:g840817
C:Gene: gp130
C:Superfamily: cytokine receptor homology
C:Keywords: glycoprotein
F:134-314/Domain: cytokine receptor homology <CRS>

Query Match 63.3%; Score 88; DB 2; Length 917;
Best Local Similarity 68.2%; Pred. No. 1e-05;
Matches 15; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 NPTLSEWATHKFPDCKAKKRT 22
|:|||||:|:|:|:|
Db 157 NYTLKSEWATEKFPDCOSKHCT 178

RESULT 3
A44257
Interleukin-6 signal transducing molecule gp130 - rat

C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 28-Jul-2000

C:Accession: A44257
R:Wang, Y.; Nesbitt, J.E.; Fuentes, N.L.; Fuller, G.M.
Genomics 14, 666-672, 1992

A:Title: Molecular cloning and characterization of the rat liver IL-6 signal transducing

A:Reference number: A44257; MUID:93052397
A:Accession: A44257

A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA

A:Residues: 1-918 <MAN>
A:Experimental source: liver

A:Note: sequence extracted from NCBI backbone (NCBIP:118488)
C:Superfamily: cytokine receptor homology

C:Keywords: transmembrane protein
F:134-315/Domain: cytokine receptor homology <CRS>

Query Match 63.3%; Score 88; DB 2; Length 918;
Best Local Similarity 68.2%; Pred. No. 1e-05;
Matches 15; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 NPTLSEWATHKFPDCKAKKRT 22
|:|||||:|:|:|:|
Db 157 NYTLKSEWATEKFPDCRKHCT 178

RESULT 4
I49059
Ly49c - mouse

C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 19-May-2000

C:Accession: I49059
R:Hong, S.; Freeman, J.D.; Kelleher, C.; Mager, D.; Taket, F.
J. Immunol. 147, 1417-1423, 1991

A:Title: Ly-49 multigene family: New members of a superfamily of type II membrane protei

A:Reference number: I49058; MUID:91332459
A:Accession: I49059

A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA

A:Residues: 1-266 <RES>
A:Cross-references: EMBL:U010305; NID:g500645; PIDN:AAA19053.1; PID:g500646

C:Superfamily: natural killer cell receptor PL; C-type lectin homology

Query Match 36.0%; Score 50; DB 2; Length 266;
Best Local Similarity 40.9%; Pred. No. 2.7;
Matches 9; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

QY 1 NPTLSEWATHKFPDCKAKKRT 22
|:|:|:|:|:|:|:|:|:|
Db 94 DFNLEKEMTLNKSIDCRPSNET 115

RESULT 5
T08437
hyperplastic discs protein - fruit fly (Drosophila melanogaster)

C:Species: Drosophila melanogaster
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 17-Nov-2000

C:Accession: T08437
R:Mansfield, E.; Hersperger, E.; Biggs, J.; Shearn, A.
Dev. Biol. 165, 507-526, 1994

A:Title: Genetic and molecular analysis of hyperplastic discs, a gene whose product i

A:Reference number: Z16419; MUID:95046871
A:Accession: T08437

A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA

A:Residues: 1-2895 <MAN>
A:Cross-references: EMBL:L14644; NID:g2673886; PID:g2673887

C:Genetics:
A:Cross-references: FlyBase:FBgn0002431

Query Match 35.3%; Score 49; DB 2; Length 2895;
Best Local Similarity 60.0%; Pred. No. 43;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 11 HKFPDCKAKKRTPTS 25
|:|:|:|:|:|:|:|:|:|
Db 1249 HKGHCKLKRTPA 1263

RESULT 6
T27066
hypothetical protein Y51A2B.6a - Caenorhabditis elegans

C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 20-Jun-2000

C:Accession: T27066
R:McMurray, A.

submitted to the EMBL Data Library, January 1998
A:Reference number: Z20305

A:Accession: T27066
A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA
A:Residues: 1-717 <WIL>

A:Cross-references: EMBL:AL021493; PIDN:CAA16394.1; GSPDB:GN00023; CESP:Y51A2B.6a

A:Experimental source: clone Y51A2B
C:Genetics:

A:Gene: CESP:Y51A2B.6a
A:Map position: 5

A:Introns: 8/1: 33/1
C:Superfamily: Caenorhabditis elegans hypothetical protein Y116A8C.33

Query Match 33.5%; Score 46.5; DB 2; Length 717;
Best Local Similarity 50.0%; Pred. No. 26;
Matches 11; Conservative 3; Mismatches 7; Indels 1; Gaps 1;

QY 4 LKSEWATHKFPDCKAKKRTPTS 25
|:|:|:|:|:|:|:|:|:|
Db 605 LKQWGDHK-ADMESLEATWTS 625

RESULT 7
T27067
hypothetical protein Y51A2B.6b - Caenorhabditis elegans

C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 20-Jun-2000

C:Accession: T27067
R:McMurray, A.

submitted to the EMBL Data Library, January 1998
A:Reference number: Z20305

A:Accession: T27067
A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA
A:Residues: 1-717 <WIL>

A:Cross-references: EMBL:AL021493; PIDN:CAA16395.1; GSPDB:GN00023; CESP:Y51A2B.6b
A:Experimental source: clone Y51A2B

C:Genetics:
A:Gene: CESP:Y51A2B.6b
A:Map position: 5
A:Introns: 8/1; 33/1
C:Superfamily: Caenorhabditis elegans hypothetical protein Y116A8C.33

Query Match 33.1%; Score 46.5; DB 2; Length 717;
Best Local Similarity 50.0%; Pred. No. 26;
Matches 11; Conservative 3; Mismatches 7; Indels 1; Gaps 1;

OY 4 LKSEMTNHFADCKAKRDPPTS 25
DB 605 LKSNQGDHK-ADMESELEAVMTS 625

RESULT 8
S74853
hypothetical protein sl10837 - *Synechocystis* sp. (strain PCC 6803)

C:Species: *Synechocystis* sp.
A:Variety: PCC 6803
C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 11-Jan-2000
C:Accession: S74853

R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
O. K. Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
DNA Res. 3, 109-136, 1996

A:Title: Sequence analysis of the genome of the unicellular cyanobacterium *Synechocystis*
s.

A:Reference number: S74322; MUID:97061201

A:Accession: S74853

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-294 <KAN>

A:Cross-references: EMBL:D90909; GB:AB001339; NID:g1652844; PIDN:BA117814.1; PID:d101854

A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

C:Superfamily: unassigned tetratricopeptide repeat proteins: tetratricopeptide repeat hc
F:117-150/Domain: tetratricopeptide repeat homology <TT1>
F:151-184/Domain: tetratricopeptide repeat homology <TT2>
F:185-218/Domain: tetratricopeptide repeat homology <TT3>
F:219-252/Domain: tetratricopeptide repeat homology <TT4>

Query Match 33.1%; Score 46; DB 2; Length 294;
Best Local Similarity 41.7%; Pred. No. 13;
Matches 10; Conservative 3; Mismatches 11; Indels 0; Gaps 0;

OY 1 NPTLKSEMTNHFADCKAKRDPPT 24
DB 256 DFLVKNLMEQLIADTKALFATPT 279

RESULT 9
T15253
hypothetical protein K07B1.3 - *Caenorhabditis elegans*

C:Species: *Caenorhabditis elegans*
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 17-Mar-2000
C:Accession: T15253

R:Pauley, A.; Gattlung, S.
submitted to the EMBL Data Library, May 1997
A:Description: The sequence of C. elegans cosmid K07B1.

A:Reference number: Z18317

A:Accession: T15253

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-343 <PAU>

A:Cross-references: EMBL:AF003384; NID:g2088817; PID:g2088821; PIDN:AA54239.1; GSPDB:GN

C:Genetics:

A:Gene: CESP:K07B1.3

A:Map position: 5

A:Introns: 81/1; 131/3; 236/3; 279/2

C:Superfamily: ADP, ATP carrier protein; ADP, ATP carrier protein repeat homology

Query Match 33.1%; Score 46; DB 2; Length 343;
Best Local Similarity 50.0%; Pred. No. 15;
Matches 9; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 1 NPTLKSEMTNHFADCKA 18
DB 232 NPELKNMPLTHAVASACA 249

RESULT 10
S13392
alpha-L-arabinofuranosidase (EC 3.2.1.55) - *Pseudomonas fluorescens* subsp. *cellulosa*

N:Alternate names: xylanase C
C:Species: *Pseudomonas fluorescens* subsp. *cellulosa*
C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 08-Oct-1999
C:Accession: S13392

R:Kellett, L.E.; Poole, D.M.; Ferreira, L.M.A.; Durrant, A.J.; Hazlewood, G.P.; Gilbe

Biochem. J. 272, 363-376, 1990

A:Title: Xylanase B and an arabinofuranosidase from *Pseudomonas fluorescens* subsp. *ce*

A:Reference number: S13391; MUID:91097447

A:Accession: S13392

A:Molecule type: DNA

A:Residues: 1-571 <KEU>

A:Cross-references: EMBL:X54523; NID:g45523; PIDN:CAA38390.1; PID:g45525

C:Genetics:

A:Gene: xycC

C:Superfamily: bacterial cellulose-binding domain homology

C:Keywords: glycosidase; hydrolase

F:38-134/Domain: bacterial cellulose-binding domain homology <RCB>

F:39-133/Disulfide bonds: #status predicted

Query Match 33.1%; Score 46; DB 2; Length 571;
Best Local Similarity 42.9%; Pred. No. 25;
Matches 9; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

OY 2 FTLKSEMTNHFADCKAKRDT 22
DB 41 YTIIDSEWSTGFTANTITLKNDF 61

RESULT 11
S36781

esterase D - *Pseudomonas fluorescens*

C:Species: *Pseudomonas fluorescens*

C:Date: 22-Jan-1994 #sequence_revision 01-Dec-1995 #text_change 08-Oct-1999

C:Accession: S36781

R:Ferreira, L.M.A.; Wood, T.M.; Williamson, G.; Faulds, C.; Hazlewood, G.P.; Black, G

Biochem. J. 294, 349-355, 1993

A:Title: A modular esterase from *Pseudomonas fluorescens* subsp. *cellulosa* contains a

A:Reference number: S36781; MUID:93384502

A:Accession: S36781

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-583 <FER>

A:Cross-references: EMBL:X58956; NID:g313110; PIDN:CAA41727.1; PID:g313111

C:Superfamily: bacterial cellulose-binding domain homology

F:37-133/Domain: bacterial cellulose-binding domain homology <RCB>

Query Match 33.1%; Score 46; DB 2; Length 583;
Best Local Similarity 42.9%; Pred. No. 26;
Matches 9; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

OY 2 FTLKSEMTNHFADCKAKRDT 22
DB 40 YTIIDSEWSTGFTANTITLKNDF 60

RESULT 12

513391
 endo-1,4-beta-xylosidase (EC 3.2.1.8) B - Pseudomonas fluorescens subsp. cellulosa
 N:Alternate names: xylanase B
 C:Species: Pseudomonas fluorescens subsp. cellulosa
 C:Date: 17-Apr-1993 #sequence_revision 11-Apr-1997 #text_change 18-Jun-1999
 C:Accession: 513391
 R:Kelllett, L.E.; Poole, D.M.; Ferreira, L.M.A.; Durrant, A.J.; Hazlewood, G.P.; Gilbert,
 Biochem. J. 272, 369-376, 1990
 A:Title: xylanase B and an arabinofuranosidase from Pseudomonas fluorescens subsp. cellul
 A:Reference number: 513391; MUID:91097447
 A:Accession: 513391
 A:Molecule type: DNA
 A:Residues: 1-592 <REL>
 A:Cross-references: EMBL:X54523; NID:g45523; PIDN:CA58389.1; PID:g45524
 C:Genetics:
 A:Gene: xynB
 C:Function:
 A:Description: catalyzes the hydrolysis of 1,4-beta-xylosidic linkages in xyans
 A:Pathway: xylan degradation
 C:Superfamily: Pseudomonas endo-1,4-beta-xylanase B; bacterial cellulose-binding domain
 C:Keywords: glycosidase; hydrolase; polysaccharide degradation
 F:38-134/Domain: bacterial cellulose-binding domain homology <BCB>
 F:337-592/Domain: Streptomyces endo-1,4-beta-xylanase A homology <SXY>
 F:39-133/Disulfide bonds: #status predicted
 F:431,530/Active site: Glu #status predicted

```

Query Match          33.1%; Score 46; DB 1; Length 592;
Best Local Similarity 42.9%; Pred. No. 26;
Matches      9; Conservative    4; Mismatches      8; Indels      0; Gaps      0;
QY      2 FTLSSEWATHKFAADCKAKRDT 22
       :::|||:| |::| ||
Db      41 YTIIDSEWSTGTANTLTNKNDT 61

```

RESULT 13
E83137
Probable nonribosomal peptide synthetase PA4078 [imported] - *Pseudomonas aeruginosa* (strain ATCC 27846) [NCBI]
C:Species: *Pseudomonas aeruginosa*
C:Date: 15-Sep-2000 #sequence, revision 15-Sep-2000 #text, change 31-Dec-2000
C:Accession: E83137
R:Stover, C.K.; Plam, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Berman, S.; Yun, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lapidis, K.; Lim, J.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic pathogen
A:Reference number: GB:AE004823; GB:AE004091; MID:g9950265; PIDN:AA607465.1; GSPDB:GN000491
A:Accession: E83137
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-991 <SMD>
A:Cross references: GB:AE004823; GB:AE004091; MID:g9950265; PIDN:AA607465.1; GSPDB:GN000491
A:Experimental source: strain PA01
C:Genetics:
A:Gene: PA4078
C:Superfamily: acyl carrier protein homology; acetate--CoA ligase homology
F:50-488/Domain: acetyl carrier protein homology <ACL>
F:50-575/Domain: acyl carrier protein homology <ACP>

Query Match	33.1%	Score 46:	DB 2:	Length 991:
Best Local	40.0%	Pred. NO. 43:		
Matches	8:	Mismatches	8:	Gaps 0
Conservative	4:			

```
QY      4 LKSEWATHKFEADCKAKRDP 23
          ::|:| | | | |
Db      790 VRSKVWMEKIADIAAERGLP 809
```

RESULT 14
T48403

hypothetical protein F17C15.180 - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C>Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
 C/Accession: T48403
 R:Bevan, M.; Pohl, T.; Weizenegger, T.; Bancroft, I.; Mewes, H.W.; Rudd, S.; Lemcke
 submitted to the Protein Sequence Database, March 2000
 A:Reference number: Z24492
 A:Accession: T48403
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1533 <BEV>
 A:Cross-references: EMBL:AL162506
 A:Experimental source: cultivar Columbia; BAC clone F17C15
 C:Genetics:
 A:Map position: 5
 A:Insertions: 110/3; 143/3; 228/1; 265/1; 310/3; 348/3; 415/2; 480/2
 A:Note: F17C15.180

Query Match	32.7%	Score 45.5	DB 2	Length 533
Best Local Similarity	52.4%	Pred. No. 28		
Matches 11	Conservative 1	Mismatches 8	Indels 1	Gaps 1
QY	6	SEW-ATHKFADCKAKRQPTTS	25	
	:			
Db	449	NEWIVTEKLDGVKAKSATKTS	469	

RESULT 15
 PLO186
 Ig lambda chain, C region - sandbar shark (fragment)
 C:Species: Carcharhinus plumbeus (sandbar shark)
 C:Date: 20-Feb-1995 #sequence,revision 20-Feb-1995 #text,change 17-Nov-2000
 C:Accession: PLO186
 R:Schluter, S.F.; Betschel, C.J.; Martin, S.A.; Marchalonis, J.J.
 Mol. Immunol. 27, 17-23, 1990
 A:Title: Sequence analysis of homogeneous peptides of shark immunoglobulin light chain
 epitopes of sharks and mammals.
 A:Reference number: PLO186; MUID:90190677
 A:Accession: PLO186
 A:Molecule type: mRNA
 A:Residues: 1-67 <SCH>
 A:Experimental source: serum
 C:Genetics:
 A:Gene: SHLC6
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin

Query Match	32.4%	Score 45:	DB 2:	Length 67:
Best Local Similarity	41.2%	Pred. No. 4.2:		
Matches	7:	Conservative	3:	Mismatches 7:
				Indels 0:
				Gaps 0:
QY	6	SEMAHKEADCKAKRDT	22	
		: :	: :	:
DB	36	SEWNSHELXCVCKHET	52	

Search completed: December 19, 2001, 16:22:40
Job time: 460 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: December 19, 2001, 16:26:17; Search time 48.45 Seconds

(without alignments)
18.919 Million cell updates/sec

Title: US-09-202-104A-8

Perfect score: 139

Sequence: 1 NFKLSEWATKFKADCKAKRDTPTS 25

Scoring table: BIOSUM62

Gapop 10.0, Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	139	100.0	918	1 IL6B_HUMAN	P40189 homo sapien
2	88	63.3	917	1 IL6B_MOUSE	Q00560 mus musculu
3	88	63.3	918	1 IL6B_RAT	P40190 rattus norv
4	50	36.0	266	1 KLR3_MOUSE	O64329 mus musculu
5	49	35.3	2895	1 HYDP_DROME	P51552 drosophila
6	47.5	34.2	394	1 AMP1_HUMAN	P53552 homo sapien
7	46	33.1	571	1 XYNB_PSEFL	P23031 pseudomonas
8	46	33.1	592	1 XYNB_PSEFL	P23030 pseudomonas
9	44	31.7	266	1 KLR8_MOUSE	O60682 mus musculu
10	44	31.7	360	1 FADH_AMEYE	P80094 amycolatops
11	44	31.7	909	1 Y4G1_RHISN	P55465 thizobidum s
12	43	30.9	2301	1 POLG_TMEVD	P13899 t genome po
13	43	30.9	2303	1 POLG_TMEVD	P08545 t genome po
14	42.5	30.6	488	1 GATB_CHELT	O84007 chlamydia t
15	42.5	30.6	569	1 TNRA3_SCHPO	P41888 schizosacch
16	42	30.2	381	1 DCOP_TTRIRE	P21594 trichoderma
17	42	30.2	437	1 EF1G_HUMAN	P26641 homo sapien
18	42	30.2	437	1 EF1G_MOUSE	O9d80 mus musculu
19	42	30.2	437	1 EF1G_MOUSE	P29694 oryctolagus
20	42	30.2	444	1 TBG_CAEEL	P44475 caenorhabdi
21	41	29.5	239	1 VV_NDVU2	O66428 newcastile d
22	41	29.5	269	1 Y474_RICPR	O92d70 rickettsia
23	41	29.5	303	1 NQRE_VIBPS	O91c32 vibrio psyc
24	41	29.5	311	1 GIAG_GALIA	P38433 giardia lam
25	41	29.5	372	1 3BH4_RAT	O62878 r 3 beta-hy
26	41	29.5	395	1 RRP_NDVU2	O66427 newcastile d
27	41	29.5	446	1 GAG_CMVYS	P16900 cytole jentl
28	41	29.5	673	1 KR74_HSV11	Q00055 icetallurid h
29	41	29.5	903	1 SYLM_HUMAN	Q15031 homo sapien
30	41	29.5	951	1 ACON_MYCAV	P37071 homo sapien
31	41	29.5	961	1 ACON_MYCAV	O08451 mycobacteri
32	41	29.5	1035	1 DPOL_RHGM6	O71121 rhesus cyto
33	40	28.8	168	1 PUR6_ECOLI	P09028 escherichia

RESULT	1	STANDARD	PRT	918 AA
IL6B_HUMAN				
ID	P40189: Q9U041:			
AC	01-FEB-1995 (Rel. 31, Created)			
DT	01-FEB-1995 (Rel. 31, Last sequence update)			
DT	20-AUG-2001 (Rel. 40, Last annotation update)			
DE	INTERLEUKIN-6 RECEPTOR BETA CHAIN PRECURSOR (IL-6R-BETA) (INTERLEUKIN			
DE	6 SIGNAL TRANSDUCER) (MEMBRANE GLYCOPROTEIN 130) (GP130) (ONCOSTATIN M			
DE	RECEPTOR) (CDM130) (CD130 ANTIGEN).			
GN	IL6ST.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A. (ISOFORM 1).			
RC	TISSUE=Myeloma, and Placenta;			
RA	MEDLINE=91084844; PubMed=2261637;			
RA	Hibi M., Murakami M., Saito M., Hirano T., Taga T., Kishimoto T.;			
RT	"Molecular cloning and expression of an IL-6 signal transducer,			
RT	gp130.";			
RL	Cell 63:1149-1157(1990).			
RN	[2]			
RP	SEQUENCE FROM N.A. (ISOFORM 2).			
RC	TISSUE=Synovium;			
RA	PubMed=10880057;			
RA	Tanaka M., Kishimura M., Ozaki S., Osakada F., Hashimoto H., Okubo M.,			
RA	Murakami M., Nakao K.;			
RT	"Cloning of novel soluble gp130 and detection of its neutralizing			
RT	autoantibodies in rheumatoid arthritis.";			
RL	J. Clin. Invest. 106:137-144(2000).			
RN	[3]			
RP	PARTIAL SEQUENCE, DISULFIDE BONDS, AND CARBOHYDRATE-LINKAGE SITES.			
RC	PubMed=11098061;			
RA	Moritz R.L., Hall N.E., Connolly L.M., Simpson N.J.;			
RT	"Determination of the disulfide structure and N-glycosylation sites of			
RT	the extracellular domain of the human signal transducer gp130.";			
RL	J. Biol. Chem. 276:8244-8253(2001).			
RN	[4]			
RP	X-RAY CRYSTALLOGRAPHY (2.0-ANGSTROMS) OF 122-325.			
RC	MEDLINE=98169383; PubMed=9501088;			
RA	Bravo J., Staunton D., Heath J.K., Jones E.Y.;			
RT	"Crystal structure of a cytokine-binding region of gp130.";			
RL	EMBO J. 17:1665-1674(1998).			
CC	-1- FUNCTION: SIGNAL-TRANSDUCING MOLECULE. THE RECEPTOR SYSTEMS FOR			
CC	IL-6, LIF, OSM, CNTF, IL-11 AND CT-1 CAN UTILIZE GP130 FOR			
CC	INITIATING SIGNAL TRANSMISSION. BINDS TO IL-6/IL-6-R (ALPHA CHAIN)			
CC	COMPLEX, RESULTING IN THE FORMATION OF HIGH-AFFINITY IL-6 BINDING			
CC	SITES. AND TRANSDUCES THE SIGNAL. DOES NOT BIND IL-6. MAY HAVE A			
CC	ROLE IN EMBRYONIC DEVELOPMENT (BY SIMILARITY).			
CC	-1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.			
CC	-1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (ISOFORM 1) AND			
CC	SECRETED (ISOFORM 2).			
CC	-1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: 1 (SHOWN HERE) AND 2/GP130-			
CC	RAFS; ARE PRODUCED BY ALTERNATIVE SPLICING.			

CC -1- TISSUE SPECIFICITY: FOUND IN ALL THE TISSUES AND CELL LINES.
 CC EXAMINED. EXPRESSION NOT RESTRICTED TO IL-6 RESPONSIVE CELLS.
 CC DISEASE: GP130-RAPS IS AN AUTOANTIGEN FOUND IN RHEUMATOID
 CC ARTHRITIS (RA) BUT IT IS NOT SPECIFIC TO PATIENTS WITH RA.
 CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
 CC -1- SIMILARITY: CONTAINS 5 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 CC -1- DATABASE: NAME-PROW; NOTE-CD guide CD130 entry;
 CC WWW: <http://www.ncbi.nlm.nih.gov/prov/cd/cd130.htm>.
 CC -----
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 CC -----
 CC EMBL: M57230; AAA59155.1; -.
 CC EMBL: AB015706; BAA78112.1; -.
 CC PIR: A36337; A36337.
 CC PDB: 1BOU; 26-AUG-98.
 CC MIM: 600694; -.
 CC InterPro: IPR002996; CRA.
 CC InterPro: IPR001777; FN_III.
 CC InterPro: IPR003529; Hematopo_receptor_L_F2.
 CC Pfam: PF00041; fn3; 3.
 CC SMART: SMO0014; FNTYPEIII.
 CC SMART: SMO0060; FN3; 3.
 CC PROSITE: PS01353; Hematopo_REC_L_F2; 1.
 CC Receptor: Transmembrane; Glycoprotein; Immunoglobulin domain; Signal;
 CC Repeat: 3d-structure; Alternative splicing.
 CC KW: Repeat: 3d-structure; Alternative splicing.
 CC FT SIGNAL 1 22
 CC FT CHAIN 23 918 INTERLEUKIN-6 RECEPTOR BETA CHAIN.
 CC FT DOMAIN 23 619 EXTRACELLULAR (POTENTIAL).
 CC FT TRANSEM 620 641 POTENTIAL.
 CC FT DOMAIN 642 918 CYTOPLASMIC (POTENTIAL).
 CC FT DOMAIN 126 120 IG-LIKE C2-TYPE DOMAIN.
 CC FT DOMAIN 124 222 FIBRONECTIN TYPE-III 1.
 CC FT DOMAIN 223 324 FIBRONECTIN TYPE-III 2.
 CC FT DOMAIN 325 423 FIBRONECTIN TYPE-III 3.
 CC FT DOMAIN 424 517 FIBRONECTIN TYPE-III 4.
 CC FT DOMAIN 518 613 FIBRONECTIN TYPE-III 5.
 CC FT DOMAIN 725 755 SER-RICH.
 CC FT DISULFID 28 54
 CC FT DISULFID 48 103
 CC FT DISULFID 134 144
 CC FT DISULFID 172 182
 CC FT DISULFID 458 466
 CC FT CARBOHYD 43 43 N-LINKED (GLCNAC. . .).
 CC FT CARBOHYD 83 83 N-LINKED (GLCNAC. . .).
 CC FT CARBOHYD 131 131 N-LINKED (GLCNAC. . .).
 CC FT CARBOHYD 157 157 N-LINKED (GLCNAC. . .).
 CC FT CARBOHYD 227 227 N-LINKED (GLCNAC. . .).
 CC FT CARBOHYD 379 379 N-LINKED (GLCNAC. . .).
 CC FT CARBOHYD 383 383 N-LINKED (GLCNAC. . .).
 CC FT CARBOHYD 553 553 N-LINKED (GLCNAC. . .).
 CC FT CARBOHYD 564 564 N-LINKED (GLCNAC. . .).
 CC FT VASAPPLIC 325 329 RPSKA -> NTRAF (IN GP130-RAPS).
 CC FT VASAPPLIC 330 918 MISSING (IN GP130-RAPS).
 CC SEQUENCE 918 AA; 103522 MW; D813F3672DD10D53 CRC64;

Query Match 100.0%; Score 139; DB 1; Length 918;
 Best Local Similarity 100.0%; Pred. No. 2.8e-14;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NFKSEWATKFKADCKAKRDTPTS 25
 DB 157 NFKSEWATKFKADCKAKRDTPTS 181

RESULT 2

IL6_MOUSE
 ID IL6_MOUSE STANDARD: PRT: 917 AA.
 AC Q00560;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE INTERLEUKIN-6 RECEPTOR BETA CHAIN PRECURSOR (IL-6R-BETA) (INTERLEUKIN
 DE 6 SIGNAL TRANSDUCER) (MEMBRANE GLYCOPROTEIN 130) (GP130).
 GN IL6ST.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ICR; TISSUE=Macrophage;
 RX MEDLINE=92291532; PubMed=1602143;
 RA Saito M., Yoshida K., Hibi M., Tega T., Kishimoto T.;
 RT "Molecular cloning of a murine IL-6 receptor-associated signal
 transducer, gp130, and its regulated expression in vivo."
 RL J. Immunol. 148:4066-4071(1992).
 CC -1- FUNCTION: SIGNAL-TRANSDUCING MOLECULE. THE RECEPTOR SYSTEMS FOR
 CC IL-6, LIF, OSM, CNTF, AND IL-11 CAN UTILIZE GP130 FOR INITIATING
 CC SIGNAL TRANSMISSION. BINDS TO IL-6/IL-6-R (ALPHA CHAIN) COMPLEX,
 CC RESULTING IN THE FORMATION OF HIGH-AFFINITY IL-6 BINDING SITES.
 CC AND TRANSDUCES THE SIGNAL. DOES NOT BIND IL-6. MAY HAVE A ROLE IN
 CC EMBRYONIC DEVELOPMENT.
 CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- TISSUE SPECIFICITY: FOUND IN TISSUES SUCH AS BRAIN, HEART, THYMUS,
 CC SPLEEN, KIDNEY, LUNG AND LIVER. FOUND IN ALL THE CELL LINES TESTED
 CC EXCEPT BAF-B03. EXPRESSION NOT RESTRICTED TO IL-6-RESPONSIVE
 CC CELLS.
 CC -1- DEVELOPMENTAL STAGE: IN EMBRYONIC STEM CELLS IT IS FOUND FROM DAY
 CC 6 OF GESTATION. IT REACHES A PEAK ON DAY 8 AND GRADUALLY DECLINES
 CC DURING THE REST OF EMBRYOGENESIS.
 CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
 CC -1- SIMILARITY: CONTAINS 5 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 CC -----
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 CC -----
 CC EMBL: X62646; CAA44515.1; -.
 CC EMBL: M83336; AAA37723.1; -.
 CC HSSP: P40189; IBOU.
 CC DR MGD; MGI:96560; Il6st.
 CC DR InterPro: IPR002996; CRA.
 CC DR InterPro: IPR001777; FN_III.
 CC DR InterPro: IPR003529; Hematopo_receptor_L_F2.
 CC Pfam: PF00041; fn3; 4.
 CC SMART: SMO0014; FNTYPEIII.
 CC SMART: SMO0060; FN3; 2.
 CC PROSITE: PS01353; Hematopo_REC_L_F2; 1.
 CC Receptor: Transmembrane; Glycoprotein; Immunoglobulin domain; Signal;
 CC Repeat:
 CC KW Repeat:
 CC FT SIGNAL 1 22
 CC FT CHAIN 23 917 INTERLEUKIN-6 RECEPTOR BETA CHAIN.
 CC FT DOMAIN 23 617 EXTRACELLULAR (POTENTIAL).
 CC FT TRANSEM 618 639 POTENTIAL.
 CC FT DOMAIN 640 917 CYTOPLASMIC (POTENTIAL).
 CC FT DOMAIN 126 120 IG-LIKE C2-TYPE DOMAIN.
 CC FT DOMAIN 124 220 FIBRONECTIN TYPE-III 1.
 CC FT DOMAIN 221 322 FIBRONECTIN TYPE-III 2.
 CC FT DOMAIN 323 420 FIBRONECTIN TYPE-III 3.
 CC FT DOMAIN 422 515 FIBRONECTIN TYPE-III 4.
 CC FT DOMAIN 516 611 FIBRONECTIN TYPE-III 5.
 CC FT DOMAIN 723 741 SER-RICH.

FT DISULFID 28 54 BY SIMILARITY.
 FT DISULFID 48 103 BY SIMILARITY.
 FT DISULFID 134 144 BY SIMILARITY.
 FT DISULFID 172 180 BY SIMILARITY.
 FT DISULFID 456 464 BY SIMILARITY.
 FT CARBOHYD 43 43 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 61 61 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 83 83 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 131 131 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 157 157 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 225 225 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 388 388 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 476 476 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 551 551 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 917 AA: 102452 MW; FCFEPD20BC2466F4 CRC64;

Query Match 63.3%; Score 88; DB 1; Length 917;
 Best Local Similarity 68.2%; Pred. No. 3.5e-06;
 Matches 15; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 1 NPTLKSEWATHKPADCKAKRDT 22
 I:||||||| I I I I I I
 Db 157 NYTLKSEWATEKPPDCQSKHGT 178

RESULT 3
 IL6B_RAT STANDARD; PRT; 918 AA.
 AC P40190;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE INTERLEUKIN-6 RECEPTOR BETA CHAIN PRECURSOR (IL-6R-BETA) (INTERLEUKIN
 DE 6 SIGNAL TRANSDUCER) (MEMBRANE GLYCOPROTEIN I30) (GP130).
 GN IL6ST.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID-10116;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE-93052397; PubMed-1477893;
 RA Wang Y., Nesbitt J.E., Fuentes N.L., Fuller G.M.;
 RT Molecular cloning and characterization of the rat liver IL-6 signal
 RL transducing molecule, gp130. "
 RL Genomics 14:666-672(1992).
 CC -1- FUNCTION: SIGNAL-TRANSDUCING MOLECULE. THE RECEPTOR SYSTEMS FOR
 CC IL-6, LIF, OSM, CNTF, AND IL-11 CAN UTILIZE GP130 FOR INITIATING
 CC SIGNAL TRANSMISSION. BINDS TO IL-6/IL-6-R (ALPHA CHAIN) COMPLEX,
 CC RESULTING IN THE FORMATION OF HIGH-AFFINITY IL-6 BINDING SITES,
 CC AND TRANSDUCES THE SIGNAL. DOES NOT BIND IL-6. MAY HAVE A ROLE IN
 CC EMBRYONIC DEVELOPMENT (BY SIMILARITY).
 CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- TISSUE SPECIFICITY: FOUND IN HEPATOCYTES, ASTROCYTES, FIBROBLASTS
 CC AND ENDOTHELIAL CELLS.
 CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
 CC -1- SIMILARITY: CONTAINS 5 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: M92340; -; NOT_ANNOTATED_CDS.
 CC PIR: A44257; A44257.
 DR HSSP: P40189; IBDU.

DR InterPro: IPR002996; CRIA.
 DR InterPro: IPR01777; FN III.
 DR InterPro: IPR003529; Hemato_p_rceptor_L_F2.
 DR Pfam: PF00061; fn3; 3.
 DR SMART: SM00060; FN3; 3.
 DR PROSITE: PS01353; HEMATOPO_REC_L_F2; 1.
 DR Receptor; Transmembrane; Glycoprotein; Immunoglobulin domain; signal;
 KW Repeat.
 FT STGNAL 1 22
 FT CHAIN 23 918
 FT DOMAIN 23 618
 FT TRANSMEM 619 640
 FT DOMAIN 641 918
 FT DOMAIN 26 120
 FT DOMAIN 124 221
 FT DOMAIN 222 323
 FT DOMAIN 324 422
 FT DOMAIN 423 516
 FT DOMAIN 517 612
 FT DOMAIN 724 754
 FT DISULFID 28 54
 FT DISULFID 48 103
 FT DISULFID 134 144
 FT DISULFID 172 181
 FT DISULFID 457 465
 FT CARBOHYD 43 43 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 61 61 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 83 83 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 131 131 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 157 157 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 205 205 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 225 225 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 382 382 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 389 389 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 477 477 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 552 552 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 918 AA: 102450 MW; 9E18B6FECF087F7 CRC64;

Query Match 63.3%; Score 88; DB 1; Length 918;
 Best Local Similarity 68.2%; Pred. No. 3.5e-06;
 Matches 15; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

OY 1 NPTLKSEWATHKPADCKAKRDT 22
 I:||||||| I I I I I I
 Db 157 NYTLKSEWATEKPPDCRTKHGT 178

RESULT 4
 KLR3_MOUSE STANDARD; PRT; 266 AA.
 AC Q64329; Q64257; Q61154;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE KILLER CELL LECTIN-LIKE RECEPTOR 3 (T-CELL SURFACE GLYCOPROTEIN
 DE LY-49C) (LY49-C ANTIGEN) (LYMPHOCYTE ANTIGEN 49C) (5E6).
 GN KLR3 OR LY49C OR LY-49C.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID-10090;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=CB.17;
 RX MEDLINE-95355830; PubMed-7629496;
 RA Strongman E.R., Bennett M., An J., Chesnut K.A., Wakeland E.K.,
 RA Schreier J.B., Siciliano M.J., Kumar V., Kumar P.A.;
 RT Cloning and characterization of 566(Ly-49C), a receptor molecule
 RT expressed on a subset of murine natural killer cells."
 RL J. Exp. Med. 182:305-313(1995).
 RN (2)
 RP SEQUENCE FROM N.A.

RC STRAIN-C57BL/6 X CBA; TISSUE=Lung;
RA MEDLINE-91332459; PubMed-1869832;
RX Wong S., Freeman J.D., Kelleher C., Mager D., Takei F.;
RT "Ly-49 multigene family. New members of a superfamily of type II
RL membrane proteins with lectin-like domains."
RN J. Immunol. 147:1417-1423(1991).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-C57BL/6, AND 129/SVJ;
RX MEDLINE-95356819; PubMed-7630404;
RA Held W., Roland J., Raullet D.H.;
RT "Allelic exclusion of Ly49-family genes encoding class I MHC-specific
RN receptors on NK cells."
RL Nature 376:355-358(1995).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN-A/SN;
RA Sundback J., Karre K., Sentman C.L.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN-C57BL/6 X CBA; TISSUE=Lung;
RX Wong S., Freeman J.D., Kelleher C., Mager D., Takei F.;
RT Submitted (JUN-1994) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/C, NZB, C57BL/6, AND BALB/C X C57BL/6;
RA Mathew P.A., Stoneman E., Bennett M., An J., Chesnut K.A.,
RL Wakeland E.K., Scheerer J.B., Siciliano M.J., Khusat V.;
RT Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
RN [7]
RP FUNCTION: RECEPTOR ON NATURAL KILLER (NK) CELLS FOR CLASS I MHC.
CC -1- SUBUNIT: HOMODIMER. DISULFIDE-LINKED.
CC -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN.
CC -1- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
CC -----
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CC or send an email to license@ebi.ac.uk).
CC -----
CC
DR EMBL: U09739; AAA86873.1; -
DR EMBL: U49865; AAA92951.1; -
DR EMBL: U49866; AAA92952.1; -
DR EMBL: U49867; AAA92953.1; -
DR EMBL: U49868; AAA92954.1; -
DR EMBL: U10305; AAA19053.1; -
DR EMBL: U56405; AAB19101.1; -
DR EMBL: U34891; AAB77066.1; -
DR EMBL: U34892; AAC17703.1; -
DR HSP: P05451; ILIT.
DR MCD: MGT101905; KIR3.
DR InterPro: IPR001304; Lectin_c.
DR Pfam: PF00059; lectin_c.1.
DR SMART: SM00034; CLECT.1.
DR PROSITE: PS00615; C-TYPE LECTIN_1; FALSE_NEG.
DR PROSITE: PS50041; C-TYPE LECTIN_2; 1.
KW T-cell; Glycoprotein; Antigen; Transmembrane; Cell adhesion;
KW Signal-anchor; Lectin; Receptor; Multigene family.
FT DOMAIN 1 44 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 45 66 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT (POTENTIAL).
FT DOMAIN 67 266 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 143 261 C-TYPE LECTIN (LONG FORM).
FT DISULFID 154 257 BY SIMILARITY.
FT DISULFID 171 249 BY SIMILARITY.
FT CARBOHYD 79 79 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 104 104 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 113 113 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 160 160 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT	VARIANT	2	2	S -> N (IN STRAINS BALB/C X C57BL/6 AND C57BL/6).
FT	VARIANT	13	13	L -> F (IN STRAIN 129/SVJ).
FT	VARIANT	22	22	Q -> L (IN STRAINS BALB/C X C57BL/6, NZB, 129/SVJ AND C57BL/6).
FT	VARIANT	34	34	V -> A (IN STRAINS BALB/C X C57BL/6, NZB, 129/SVJ AND C57BL/6).
FT	VARIANT	41	42	AP -> VS (IN STRAINS BALB/C X C57BL/6, NZB, 129/SVJ AND C57BL/6).
FT	VARIANT	60	60	T -> I (IN STRAINS BALB/C X C57BL/6, NZB, 129/SVJ AND C57BL/6).
FT	VARIANT	65	66	AV -> TI (IN STRAINS BALB/C X C57BL/6, NZB, 129/SVJ AND C57BL/6).
FT	VARIANT	72	72	N -> S (IN STRAINS BALB/C X C57BL/6, NZB, 129/SVJ AND C57BL/6).
FT	VARIANT	85	85	H -> Y (IN STRAINS BALB/C X C57BL/6, NZB, 129/SVJ AND C57BL/6).
FT	VARIANT	93	93	S -> R (IN NZB AND 129/SVJ).
FT	VARIANT	115	115	T -> L (IN STRAINS BALB/C X C57BL/6, NZB AND C57BL/6).
FT	VARIANT	115	115	T -> I (IN STRAIN 129/SVJ).
FT	VARIANT	117	117	E -> D (IN STRAINS BALB/C X C57BL/6 AND C57BL/6).
FT	VARIANT	127	127	D -> N (IN STRAINS BALB/C X C57BL/6 AND C57BL/6).
FT	VARIANT	129	129	K -> E (IN STRAINS BALB/C X C57BL/6, NZB, 129/SVJ AND C57BL/6).
FT	VARIANT	131	131	K -> N (IN STRAIN NZB).
FT	VARIANT	133	133	V -> I (IN STRAIN NZB).
FT	VARIANT	146	146	Y -> H (IN STRAINS BALB/C X C57BL/6 AND C57BL/6).
FT	VARIANT	151	151	S -> G (IN STRAINS BALB/C X C57BL/6, NZB, 129/SVJ AND C57BL/6).
FT	VARIANT	174	174	F -> Y (IN STRAINS BALB/C X C57BL/6, NZB, 129/SVJ AND C57BL/6).
FT	VARIANT	179	179	L -> V (IN STRAINS BALB/C X C57BL/6, NZB AND C57BL/6).
FT	VARIANT	189	189	F -> S (IN STRAIN NZB).
FT	VARIANT	198	198	N -> S (IN STRAINS BALB/C X C57BL/6, NZB AND C57BL/6).
FT	VARIANT	219	219	P -> Q (IN STRAINS BALB/C X C57BL/6, NZB AND C57BL/6).
FT	VARIANT	222	222	L -> F (IN STRAIN 129/SVJ).
FT	VARIANT	226	226	I -> T (IN STRAINS BALB/C X C57BL/6 AND C57BL/6).
FT	VARIANT	232	232	K -> T (IN STRAIN NZB).
FT	VARIANT	247	247	I -> T (IN STRAINS BALB/C X C57BL/6, NZB, 129/SVJ AND C57BL/6).
FT	VARIANT	251	251	I -> T (IN STRAIN NZB).
FT	VARIANT	260	260	K -> R (IN STRAIN NZB).
FT	SEQUENCE	266 AA;	31285 MW;	409F61E5DFAD299A CRC64;

Query Match 36.0%; Score 50; DB 1; Length 266;
Best Local Similarity 40.9%; Pred. No. 1;
Matches 9; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

Oy 1 NETKSEWATHKADCKAKRDT 22
Db 94 DFNKKEMLTKNSIDCRSNET 115

RESULT 5
HYDP_DROME STANDARD: PRT: 2895 AA.
AC P51592; 01-OCT-1996 (Rel. 34, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DI 20-AUG-2001 (Rel. 40, Last annotation update)
DE HYPERPLASTIC DISCS PROTEIN (HYD PROTEIN) (EC 6.3.2.-).
GN HYD OR L(3)CA3.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Insecta;

OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95046871; PubMed=7958417;
 RA Mansfield E., Hersperger E., Biggs J., Shearn A.;
 RT "Genetic and molecular analysis of hyperplastic discs, a gene whose
 product is required for regulation of cell proliferation in
 Drosophila melanogaster imaginal discs and germ cells.";
 RL Dev. Biol. 165:507-526(1994).
 RN [2]
 RP REVISIONS.
 RA Shearn A.;
 RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: REQUIRED FOR REGULATION OF CELL PROLIFERATION IN
 CC IMAGINAL DISCS AND GERM CELLS.
 CC -1- FUNCTION: E3 UBIQUITIN-PROTEIN LIGASE WHICH ACCEPTS UBIQUITIN FROM
 CC AN E2 UBIQUITIN-CONJUGATING ENZYME IN THE FORM OF A THIOESTER AND
 CC THEN DIRECTLY TRANSFERS THE UBIQUITIN TO TARGETED SUBSTRATES (BY
 CC SIMILARITY).
 CC -1- DEVELOPMENTAL STAGE: PUPAE AND LARVAE.
 CC -1- MISCELLANEOUS: A CYSTEINE RESIDUE IS REQUIRED FOR UBIQUITIN-
 CC THIOESTER FORMATION.
 CC -1- SIMILARITY: CONTAINS 1 HECT-TYPE E3 UBIQUITIN-PROTEIN LIGASE
 CC DOMAIN.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; L14644; AAB88625.1; -
 DR F1; EMBL; EFGN0002431; hyd.
 DR InterPro: IPR000569; HECT.
 DR InterPro: IPR002004; PABP.
 DR InterPro: IPR000449; UBA.
 DR InterPro: IPR003126; ZNF_UBR1.
 DR Pfam; PF00632; HECT; 1.
 DR Pfam; PF00658; PABP; 1.
 DR Pfam; PF02307; zf-UBR1; 1.
 DR SMART; SM00119; HECTC; 1.
 DR SMART; SM00517; POLYA; 1.
 DR SMART; SM00396; ZNF_UBR1; 1.
 DR PROSITE; PS50237; HECT; 1.
 DR Ubiquitin conjugation; Llgase; Repeat.
 FT DOMAIN 621 626 POLY-PRO.
 FT DOMAIN 700 709 POLY-ALA.
 FT DOMAIN 2587 2590 POLY-VAL.
 FT DOMAIN 2792 2895 HECT.
 FT BINDING 2864 2864 UBIQUITIN (BY SIMILARITY).
 SQ SEQUENCE 2895 AA; 319672 MW; 4E172B8D5A12B156 CRC64;

Query Match 35.3%; Score 49; DB 1; Length 2895;
 Best Local Similarity 60.0%; Pred. No. 18;
 Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

OY 11 HKPADCKARDPPTS 25
 DB 1249 HKGHCKLKRTAFTA 1263

RESULT 6
 ID AMPL_HUMAN STANDARD; PRT; 394 AA.
 AC P53582;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE PUTATIVE METHIONINE AMINOPEPTIDASE 1 (EC 3.4.11.18) (METAP 1)
 GN (PEPTIDASE M 1) (FRAGMENT).
 DE KIAA0094.
 GN KIAA0094.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Bone marrow;
 RX MEDLINE=95308325; PubMed=7788527;
 RA Nagase T., Miyajima N., Tanaka A., Sazuka T., Seki N., Sato S.,
 RA Tabata S., Ishikawa K.-I., Kawarabayashi Y., Kotani H., Nomura N.;
 RT "Prediction of the coding sequences of 40 new genes (KIA0081-KIA0120) deduced by
 RT analysis of cDNA clones from human cell line KG-1.";
 RL DNA Res. 2:37-43(1995).
 CC -1- FUNCTION: REMOVES THE AMINO-TERMINAL METHIONINE FROM NASCENT
 CC PROTEINS (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: L-METHIONYLPEPTIDE + H(2)O = L-METHIONINE
 CC + PEPTIDE.
 CC -1- COFACTOR: COBALT (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M24A; ALSO KNOWN AS THE
 CC MAP FAMILY 1.
 CC -----
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 CC -----
 DR EMBL; D42084; BAA07679.1; -
 DR HSSP; P07906; 1MAT.
 DR MEROPS; M24.001; -
 DR InterPro: IPR002467; MAP_1.
 DR InterPro: IPR000994; Peptidase_M24.
 DR Pfam; PF00557; Peptidase_M24; 1.
 DR PROSITE; PS00680; MAP_1; 1.
 DR Hydrolyase; Amino-peptidase; Cobalt.
 FT METAL 1 1
 FT METAL 228 228 COBALT (BY SIMILARITY).
 FT METAL 239 239 COBALT (BY SIMILARITY).
 FT METAL 302 302 COBALT (BY SIMILARITY).
 FT METAL 335 335 COBALT (BY SIMILARITY).
 FT METAL 367 367 COBALT (BY SIMILARITY).
 SQ SEQUENCE 394 AA; 44046 MW; 4B37DE9282ACD40 CRC64;

Query Match 34.2%; Score 47.5; DB 1; Length 394;
 Best Local Similarity 50.0%; Pred. No. 3.8;
 Matches 11; Conservative 1; Mismatches 5; Indels 5; Gaps 1;

OY 5 KSEWATHKFR-----ADCKARD 21
 DB 50 KGSWATHKLIHKRAKDKAKRE 71

RESULT 7
 ID XYNC_PSEFL STANDARD; PRT; 571 AA.
 AC P23031;
 DT 01-NOV-1991 (Rel. 20, Created)
 DT 01-NOV-1991 (Rel. 20, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE ALPHA-L-ARABINOFURANOSIDASE C PRECURSOR (EC 3.2.1.55) (XYLANASE C).
 GN XYNC.
 OS Pseudomonas fluorescens.
 OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
 OC Pseudomonas.
 OX NCBI_TaxID=294;

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RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 39-56.
RC STRAIN-SP. CELLULOZA;
RA MEDLINE-91097447; PubMed-2125205;
RA Kellelt L.E., Poole D.M., Ferreira L.M.A., Durrant A.J.,
RA Hazlewood G.P., Gilbert H.J.;
RA "Xylanase B and an arabinofuranosidase from Pseudomonas fluorescens
RT subsp. cellulosa contain identical cellulose-binding domains and are
RT encoded by adjacent genes.";
RT Biochem. J. 272:369-376(1990).
CC -1- FUNCTION: XYLANASE C CONTRIBUTES TO HYDROLYSE HEMICELLULOSE, THE
CC MAJOR COMPONENT OF PLANT CELL-WALLS.
CC -1- CATALYTIC ACTIVITY: HYDROLYSIS OF TERMINAL NON-REDUCING ALPHA-L-
CC ARABINOFURANOSIDE RESIDUES IN ALPHA-L-ARABINOSIDES.
CC -1- PATHWAY: HEMICELLULOSE DEGRADATION.
CC -1- SUBCELLULAR LOCATION: SECRETED.
CC -1- MISCELLANEOUS: ACTS ONLY ON HIGH MW SUBSTRATES, IN WHICH ARABINOSE
CC IS LINKED TO A POLYMERIC BACKBONE.
CC -1- SIMILARITY: CONTAINS 1 BACTERIAL-TYPE CELLULOSE-BINDING DOMAIN
CC (CBD).
CC -----
CC -1- SIMILARITY: BELONGS TO FAMILY 62 OF GLYCOSYL HYDROLASES.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC DR EMBL; X54523; CA38390.1; -.
CC DR PIR; S13392; S13392.
CC DR HSSP; P01086; 1BFA.
CC DR InterPro: IPR001919; CBD_2.
CC DR Pfam; PF00553; CBD_2; 1.
CC DR PROSITE; PS00561; CBD_BACTERIAL; 1.
CC DR KMW HYDROLASE; Glycosidase; Signal.
CC FT SIGNAL 1 38
CC FT CHAIN 39 571 ALPHA-L-ARABINOFURANOSIDASE C.
CC FT DOMAIN 39 134 CELLULOSE-BINDING (BY SIMILARITY).
CC FT DOMAIN 135 160 SER-RICH (LINKER).
CC FT DOMAIN 300 320 SER-RICH (LINKER).
CC FT ACT_SITE 39 133 BY SIMILARITY.
CC FT DISULFID 39 133
CC FT SEQUENCE 571 AA; 61072 MW; AD19585F5E3D5555 CRC64;
SQ
Query Match 33.1%; Score 46; DB 1; Length 571;
Best Local Similarity 42.9%; Pred. No. 9.8;
Matches 9; Conservative 4; Mismatches 8; Indels 0; Gaps 0;
QY 2 FTLKSEWATHKFAADCKAKRDT 22
DB 41 YTISEWSTGFTANTITLKNPT 61
:|:|||||:|:|
RESULT 8
XYNB_PSEFL
ID XYNB_PSEFL STANDARD; PRT; 592 AA.
AC P23030;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE ENDO-1,4-BETA-XYLANASE B PRECURSOR (EC 3.2.1.8) (XYLANASE B)
DE (1,4-BETA-D-XYLAN XYLANOHYDROLASE B).
GN XYNB.
OS Pseudomonas fluorescens.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_Taxid=294;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 39-56.
RC STRAIN-SP. CELLULOZA;
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RX MEDLINE-91097447; PubMed-2125205;
RA Kellelt L.E., Poole D.M., Ferreira L.M.A., Durrant A.J.,
RA Hazlewood G.P., Gilbert H.J.;
RA "Xylanase B and an arabinofuranosidase from Pseudomonas fluorescens
RT subsp. cellulosa contain identical cellulose-binding domains and are
RT encoded by adjacent genes.";
RT Biochem. J. 272:369-376(1990).
CC -1- FUNCTION: XYLANASE B CONTRIBUTES TO HYDROLYSE HEMICELLULOSE, THE
CC MAJOR COMPONENT OF PLANT CELL-WALLS.
CC -1- CATALYTIC ACTIVITY: ENDOMYDOLYSIS OF 1,4-BETA-D-XYLOSIDIC
CC LINKAGES IN XYLANS.
CC -1- PATHWAY: HEMICELLULOSE DEGRADATION.
CC -1- SIMILARITY: BELONGS TO CELLULOSE FAMILY F (FAMILY 10 OF GLYCOSYL
CC HYDROLASES).
CC -1- SIMILARITY: CONTAINS 1 BACTERIAL-TYPE CELLULOSE-BINDING DOMAIN
CC (CBD).
CC -----
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CC -----
CC DR EMBL; X54523; CA38389.1; -.
CC DR PIR; S13391; S13391.
CC DR HSSP; P07986; 1EXH.
CC DR InterPro: IPR001919; CBD_2.
CC DR InterPro: IPR001000; Glyco_hydro_10.
CC DR Pfam; PF00553; CBD_2; 1.
CC DR Pfam; PF00331; Glyco_hydro_10; 1.
CC DR PRINTS; PR00134; GLHYDRLASE10.
CC DR PROSITE; PS00591; GLYCOSYL_HYDROL_F10; 1.
CC DR PROSITE; PS00561; CBD_BACTERIAL; 1.
CC DR KMW Cellulose degradation; Xylan degradation; Hydrolase; Glycosidase;
CC FT Signal.
CC FT SIGNAL 1 38
CC FT CHAIN 39 592 ENDO-1,4-BETA-XYLANASE B.
CC FT DOMAIN 39 134 CELLULOSE-BINDING (BY SIMILARITY).
CC FT DOMAIN 135 160 SER-RICH (LINKER).
CC FT DOMAIN 300 320 SER-RICH (LINKER).
CC FT ACT_SITE 431 431 PROTON-DONOR (BY SIMILARITY).
CC FT ACT_SITE 530 530 NUCLEOPHILE (BY SIMILARITY).
CC FT DISULFID 39 133 BY SIMILARITY.
CC FT SEQUENCE 592 AA; 63410 MW; E081F6308EA2B93A CRC64;
SQ
Query Match 33.1%; Score 46; DB 1; Length 592;
Best Local Similarity 42.9%; Pred. No. 10;
Matches 9; Conservative 4; Mismatches 8; Indels 0; Gaps 0;
QY 2 FTLKSEWATHKFAADCKAKRDT 22
DB 41 YTISEWSTGFTANTITLKNPT 61
:|:|||||:|:|
RESULT 9
KLRS_MOUSE
ID KLRS_MOUSE STANDARD; PRT; 266 AA.
AC Q60682; Q78027;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE KILLER CELL LECTIN-LIKE RECEPTOR 8 (T-CELL SURFACE GLYCOPROTEIN
DE LY-49H) (LY49-H ANTIGEN).
GN KLRS OR LY49H OR LY-49H OR LY49-H.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
```

RP SEQUENCE FROM N.A. (ISOFORM H1).
 RC STRAIN-C57BL/6 X CBA: TISSUE-LUNG;
 RX MEDLINE-95053763; PubMed-7964501;
 RA Brennan J., Mager D., Jefferies W., Taket F.;
 RT "Expression of different members of the Ly-49 gene family defines
 RT distinct natural killer cell subsets and cell adhesion properties.";
 RL J. Exp. Med. 180:2287-2295(1994).
 [2]
 RN SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
 RP STRAIN-C57BL/6;
 RX MEDLINE-96421544; PubMed-8824161;
 RA Silver E.T., Elliott J.F., Kane K.P.;
 RT "Alternatively spliced Ly-49D and H transcripts are found in IL-2-
 RT activated NK cells.";
 RL Immunogenetics 44:478-482(1996).
 CC -1- FUNCTION: RECEPTOR ON NATURAL KILLER (NK) CELLS FOR CLASS I MHC.
 CC -1- SUBUNIT: HOMODIMER; DISULFIDE-LINKED.
 CC -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN.
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; H1 (SHOWN HERE) AND H2; ARE
 CC PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
 CC -----
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 CC -----
 DR EMBL: U12889; AAA58704.1; -;
 DR EMBL: L78253; AAC32668.1; -;
 DR MGD: MGI:102968; Klrab.
 DR InterPro: IPR001304; Lectin_c.
 DR Pfam: PF00059; Lectin_g; 1.
 DR SMART: SM00034; CLECT; 1.
 DR PROSITE: PS00615; C_TYPE_LLECTIN_1; FALSE_NEG.
 DR PROSITE: PS00041; C_TYPE_LLECTIN_2; 1.
 KM T-cell; Glycoprotein; Antigen; Transmembrane; Cell adhesion;
 KW Signal-anchor; Lectin; Receptor; Multigene family;
 KM Alternative splicing.
 FT DOMAIN 1 44
 FT TRANSMEM 45 66
 FT SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
 FT (POTENTIAL).
 FT DOMAIN 67 266
 FT DOMAIN 143 261
 FT DISULFID 171 257
 FT DISULFID 236 249
 FT CARBOHYD 87 87
 FT CARBOHYD 104 104
 FT VARSPLIC 39 41
 FT SEQUENCE 266 AA; 31393 MW; 3CB5ABFE2EB401E2 CRC64;
 SQ
 Query Match 31.7%; Score 44; DB 1; Length 266;
 Best Local Similarity 47.1%; Pred. No. 9.1;
 Matches 8; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
 Oy 1 NFKSEWATHKFPADCK 17
 Db 94 DFLKKEMLTKNSIDCR 110
 RESULT 10
 FADH_ARYME STANDARD; PRT; 360 AA.
 ID P80094;
 AC 01-DEC-1992 (Rel. 24, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE NAD/MYCOTHIOL-DEPENDENT FORMALDEHYDE DEHYDROGENASE (EC 1.2.1.66) (MD-
 DE FALDH).
 OS Amycolatopsis methanolica.

OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Pseudonocardiaceae; Pseudonocardiaceae;
 OC Amycolatopsis
 OC NCBI_TaxID-1814;
 OX
 RN
 RP SEQUENCE.
 RX MEDLINE-98004265; PubMed-9346279;
 RA Norin A., van Ophem P.W., Piersma S.R., Persson B., Duine J.A.,
 RA Joernvall H.;
 RT "Mycotoxin-dependent formaldehyde dehydrogenase, a prokaryotic
 RT medium-chain dehydrogenase/reductase, phylogenetically links
 RT different eukaryotic alcohol dehydrogenases -- primary structure,
 RT conformational modelling and functional correlations.";
 RL Eur. J. Biochem. 248:282-289(1997).
 [2]
 RN PRELIMINARY SEQUENCE OF 1-31.
 RP MEDLINE-92283278; PubMed-1597190;
 RX van Ophem P.W., van Beeumen J., Duine J.A.;
 RA "NAD-linked, factor-dependent formaldehyde dehydrogenase or trimetric,
 RT zinc-containing, long-chain alcohol dehydrogenase from Amycolatopsis
 RT methanolica.";
 RL Eur. J. Biochem. 206:511-518(1992).
 [3]
 RN CHARACTERIZATION.
 RP MEDLINE-97345657; PubMed-9202149;
 RX Misset-Smits M., van Ophem P.W., Sakuda S., Duine J.A.;
 RA "Mycotoxin 1-O-(2'-[N-acetyl-L-cysteinyl]amido-2'-deoxy-alpha-
 RT D-glucopyranosyl)-D-myo-inositol, is the factor of NAD/factor-
 RT dependent formaldehyde dehydrogenase.";
 RL FEBS Lett. 409:221-222(1997).
 CC -1- CATALYTIC ACTIVITY: FORMALDEHYDE + MYCOTHIOL + NAD(+) =
 CC S-FORMALMYCOTHIOL + NADH.
 CC -1- COFACTOR: EACH SUBUNIT BINDS 6 IONS OF ZINC.
 CC -1- SUBUNIT: HOMOTRIMER.
 DR PIR: S23181; S23181.
 DR InterPro: IPR002328; ADH_zinc.
 DR InterPro: IPR002085; Adh_zinc.
 DR InterPro: IPR000205; NAD_binding.
 DR Pfam: PRO0107; adh_zinc; 1.
 DR PROSITE: PS00059; ADH_ZINC; 1.
 KM Oxidoreductase; NAD; Zinc.
 FT METAL 41 41
 FT METAL 62 62
 FT ACT SITE 89 89
 FT METAL 92 92
 FT METAL 95 95
 FT METAL 98 98
 FT METAL 106 106
 FT METAL 161 161
 FT SEQUENCE 360 AA; 37757 MW; 48BED1F70BAB2CB7 CRC64;
 SQ
 Query Match 31.7%; Score 44; DB 1; Length 360;
 Best Local Similarity 45.0%; Pred. No. 13;
 Matches 9; Conservative 2; Mismatches 5; Indels 4; Gaps 1;
 Oy 4 LKSEWATHKFPADCKARDTP 23
 Db 300 LKSSW----YDCLPERDEP 315
 RESULT 11
 Y4GI_RHISN STANDARD; PRT; 909 AA.
 ID Y4GI_RHISN
 AC P55465;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE HYPOTHETICAL 102.8 KDA PROTEIN Y4GI.
 GN Y4GI.
 OS Rhizobium sp. (strain NGR234).
 OG Plasmid sym pNGR234a.
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;

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OC Rhizobiaceae; Rhizobium.
OX NCBI_TaxID=394;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97305956; PubMed=9163424;
RA Freiberg C.A., Fellay R., Balroch A., Broughton W.J., Rosenthal A.,
RT Perret X.;
RL "Molecular basis of symbiosis between Rhizobium and legumes. ";
RL Nature 387:394-401(1997).
CC -1- SIMILARITY: STRONG TO M.XANTHUS O-ANTIGEN BIOSYNTHESIS PROTEIN
CC RBBC (NOT TO BE CONFUSED WITH ENTEROBACTERIAL RBBC).
CC -----
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CC -----
DR EMBL; AE000074; AAB91683.1; -
DR InterPro; IPR001173; Glycos_transf_2.
DR Pfam; PF00535; Glycos_transf_2; 2.
KW Hypothetical protein; Plasmid.
SO SEQUENCE 909 AA; 102827 MW; 3985D69722E43962 CRC64;

Query Match 31.7%; Score 44; DB 1; Length 909;
Best Local Similarity 58.3%; Pred. No. 33;
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 4 LKSEWATKFPAD 15
      : 1 1 1 1 1 1 1
Db 870 MKRRWTKHDFAD 881

RESULT 12
POLG.TMEVD STANDARD: PRT; 2301 AA.
AC P18899; Q88564; Q88565; Q88566; Q88567; Q88568; Q88569; Q88570;
AC Q88571; Q88572; Q88573; Q88574; Q88580;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE GENOME POLYPEPTIDE [CONTAINS: COAT PROTEINS VP1 TO VP4; CORE PROTEINS
DE P2A TO P2C; P3A; GENOME-LINKED PROTEIN VP3; PICORNAIN 3C
DE (EC 3.4.22.28) (PROTEASE 3C) (P3C); RNA-DIRECTED RNA POLYMERASE P3D
DE (EC 2.7.7.48)].
OS Theiler's murine encephalomyelitis virus (strain DA) (TMEV)
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC Cardiovirus.
OX NCBI_TaxID=12126;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=68206072; PubMed=2834872;
RA Ohara Y., Stein S., Fu J., Stillman L., Klman L., Roos R.P.;
RT "Molecular cloning and sequence determination of DA strain of
RT Theiler's murine encephalomyelitis viruses. ";
RL Virology 164:245-255(1988).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).
RX MEDLINE=92196057; PubMed=1549565;
RA Grant R.A., Filman D.J., Fujinami R.S., Icenogle J.P., Hogle J.M.;
RT "Three-dimensional structure of Theiler virus. ";
RL Proc. Natl. Acad. Sci. U.S.A. 89:2061-2065(1992).
CC -1- FUNCTION: IT IS THOUGHT THAT THE P2C PROTEIN ATTACHES TO VESICULAR
CC MEMBRANES AND IS ASSOCIATED WITH VIRAL RNA SYNTHESIS.
CC -1- FUNCTION: P2C POLYPEPTIDE IS A PROTEASE THAT CLEAVES AT CERTAIN
CC Q/G SITES IN THE POLYPEPTIDE. IT MAY BE A CYSTEINE PROTEASE.
CC -1- SUBUNIT: THE VIRUS CAPSID IS COMPOSED OF 60 ICOSAEDRAL UNITS,
CC EACH OF WHICH IS COMPOSED OF ONE COPY EACH OF PROTEINS VP1, VP2,
CC VP3, AND VP4.
CC -1- PTM: SPECIFIC ENZYMAIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS.

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CC	-1- SIMILARITY: CLOSELY RELATED TO ENCEPHALOMYOCARDITIS VIRUS.	
CC	-1- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY C3.	
CC	-----	
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CC	-----	
DR	EMBL; M20301; AAA47928.1; -.	
DR	PIR: A31228; GNNVTN.	
DR	PDB: 1TME; 31-JAN-94.	
DR	MEROPS; C03.009; -.	
DR	MEROPS; 029.001; -.	
DR	InterPro: IPR000605; RNA_helicase.	
DR	InterPro: IPR001205; RNA_pol_P3L.	
DR	InterPro: IPR001676; RHV.	
DR	Pfam; PF00073; rhv; 3.	
DR	Pfam; PF00680; RNA_dep_RNA_pol; 1.	
DR	Pfam; PF00910; RNA_helicase; 1.	
KW	Polypeptide; Coat protein; Core protein; Transferase;	
KW	RNA-directed RNA polymerase; Core protein; Core protein; Myristate;	
KW	3D-structure.	
FT	PROPEP	1
FT	CHAIN	77
FT	CHAIN	147
FT	CHAIN	148
FT	CHAIN	415
FT	CHAIN	647
FT	CHAIN	921
FT	CHAIN	1063
FT	CHAIN	1190
FT	CHAIN	1516
FT	CHAIN	1516
FT	CHAIN	1623
FT	CHAIN	1624
FT	CHAIN	1841
FT	LITID	77
FT	ACT_SITE	1791
FT	ACT_SITE	1809
FT	TURN	96
FT	HELIX	103
FT	STRAND	109
FT	STRAND	162
FT	TURN	167
FT	STRAND	169
FT	STRAND	173
FT	HELIX	179
FT	HELIX	182
FT	TURN	193
FT	STRAND	200
FT	HELIX	204
FT	STRAND	210
FT	TURN	219
FT	TURN	223
FT	STRAND	226
FT	TURN	232
FT	HELIX	233
FT	HELIX	238
FT	TURN	248
FT	STRAND	250
FT	TURN	267
FT	STRAND	270
FT	TURN	280
FT	STRAND	286
FT	TURN	289
FT	STRAND	294
FT	TURN	297
FT	STRAND	305
FT	TURN	324
FT	STRAND	325
FT	TURN	330
FT	HELIX	338
FT	STRAND	342
FT	TURN	343
FT	TURN	345
FT	LEADER PEPTIDE.	
FT	COAT PROTEIN VP4 (P1A).	
FT	COAT PROTEIN VP2 (P1B).	
FT	COAT PROTEIN VP3 (P1C).	
FT	COAT PROTEIN VP1 (P1D).	
FT	COAT PROTEIN P2A.	
FT	CORE PROTEIN P2B.	
FT	CORE PROTEIN P2C.	
FT	CORE PROTEIN P3A.	
FT	GENOME-LINKED PROTEIN VP6 (P3B).	
FT	PICORNAIN 3C.	
FT	RNA-DIRECTED RNA POLYMERASE P3D.	
FT	MYRISTATE (BY SIMILARITY).	
FT	PROTEASE (POTENTIAL).	
FT	PROTEASE (POTENTIAL).	

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FT STRAND 348 353
FT STRAND 362 362
FT HELIX 366 366
FT STRAND 367 367
FT STRAND 370 381
FT TURN 384 385
FT STRAND 390 406
FT TURN 423 426
FT TURN 430 431
FT STRAND 438 438
FT STRAND 444 445
FT STRAND 449 450
FT STRAND 454 455
FT STRAND 457 457
FT HELIX 458 463
FT STRAND 466 467
FT STRAND 470 471
FT TURN 473 474
FT STRAND 477 478
FT STRAND 480 484
FT STRAND 493 496
FT TURN 499 500
FT TURN 503 506
FT HELIX 508 513
FT TURN 514 515
FT STRAND 516 520
FT STRAND 523 529
FT TURN 533 534
FT STRAND 536 544
FT HELIX 554 557
FT TURN 558 559
FT STRAND 561 566
FT STRAND 572 577
FT STRAND 586 587
FT STRAND 601 611
FT TURN 614 615
FT STRAND 619 628
FT TURN 630 631
FT STRAND 633 637
FT STRAND 648 649
FT HELIX 651 653
FT TURN 661 664
FT TURN 676 677
FT STRAND 678 678
FT HELIX 679 683
FT STRAND 687 692
FT TURN 698 699
FT STRAND 706 707
FT TURN 708 709
FT STRAND 710 711
FT STRAND 713 715
FT STRAND 721 722
FT TURN 727 728
FT TURN 732 733
FT STRAND 737 738
FT STRAND 741 741
FT STRAND 744 744
FT STRAND 752 752
FT STRAND 755 755
FT HELIX 758 763
FT TURN 763 763
FT STRAND 766 779
FT STRAND 786 792
FT TURN 794 795
FT HELIX 806 807
FT TURN 810 812
FT STRAND 818 822
FT TURN 824 825
FT STRAND 828 833
FT STRAND 842 843
FT STRAND 847 847
FT STRAND 849 849
FT TURN 853 854

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FT TURN 859 859
FT STRAND 860 860
FT TURN 863 864
FT STRAND 869 874
FT STRAND 878 892
SQ SEQUENCE 2301 AA; 256159 MW; 0B6095DF153DBDF CRC64;

Query Match 30.9%; Score 43; DB 1; Length 2301;
Best Local Similarity 38.9%; Pred. No. 1.3e+02;
Matches 7; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 5 KSEWATHKFEADCKAKRDT 22
DB 1681 ETETMTAFKLDVHERDT 1698

RESULT 13
POLG_TMIEVG STANDARD; PRT; 2303 AA.
AC P08545; 088593; 088594;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE GENOME POLYPROTEIN [CONTAINS: COAT PROTEINS VP1 TO VP4; CORE PROTEINS
DE P2A TO P2C; P3A: GENOME-LINKED PROTEIN VPG; PICORNAIN 3C
DE (EC 3.4.22.28) (PROTEASE 3C) (P3C); RNA-DIRECTED RNA POLYMERASE P3D
DE (EC 2.7.7.48)].
OS Theiler's murine encephalomyelitis virus (strain GDVII) (TMIEV).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC Cardiovirus.
OX NCBI_Taxid-12127;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-88265847; PubMed-2838951;
RA Pevear D.C., Borkowski J., Calenoff M., Oh C.K., Ostrowski B.,
RA Lipion H.L.;
RT "Insights into Theiler's virus neurovirulence based on a genomic
RT comparison of the neurovirulent GDVII and less virulent bean
RT strains."
RL Virology 165:1-12(1988).
RN [2]
RP SEQUENCE OF 1704-2303 FROM N.A.
RX MEDLINE-87061197; PubMed-3023668;
RA Ozden S., Tangy F., Chamorro M., Brabic M.;
RT "Theiler's virus genome is closely related to that of
RT encephalomyocarditis virus, the prototype cardiovirus."
RL J. Virol. 60:1163-1165(1986).
CC -1- FUNCTION: IT IS THOUGHT THAT THE P2C PROTEIN ATTACHES TO VESICULAR
CC MEMBRANES AND IS ASSOCIATED WITH VIRAL RNA SYNTHESIS.
CC -1- FUNCTION: P3C POLYPEPTIDE IS A PROTEASE THAT CLEAVES AT CERTAIN
CC Q/G SITES IN THE POLYPROTEIN. IT MAY BE A CYSTEINE PROTEASE.
CC -1- SUBUNIT: THE VIRUS CAPSID IS COMPOSED OF 60 ICOSAEDRAL UNITS,
CC EACH OF WHICH IS COMPOSED OF ONE COPY EACH OF PROTEINS VP1, VP2,
CC VP3, AND VP4.
CC -1- PTM: SPECIFIC ENZYMAIC CLEAVAGES. IN VIVO YIELD MATURE PROTEINS.
CC -1- SIMILARITY: CLOSELY RELATED TO ENCEPHALOMYOCARDITIS VIRUS.
CC -1- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY C3.
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CC -----
DR EMBL: M20562; AAA47929.1; -
DR EMBL: M14703; AAA47933.1; -
DR PIR: A29193; GNNYTP.
DR PIR: A26100; A26100.
DR HSSP: P13899; ITME.
DR MEROPS: C03.009; -.

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SO SEQUENCE 569 AA: 64235 MW: 5118042478DF00FC CRC64;

Query Match 30.6%; Score 42.5; DB 1; Length 569;

Best Local Similarity 52.4%; Pred. No. 35;

Matches 11; Conservative 2; Mismatches 7; Indels 1; Gaps 1;

OY 5 KSEWATHKFPADCKA-KRDYPT 24

1 : ||| : | || | | |

DB 329 KPQKATHQIAPCKAMLRDXYDT 349

Search completed: December 19, 2001, 16:26:18
Job time: 573 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: December 19, 2001, 16:25:24 ; Search time 157.32 Seconds
(without alignments) 23.244 Million cell updates/sec

Title: US-09-202-104a-8
Perfect score: 139
Sequence: 1 NPTLKSEWATHKFAADCKAKRDPTPS 25

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues
Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: SPREMBL_17:*
2: sp.archaea:*
3: sp.bacteria:*
4: sp.fungi:*
5: sp.human:*
6: sp.invertebrate:*
7: sp.mammal:*
8: sp.mhc:*
9: sp.organelle:*
10: sp.phage:*
11: sp.plant:*
12: sp.rodent:*
13: sp.virus:*
14: sp.vertibrate:*
15: sp.unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	139	100.0	329	4 Q9U041	Q9U041 homo sapien
2	50	36.0	361	2 Q9CBN2	Q9CBN2 mycobacteri
3	50	36.0	2798	4 Q9NPI3	Q9NPI3 homo sapien
4	49	33.3	266	11 Q6I198	Q6I198 mus musculu
5	49	33.3	2165	5 Q9VH88	Q9VH88 drosophila
6	48	34.5	93	12 Q67603	Q67603 squash leaf
7	48	34.5	131	9 Q9A242	Q9A242 bacterioph
8	48	34.5	416	5 Q9N3L6	Q9N3L6 caenorhabd
9	48	34.5	530	5 Q9Y755	Q9Y755 drosophila
10	48	34.5	1456	5 Q9W3M3	Q9W3M3 drosophila
11	47	33.8	60	11 Q88362	Q88362 mus musculu
12	47	33.8	698	2 Q9Z486	Q9Z486 aeromonas p
13	46.5	33.5	717	5 Q45958	Q45958 caenorhabd
14	46.5	33.5	717	5 Q45959	Q45959 caenorhabd
15	46	33.1	196	12 Q55275	Q55275 fowl adenov
16	46	33.1	294	2 P73762	P73762 synecocyst
17	46	33.1	343	5 Q01883	Q01883 caenorhabd
18	46	33.1	565	10 Q9M5Q1	Q9M5Q1 plasm sativ
19	46	33.1	583	2 Q51815	Q51815 pseudomonas

20	46	33.1	751	11 Q99MK1	Q99MK1 mus musculu
21	46	33.1	778	11 Q99MP4	Q99MP4 mus musculu
22	46	33.1	830	12 Q83863	Q83863 nillaparvata
23	46	33.1	887	5 Q9VXG1	Q9VXG1 drosophila
24	46	33.1	991	2 Q9HNV0	Q9HNV0 pseudomonas
25	45.5	32.7	533	10 Q9L2R3	Q9L2R3 arabidopsis
26	45	32.4	59	11 Q88360	Q88360 mus musculu
27	45	32.4	59	11 Q88365	Q88365 mus musculu
28	45	32.4	266	11 Q9R1G6	Q9R1G6 mus musculu
29	45	32.4	266	11 Q9JHN9	Q9JHN9 mus musculu
30	45	32.4	286	10 Q9SZ14	Q9SZ14 arabidopsis
31	45	32.4	289	10 Q38810	Q38810 arabidopsis
32	45	32.4	356	5 Q9B1G4	Q9B1G4 caenorhabd
33	45	32.4	381	5 Q18873	Q18873 caenorhabd
34	45	32.4	552	5 P91765	P91765 myzus persi
35	44.5	32.0	331	10 Q9SM90	Q9SM90 oryza sativ
36	44.5	32.0	331	10 Q9SC68	Q9SC68 oryza sativ
37	44.5	32.0	994	4 Q9Y489	Q9Y489 homo sapien
38	44.5	32.0	1003	2 Q9AHP2	Q9AHP2 arcobacte
39	44.5	32.0	1657	5 Q9XUC3	Q9XUC3 caenorhabd
40	44	31.7	201	2 Q9X407	Q9X407 methylsul
41	44	31.7	214	5 Q9NEA4	Q9NEA4 leishmania
42	44	31.7	263	7 Q78027	Q78027 mus musculu
43	44	31.7	266	11 Q9JHV1	Q9JHV1 mus musculu
44	44	31.7	362	2 Q9EWT0	Q9EWT0 streptomyce
45	44	31.7	957	5 Q9VGY4	Q9VGY4 drosophila

ALIGNMENTS

RESULT	ID	PRELIMINARY:	PRT:	329 AA.
Q9U041	Q9U041	PRELIMINARY:	PRT:	329 AA.
AC	Q9U041	01-MAY-2000 (TREMBLrel. 13, Created)		
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)			
DT	01-JUN-2001 (TREMBLrel. 17, Last annotation update)			
DE	GP130 OF THE RHEUMATOID ARTHRITIS ANTIGENIC PEPTIDE-BEARING SOLUBLE FORM (GP130-RAPS).			
GN	GP130.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=SYNOVIAL;			
RA	Tanaka M., Kishimura M., Ozaki S., Hashimoto H., Osakada F., Okubo M., Murekami M., Nakao K.;			
RT	"Cloning of novel soluble gp130 and detection of its neutralizing autoantibodies in rheumatoid arthritis."			
RT	Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.			
RL	EMBL: AB015706; BAA78112.1; -			
DR	HSSP: P40189; 1B0J.			
DR	InterPro: IPR002996; CRIA.			
DR	InterPro: IPR003962; FN1L-repeat.			
DR	InterPro: IPR003961; FN-IT1.			
DR	Pfam: PF00041; fn3; 1.			
DR	PRINTS: PR00014; FNTYPEIT1.			
DR	SMART: SM00060; FN3; 1.			
KW	Repeat.			
SO	SEQUENCE	329 AA; 37484 MW; D9776576B34FC596 CRC64;		

Query Match 100.0%; Score 139; DB 4; Length 329;
Best local Similarity 100.0%; Pred. No. 5.1e-15;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NPTLKSEWATHKFAADCKAKRDPTPS 25
DB 157 NPTLKSEWATHKFAADCKAKRDPTPS 181

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RESULT 2
Q9CBN2 PRELIMINARY; PRT; 361 AA.
AC Q9CBN2;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DE PUTATIVE ALCOHOL DEHYDROGENASE (ZN DEPENDENT).
GN ADH2 OR ML1784.
OS Mycobacterium leprae.
OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_Taxid=1769;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TN;
RX MEDLINE=21128732; PubMed=11234002;
RA Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R.,
RA Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,
RA Mungall K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N.,
RA Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S.,
RA Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M.,
RA Rutter S., Seeger K., Simon S., Simmonds M., Skellon J., Squares R.,
RA Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
RA Barrall B.G.;
RT "Massive gene decay in the leprosy bacillus.";
RL Nature 409:1007-1011(2001).
CC -1- COFACTOR: REQUIRES ZINC FOR ITS ACTIVITY (BY SIMILARITY).
CC -1- SIMILARITY: TO THE ZINC-CONTAINING ALCOHOL DEHYDROGENASE FAMILY.
DR EMBL: AL883923; CAC30737.1; -
DR InterPro: IPR002085; Adh_zinc.
DR InterPro: IPR002328; Adh_zinc.
DR InterPro: IPR002025; NAD_binding.
DR Pfam: PF00107; adh_zinc.1.
DR PROSITE: PS00059; ADH_ZINC; 1.
KW Complete proteome; Oxidoreductase; Zinc.
SQ SEQUENCE 361 AA; 38109 MW; 464713FPB2919F82 CRC64;

Query Match 36.0%; Score 50; DB 2; Length 361;
Best Local Similarity 45.5%; Pred. No. 3.2;
Matches 10; Conservative 3; Mismatches 5; Indels 4; Gaps 1;

OY 3 TLKSEWATHKPADCKAKRDPT 24
Db 300 SLKSSW-----YGDCLPERDPT 317

RESULT 3
Q9NPL3 PRELIMINARY; PRT; 2798 AA.
AC Q9NPL3;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE HYD PROTEIN.
GN HYD.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RA Honda Y., Sava H., Nakao M.;
RT Cloning and identification of human homolog of drosophila hyd.;
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: U95000; AAF88143.1; -
DR InterPro: IPR000569; HECT.
DR InterPro: IPR002044; PABP.
DR InterPro: IPR002114; PTS_HPr_ser.
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DR InterPro: IPR000449; UBA.
DR InterPro: IPR003126; ZnF_UBR1.
DR Pfam: PF00632; HECT; 1.
DR Pfam: PF00658; PABP; 1.
DR Pfam: PF00627; UBA; 1.
DR Pfam: PF02207; zf-UBR1; 1.
DR SMART: SM00119; HECTC; 1.
DR SMART: SM00517; POLYA; 1.
DR SMART: SM00396; ZnF_UBR1; 1.
DR PROSITE: PS50237; HECT; 1.
DR PROSITE: PS00589; PTS_HPr_SER; UNKNOWN_1.
SQ SEQUENCE 2798 AA; 309449 MW; B3FD1E13E9D90DB7 CRC64;

Query Match 36.0%; Score 50; DB 4; Length 2798;
Best Local Similarity 60.0%; Pred. No. 26;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 11 HKFADCKAKRDPTPS 25
Db 1215 HKGDCKLKRTPRA 1229

RESULT 4
Q61198 PRELIMINARY; PRT; 266 AA.
AC Q61198;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE Ly-49C.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=97047784; PubMed=8892625;
RA Sundback J., Karre K., Sentman C.L.;
RT "Cloning of minimally divergent allelic forms of the natural killer
RT (NK) receptor Ly-49C, differentially controlled by host genes in the
RT MHC and NK gene complexes.";
RL J. Immunol. 157:3936-3942(1996).
DR EMBL: U56404; AAB19100.1; -
DR HSPB: P05451; ILIT.
DR InterPro: IPR001304; lectin_C.
DR InterPro: IPR00059; lectin_C; 1.
DR SMART: SM00034; CLECT; 1.
DR PROSITE: PS50041; C_TYPE_LECTIN_2; 1.
SQ SEQUENCE 266 AA; 31311 MW; BF9B10D9B6EFD628 CRC64;

Query Match 35.3%; Score 49; DB 11; Length 266;
Best Local Similarity 42.9%; Pred. No. 3.5;
Matches 9; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

OY 2 FTLKSEWATHKPADCKAKRDPT 22
Db 95 FNLKEEMITKNSIDCPSPNET 115

RESULT 5
Q9VH88 PRELIMINARY; PRT; 2165 AA.
AC Q9VH88;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE HYD PROTEIN.
GN HYD OR CG9484.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
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OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OC NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BERKELEY;
 RA MEDLINE-20196006; PubMed-10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amaralides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blaise R.G., Champagne M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Brill J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borokova D., Botchan M.R., Bouck J., Brooksstein P., Brotler P.,
 RA Burks K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
 RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodex A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris K.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kaulush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko F., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Maltel B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muszy D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puti V., Reese M.G.,
 RA Reibert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos A.C., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svrtkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weissstock G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh K.F., Zaveri J.S., Zhao W., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA GDBS R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster";
 RL Science 287:2185-2195(2000);
 DR EMBL: AF003684; AAF5431.1; -;
 DR EMBL: AF003684; AAF5431.1; -;
 DR Flybase; FBgn002431; hyd.
 DR InterPro; IPR000449; UBA.
 DR InterPro; IPR003126; znf_UBR1.
 DR Pfam; PF00627; UBA; 1.
 DR Pfam; PF02307; zf-UBR1; 1.
 DR SMART; SM00396; znf_UBR1; 1.
 SQ SEQUENCE 2165 AA; 237609 MW; A4DEF6C8AC15B4CD CRC64;

Query Match 35.3%; Score 49; DB 5; Length 2165;
 Best Local Similarity 60.0%; Pred. No. 29;
 Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 11 HKFADCKAKRDTPTS 25
 DB 1253 HKGHCKLKRTPA 1267

RESULT 6
 ID 067603 PRELIMINARY; PRT; 93 AA.
 AC 067603;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE REPLICATION-ASSOCIATED PROTEIN (FRAGMENT).
 GN AC1.

OS Squash leaf curl virus.
 OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
 OC NCBI_TaxID=10829;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-LOS MOCHIS 1;
 RA Loniello A.O., Ford R.E., Salinas R.A., Morales F.J., Maxwell D.P.;
 RL Submitted (JAN-1994) to the EMBL/Genbank/DBJ databases.
 DR EMBL: U27272; AAA47819.1; -;
 DR InterPro; IPR001191; GeminV_AL1.
 DR Pfam; PF00799; GeminV_AL1; 1.
 DR Prodom; PD000736; GeminV_AL1; 1.
 FT NON_TER 1 1
 FT NON_TER 93 93
 SQ SEQUENCE 93 AA; 10550 MW; 35CDB388C50B765D CRC64;

Query Match 34.5%; Score 48; DB 12; Length 93;
 Best Local Similarity 50.0%; Pred. No. 17;
 Matches 9; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 8 WATKPADCKAKRDTPTS 25
 DB 71 WADDFNECSAARPTPS 88

RESULT 7
 ID 09A242 PRELIMINARY; PRT; 131 AA.
 AC 09A242;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE COAT PROTEIN.
 OS Bacteriophage AP205.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
 OC Levivirus.
 OC NCBI_TaxID=154784;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Klovins J., Overbeek G.P., Ackermann H.W., Van Duin J.;
 RT "Nucleotide sequence of a single-stranded RNA phage from
 RT Acinetobacter: an unusual genetic map.";
 RL Submitted (JAN-2001) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AF334111; AAK20390.1; -;
 SQ SEQUENCE 131 AA; 14009 MW; FB4ECBCB8E129B2 CRC64;

Query Match 34.5%; Score 48; DB 9; Length 131;
 Best Local Similarity 80.0%; Pred. No. 2.5;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 TLKSEWATHK 12
 DB 92 TLKAEWETHK 101

RESULT 8
 ID 09N316 PRELIMINARY; PRT; 416 AA.
 AC 09N316;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE HYPOTHETICAL PROTEIN Y49F6A.5.
 GN Y49F6A.5.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OC NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;

RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasako P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Maitel B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclet J.M.,
 RA Palazzolo M., Peltman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Palzeret K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spletter E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svrtkars R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weisslock G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C., Smith H.O.,
 RT "The genome sequence of Drosophila melanogaster."
 RL Science 287:2185-2195(2000).
 DR EMBL: AE003442; AAF46302.1; -
 DR Flybase: FBgn0029985; CG1531.
 DR InterPro: IPR001841; znf_ring.
 DR SMART: SM00184; RING; 1
 SQ SEQUENCE 1456 AA; 161358 MW; 61C55D04E4067893 CRC64;

Query Match 34.5%; Score 48; DB 5; Length 1456;
 Best Local Similarity 57.1%; Pred. No. 28;
 Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 4 LKSEWATHKFPADCK 17
 DB 1433 LESQWLSHKFAHTK 1446

RESULT 11
 ID 088362 PRELIMINARY; PRT; 60 AA.
 AC 088362;
 DT 01-NOV-1998 (TREMBLrel. 08, Created)
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE NATURAL KILLER CELL RECEPTOR (FRAGMENT).
 GN KIR414 OR LY49N.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6;
 RX MEDLINE=96850123; PubMed=9683662;
 RA McQueen K.U., Freeman J.D., Takel F., Mager D.L.;
 RT "Localizaton of five new Ly49 genes, including three closely related
 to Ly49C."
 RL Immunogenetics 48:174-183(1998).
 DR EMBL: AF028128; AAC33258.1; -
 DR MGD: MGI:1321089; Klr414.
 FT NON_TER 1 1
 FT NON_TER 60 60
 SQ SEQUENCE 60 AA; 7261 MW; 854B4DB71E20C05A CRC64;

Query Match 33.8%; Score 47; DB 11; Length 60;
 Best Local Similarity 38.1%; Pred. No. 1.6;
 Matches 8; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY 1 NPTLKSEWATHKFPADCKAKRD 21
 DB 20 DPNLKSEWATHKSIDCRPSNF 40

RESULT 12
 092486

ID 092486 PRELIMINARY; PRT; 698 AA.
 AC 092486;
 DT 01-MAY-1999 (TREMBLrel. 10, Created)
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE ALPHA-GLUCURONIDASE.
 GN XYG.
 OS Aeromonas punctata (Aeromonas caviae).
 OC Bacteria; Proteobacteria; gamma subdivision; Aeromonadaceae;
 OC Aeromonas.
 OC NCBI_TaxID=648;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ME-1;
 RA Kitagawa E., Suzuki T., Kawai K.;
 RT "Xylosidase gene(xys) and alpha-galacturonidase gene(xyg) of Aeromonas
 caviae ME-1."
 RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AB022788; BAA74508.1; -
 DR SMART: SM00453; WSN; 1.
 SQ SEQUENCE 698 AA; 78166 MW; 064958F83654252 CRC64;

Query Match 33.8%; Score 47; DB 2; Length 698;
 Best Local Similarity 63.6%; Pred. No. 20;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 6 SEWATHKFPADC 16
 DB 573 SKWGYHFADC 583

RESULT 13
 ID 045958 PRELIMINARY; PRT; 717 AA.
 AC 045958;
 DT 01-JUN-1998 (TREMBLrel. 06, Created)
 DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE Y51A2B.6A PROTEIN.
 GN Y51A2B.6A.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OC NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA McMurtry A.;
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94150718; PubMed=7906398;
 RA Willson R., Almscough R., Anderson K., Baynes C., Berks M.,
 RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
 RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
 RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
 RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
 RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
 RA Parsons J., Percy C., Ritken L., Roopra A., Saunders D., Showmken R.,
 RA Smailson N., Smith A., Sonhammer E., Staden R., Sulston J.,
 RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
 RA Watson A., Weisslock L., Wilkinson-Sproat J., Wohlman P.;
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 elegans."
 RL Nature 368:32-38(1994).
 DR EMBL: AL021493; CAI6394.1; -
 DR InterPro: IPR003125; WSN.
 DR Pfam: PF02206; WSN; 1.
 DR SMART: SM00453; WSN; 1.
 SQ SEQUENCE 717 AA; 81475 MW; EA9C79E40E7FBD6E CRC64;

Query Match 33.5%; Score 46.5; DB 5; Length 717;
 Best Local Similarity 50.0%; Pred. No. 24;

Matches 11; Conservative 3; Mismatches 7; Indels 1; Gaps 1;
QY 4 LKSEWATHKFPADCKAKRDPPTS 25
|||:| || || || ||
Db 605 LKSQMGDHK-ADMESLENTMTS 625

RESULT 14
ID 045959 PRELIMINARY; PRT; 717 AA.
AC 045959;
DT 01-JUN-1998 (TREMBlrel. 06, Created)
DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
DE 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE Y5IA2B.68 PROTEIN.
GN Y5IA2B.68.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA McMurray A.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=94150718; PubMed=7906398;
RA Wilson R., Alnsough R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jler M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Lalster N., Latreille P.,
Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Showkeen R.,
Smaldon N., Smith A., Sonhammer E., Staden R., Sulston J.,
Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
Watson A., Weinstock L., Wilkinson-Sproat J., Wohlman P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
elegans.";
RL Nature 368:32-38(1994).
DR EMBL: AL021493; CAA16395.1; -.
DR InterPro: IPR003125; WSN.
DR Pfam: PF02206; WSN; 1.
DR SMART: SM00453; WSN; 1.
SQ SEQUENCE 717 AA; 81489 MW; 14E394886B373AB CRC64;

Query Match 33.5%; Score 46.5; DB 5; Length 717;
Best Local Similarity 50.0%; Pred. No. 24;
Matches 11; Conservative 3; Mismatches 7; Indels 1; Gaps 1;

QY 4 LKSEWATHKFPADCKAKRDPPTS 25
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Db 605 LKSQMGDHK-ADMESLENTMTS 625

RESULT 15
ID 055275 PRELIMINARY; PRT; 196 AA.
AC 055275;
DT 01-JUN-1998 (TREMBlrel. 06, Created)
DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
DE 01-AUG-1998 (TREMBlrel. 07, Last annotation update)
DE 33K PROTEIN.
GN 33K.
OS fowl adenovirus.
OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Aviadenovirus.
OX NCBI_TaxID=31540;
RN [1]
RP SEQUENCE FROM N.A.
RA Johnson M.A., Sheppard M., Teatas E.;
RL Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
DR EMBL: AF006739; AAB88279.1; -.

SQ SEQUENCE 196 AA; 21919 MW; 5E0F81A3FBA5DB83 CRC64;
Query Match 33.1%; Score 46; DB 12; Length 196;
Best Local Similarity 53.3%; Pred. No. 8;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 8 WATHKFPADCKAKRDT 22
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Db 133 WARYRVAICQALRDT 147

Search completed: December 19, 2001, 16:25:26
Job time: 551 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: December 19, 2001, 16:21:01 ; Search time 78.52 Seconds
(without alignments)
7.165 Million cell updates/sec

Title: US-09-202-104A-8

Perfect score: 139
Sequence: 1 NPTLKSEMANHFKADCKAKRDPTPS 25

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_AA:*
1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/PCITUS.COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/Backfill1es1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	139	100.0	US-08-599-455B-5	Sequence 5, Appl1
2	139	100.0	US-09-069-781B-5	Sequence 5, Appl1
3	139	100.0	US-08-419-652-5	Sequence 5, Appl1
4	139	100.0	US-08-825-558-4	Sequence 4, Appl1
5	139	100.0	US-07-797-556-2	Sequence 2, Appl1
6	139	100.0	US-08-308-881-2	Sequence 2, Appl1
7	139	100.0	US-09-058-263-2	Sequence 2, Appl1
8	139	100.0	US-09-058-099-2	Sequence 2, Appl1
9	139	100.0	US-09-058-264-2	Sequence 2, Appl1
10	139	100.0	PCR-US95-06530-2	Sequence 2, Appl1
11	139	100.0	US-08-825-558-6	Sequence 6, Appl1
12	46	30.6	US-08-217-327-8	Sequence 8, Appl1
13	42.5	30.6	US-08-910-313-2	Sequence 2, Appl1
14	42	30.2	US-08-666-405-28	Sequence 28, Appl1
15	41	29.5	US-08-077-939-19	Sequence 19, Appl1
16	41	29.5	US-08-461-599-19	Sequence 19, Appl1
17	41	29.5	US-08-461-621-19	Sequence 19, Appl1
18	41	29.5	US-08-465-334-19	Sequence 19, Appl1
19	40	28.8	US-08-803-346-62	Sequence 62, Appl1
20	40	28.8	US-08-803-346-63	Sequence 63, Appl1
21	40	28.8	US-07-949-812-7	Sequence 7, Appl1
22	40	28.8	US-08-855-261A-1	Sequence 1, Appl1
23	40	28.8	US-08-960-022-14	Sequence 14, Appl1
24	40	28.8	US-08-599-455B-2	Sequence 2, Appl1
25	40	28.8	US-09-069-781B-2	Sequence 2, Appl1
26	40	28.8	US-08-827-962-19	Sequence 19, Appl1
27	40	28.8	US-08-827-962-21	Sequence 21, Appl1

28	40	28.8	896	2	US-08-640-389A-12	Sequence 12, Appl1
29	40	28.8	1162	2	US-08-599-455B-43	Sequence 43, Appl1
30	40	28.8	1162	4	US-08-827-962-15	Sequence 15, Appl1
31	40	28.8	1162	4	US-08-827-962-20	Sequence 20, Appl1
32	40	28.8	1162	4	US-08-803-346-1	Sequence 1, Appl1
33	40	28.8	1162	4	US-09-069-781B-43	Sequence 43, Appl1
34	40	28.8	1824	4	US-08-680-327-3	Sequence 3, Appl1
35	40	28.8	1824	4	US-09-228-246-2	Sequence 2, Appl1
36	39	28.1	53	2	US-08-799-173A-13	Sequence 13, Appl1
37	39	28.1	55	1	US-07-862-021B-20	Sequence 20, Appl1
38	39	28.1	55	5	PCR-US93-03164-20	Sequence 20, Appl1
39	39	28.1	213	3	US-08-486-099-110	Sequence 110, App
40	39	28.1	213	3	US-08-360-107A-120	Sequence 120, App
41	39	28.1	213	3	US-08-484-223B-110	Sequence 110, App
42	39	28.1	213	3	US-08-919-597-110	Sequence 110, App
43	39	28.1	213	3	US-08-475-666A-110	Sequence 110, App
44	39	28.1	213	3	US-08-485-551A-110	Sequence 110, App
45	39	28.1	213	3	US-08-471-913A-110	Sequence 110, App

ALIGNMENTS

RESULT 1
US-08-599-455B-5
; Sequence 5, Application US/08599455B
; Patent No. 5972621
; GENERAL INFORMATION:
; APPLICANT: Tartaglia, Louis A.
; APPLICANT: Tepper, Robert I.
; TITLE OF INVENTION: METHODS OF IDENTIFYING COMPOUNDS THAT
; TITLE OF INVENTION: MODULATE BODY WEIGHT USING THE OB RECEPTOR
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/599,455B
; FILING DATE: 22-JAN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/583,153
; FILING DATE: 28-DEC-1995
; APPLICATION NUMBER: 08/570,142
; FILING DATE: 11-DEC-1995
; APPLICATION NUMBER: 08/569,485
; FILING DATE: 08-DEC-1995
; APPLICATION NUMBER: 08/566,622
; FILING DATE: 04-DEC-1995
; APPLICATION NUMBER: 08/562,663
; FILING DATE: 27-NOV-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Melkior, Ph.D., Anita L.
; REGISTRATION NUMBER: 35,283
; REFERENCE/DOCKET NUMBER: 07334/017001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 488 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

MOLECULE TYPE: protein
US-08-599-455B-5

Query Match 100.0%; Score 139; DB 2; Length 488;
Best Local Similarity 100.0%; Pred. No. 1,4e-14;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NPTLKSEWATHKFKADCKAKKRDPTPS 25
DB 128 NPTLKSEWATHKFKADCKAKKRDPTPS 152

RESULT 2
US-09-069-781B-5
Sequence 5, Application US/09069781B
Patent No. 6287782
GENERAL INFORMATION:
APPLICANT: Tartaglia, Louis A.
APPLICANT: Tepper, Robert I.
APPLICANT: Culpepper, Janice A.
APPLICANT: White, David W.
TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR
TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR
TITLE OF INVENTION: INCLUDING OBESITY AND CACHEXIA
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/069,781B
FILING DATE: 29-APRIL-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/864,564
FILING DATE: 28-MAY-1997
APPLICATION NUMBER: US 08/708,123
FILING DATE: 03-SEP-1996
APPLICATION NUMBER: US 08/638,524
FILING DATE: 26-APR-1996
APPLICATION NUMBER: US 08/599,455
FILING DATE: 22-JAN-1996
APPLICATION NUMBER: US 08/583,153
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: US 08/570,142
FILING DATE: 11-DEC-1995
APPLICATION NUMBER: US 08/569,485
FILING DATE: 08-DEC-1995
APPLICATION NUMBER: US 08/566,622
FILING DATE: 04-DEC-1995
APPLICATION NUMBER: US 08/562,663
FILING DATE: 27-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: Melkilejohn, Ph.D., Anita L.
REGISTRATION NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 07334/082001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 488 amino acids
TYPE: amino acid
TOPOLOGY: unknown

MOLECULE TYPE: protein
US-09-069-781B-5

Query Match 100.0%; Score 139; DB 4; Length 488;
Best Local Similarity 100.0%; Pred. No. 1,4e-14;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NPTLKSEWATHKFKADCKAKKRDPTPS 25
DB 128 NPTLKSEWATHKFKADCKAKKRDPTPS 152

RESULT 3
US-08-419-652-5
Sequence 5, Application US/08419652
Patent No. 5831007
GENERAL INFORMATION:
APPLICANT: Chua, Anne O
APPLICANT: Gubler, Ulrich A
TITLE OF INVENTION: INTERLEUKIN-12 RECEPTOR
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
CITY: Nutley
STATE: New Jersey
COUNTRY: United States of America
ZIP: 07110-1199
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: PC compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/419,652
FILING DATE: 11-APR-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/248,532
FILING DATE: 31-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/094,713
FILING DATE: 19-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Kass, Alan P
REGISTRATION NUMBER: 32142
REFERENCE/DOCKET NUMBER: CD 9174
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201) 235-4205
TELEFAX: (201) 235-3500
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 572 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Region
LOCATION: 1..572
OTHER INFORMATION: /note- "Represents residues 124 to
OTHER INFORMATION: 742 of human gp130."
US-08-419-652-5

Query Match 100.0%; Score 139; DB 2; Length 572;
Best Local Similarity 100.0%; Pred. No. 1.7e-14;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NPTLKSEWATHKFKADCKAKKRDPTPS 25
DB 34 NPTLKSEWATHKFKADCKAKKRDPTPS 58

```
RESULT 4
US-08-825-558-4
; Sequence 4, Application US/08825558
; Patent No. 5965724
; GENERAL INFORMATION:
; APPLICANT: SHARKEY, ANDREW
; APPLICANT: SMITH, STEPHEN K.
; APPLICANT: DELLOW, KIMBERLEY A.
; TITLE OF INVENTION: Gp 130 Lacking the Transmembrane Domain
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX
; STREET: 1100 NEW YORK AVENUE
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/825,558
; FILING DATE: 19-MAR-1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: ESMOND, ROBERT W.
; REGISTRATION NUMBER: 32, 893
; REFERENCE/DOCKET NUMBER: 0623.0530001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)371-2600
; TELEFAX: (202)371-2340
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 658 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-825-558-4

Query Match 100.0%; Score 139; DB 2; Length 658;
Best Local Similarity 100.0%; Pred. No. 2e-14;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NPTLKSEWATHKRFADCKAKRDPTPS 25
Db 157 NPTLKSEWATHKRFADCKAKRDPTPS 181

RESULT 5
US-07-797-556-2
; Sequence 2, Application US/07797556
; Patent No. 5262522
; GENERAL INFORMATION:
; APPLICANT: Gearing, David P.
; TITLE OF INVENTION: Receptor for Oncostatin M and Leukemia
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
```

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/797,556
; FILING DATE: 19911122
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Seese, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2607
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-587-0606
; TELEFAX: 206-587-0430
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 708 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-797-556-2

Query Match 100.0%; Score 139; DB 1; Length 708;
Best Local Similarity 100.0%; Pred. No. 2.1e-14;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NPTLKSEWATHKRFADCKAKRDPTPS 25
Db 157 NPTLKSEWATHKRFADCKAKRDPTPS 181

RESULT 6
US-08-308-881-2
; Sequence 2, Application US/08308881
; Patent No. 5783672
; GENERAL INFORMATION:
; APPLICANT: Mosley, Bruce
; APPLICANT: Cosman, David J.
; TITLE OF INVENTION: Receptor for Oncostatin M
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple 7.1
; SOFTWARE: Microsoft Word, Version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/308,881
; FILING DATE: 12-SEP-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/249,553
; FILING DATE: 26-MAY-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Seese, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2614-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; TELEEX: 756822
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 708 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-308-881-2
```

Query Match 100.0%; Score 139; DB 1; Length 708;
Best Local Similarity 100.0%; Pred. No. 2,1e-14;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NFTLKSEWATHKFKADCKAKKRDTPS 25
Db 157 NFKLSEWATHKFKADCKAKKRDTPS 181

RESULT 7
US-09-058-263-2
; Sequence 2, Application US/09058263
; Patent No. 5891997
; GENERAL INFORMATION:
; APPLICANT: Mosley, Bruce
; APPLICANT: Cosman, David J.
; TITLE OF INVENTION: Receptor for Oncostatin M
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; City: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple 7.1
; SOFTWARE: Microsoft Word, Version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/058,263
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/308,881
; FILING DATE: 12-SEP-1994
; APPLICATION NUMBER: US 08/249,553
; FILING DATE: 26-MAY-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Seese, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2614-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 708 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-058-263-2

Query Match 100.0%; Score 139; DB 2; Length 708;
Best Local Similarity 100.0%; Pred. No. 2,1e-14;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NFKLSEWATHKFKADCKAKKRDTPS 25
Db 157 NFKLSEWATHKFKADCKAKKRDTPS 181

RESULT 8
US-09-059-099-2
; Sequence 2, Application US/09059099
; Patent No. 5925740
; GENERAL INFORMATION:
; APPLICANT: Mosley, Bruce
; APPLICANT: Cosman, David J.
; FILING DATE:

; TITLE OF INVENTION: Receptor for Oncostatin M
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; City: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple 7.1
; SOFTWARE: Microsoft Word, Version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/059,099
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/308,881
; FILING DATE: 12-SEP-1994
; APPLICATION NUMBER: US 08/249,553
; FILING DATE: 26-MAY-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Seese, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2614-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 708 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-059-099-2

Query Match 100.0%; Score 139; DB 2; Length 708;
Best Local Similarity 100.0%; Pred. No. 2,1e-14;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NFKLSEWATHKFKADCKAKKRDTPS 25
Db 157 NFKLSEWATHKFKADCKAKKRDTPS 181

RESULT 9
US-09-058-264-2
; Sequence 2, Application US/09058264
; Patent No. 6010886
; GENERAL INFORMATION:
; APPLICANT: Mosley, Bruce
; APPLICANT: Cosman, David J.
; TITLE OF INVENTION: Receptor for Oncostatin M
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; City: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple 7.1
; SOFTWARE: Microsoft Word, Version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/058,264
; FILING DATE:

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; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/308,881
; FILING DATE: 12-SEP-1994
; APPLICATION NUMBER: US 08/249,553
; FILING DATE: 26-MAY-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Seese, Kathryn A.
; REGISTRATION NUMBER: 32,172
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 708 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-058-264-2

Query Match          100.0%; Score 139; DB 3; Length 708;
Best Local Similarity 100.0%; Pred. No. 2.1e-14;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NPTLKSEWATHKFPADCKAKRDPTPS 25
    |||
DB 157 NPTLKSEWATHKFPADCKAKRDPTPS 181

RESULT 10
PCT-US95-06530-2
; Sequence 2, Application PC/TUS9506530
; GENERAL INFORMATION:
; APPLICANT: Mosley, Bruce
; APPLICANT: Cosman, David J.
; TITLE OF INVENTION: Receptor for Oncostatin M
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/06530
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/308,881
; FILING DATE: 09-SEP-1994
; APPLICATION NUMBER: US 08/249,553
; FILING DATE: 26-MAY-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Anderson, Kathryn A.
; REGISTRATION NUMBER: 32,172
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 708 amino acids
; TYPE: amino acid
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```

; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US95-06530-2

Query Match          100.0%; Score 139; DB 5; Length 708;
Best Local Similarity 100.0%; Pred. No. 2.1e-14;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NPTLKSEWATHKFPADCKAKRDPTPS 25
    |||
DB 157 NPTLKSEWATHKFPADCKAKRDPTPS 181

RESULT 11
US-08-825-558-6
; Sequence 6, Application US/08825558
; Patent No. 5965724
; GENERAL INFORMATION:
; APPLICANT: SHARKEY, ANDREW
; APPLICANT: SMITH, STEPHEN K.
; APPLICANT: DELION, KIMBERLEY A.
; TITLE OF INVENTION: Gp 130 Lacking the Transmembrane Domain
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX
; STREET: 1100 NEW YORK AVENUE
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/825,558
; FILING DATE: 19-MAR-1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: ESMOND, ROBERT W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 0623.0530001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)371-2600
; TELEFAX: (202)371-2540
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 918 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-825-558-6

Query Match          100.0%; Score 139; DB 2; Length 918;
Best Local Similarity 100.0%; Pred. No. 2.8e-14;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NPTLKSEWATHKFPADCKAKRDPTPS 25
    |||
DB 157 NPTLKSEWATHKFPADCKAKRDPTPS 181

RESULT 12
US-08-217-327-8
; Sequence 8, Application US/08217327
; Patent No. 5474925
; GENERAL INFORMATION:
; APPLICANT: John, Malliyakal E
; APPLICANT: Barton, Kenneth A
; TITLE OF INVENTION: Immobilized Proteins in Cotton Fiber
```

NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Quarles and Brady
STREET: P.O. Box 2113
CITY: Madison
STATE: WI
COUNTRY: USA
ZIP: 53701-2113
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/217,327
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/812,233
FILING DATE: 19-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J
REGISTRATION NUMBER: 27,386
REFERENCE/DOCKET NUMBER: 1122990831
TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-251-5000
TELEFAX: 608-251-9166
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 592 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-217-327-8

Query Match 33.18; Score 46; DB 1; Length 592;
Best Local Similarity 42.9%; Pred. No. 16;
Matches 9; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 2 FTLSSEWATHKFKADCKAKRDT 22
DB 41 YTDSEWSTGFTANTTKNDT 61

RESULT 13
US-08-910-313-2
Sequence 2, Application US/08910313
Patent No. 6171838
GENERAL INFORMATION:
APPLICANT: Black, Michael Terence
TITLE OF INVENTION: NO. 6171838el Ratb
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dechert Price & Rhoads
STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre
CITY: Philadelphia
STATE: PA
COUNTRY: US
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/910,313
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:

NAME: Dickinson, Todd O
REGISTRATION NUMBER: 28,354
REFERENCE/DOCKET NUMBER: GM10072
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-994-2252
TELEFAX: 215-994-2222
TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 488 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-910-313-2

Query Match 30.6%; Score 42.5; DB 4; Length 488;
Best Local Similarity 43.5%; Pred. No. 48;
Matches 10; Conservative 3; Mismatches 9; Indels 1; Gaps 1;

QY 1 NPTLSEWATHKFKAD-CKAKRDT 22
DB 347 NYRLSNWITVEFAGRCARCKT 369

RESULT 14
US-08-666-405-28
Sequence 28, Application US/08666405
Patent No. 5874220
GENERAL INFORMATION:
APPLICANT: FACH, Patrick; GUILLOU, Jean-Pierre; POPOFF, Michel
TITLE OF INVENTION: PRIMERS FOR THE
TITLE OF INVENTION: AMPLIFICATION OF GENES CODING FOR THE
TITLE OF INVENTION: ENTEROTOXIN AND THE LECTININASE OF CLOSTRIDIUM
TITLE OF INVENTION: BACTERIOXINS AND THEIR APPLICATION TO THE
TITLE OF INVENTION: DETECTION AND NUMERATION OF THESE BACTERIAE
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIERMAN & MUSERLIAN
STREET: 600 THIRD AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DCS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/666,405
FILING DATE: 08-NOV-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP94/04292
FILING DATE: 22-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/172,026
FILING DATE: 22-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: MUSERLIAN, CHARLES A
REGISTRATION NUMBER: 19,683
REFERENCE/DOCKET NUMBER: 102,164
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 661-8000
TELEFAX: (212) 661-8002
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 336 amino acids
TYPE: amino acids
STRANDEDNESS: single
TOPOLOGY: linear

HYPOTHEICAL: NO
ORIGINAL SOURCE:
ORGANISM: Clostridium perfringens
FEATURE:
NAME/KEY: beta 1
US-08-666-405-28

Query Match 30.2%; Score 42; DB 2; Length 336;
Best Local Similarity 63.6%; Pred. No. 39;
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 2 FPKSEWATHK 12
|| | | ||
Db 322 FPKXINMLTK 332

RESULT 15

US-08-077-939-19
Sequence 19, Application US/08077939
Patent No. 5521088

GENERAL INFORMATION:

APPLICANT: FUJII, Toshio

APPLICANT: IWAMATSU, Akihiro

APPLICANT: YOSHIMOTO, Hiroyuki

APPLICANT: MINETOKI, Toshitaka

APPLICANT: BOGAKI, Takayuki

APPLICANT: NAGASAWA, Naoshi

TITLE OF INVENTION: ALCOHOL ACETYLTRANSFERASE GENES AND USE

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:

ADDRESSEE: Foley & Lardner

STREET: 3000 K Street, N.W., Suite 500

CITY: Washington, D.C.

COUNTRY: USA

ZIP: 20007-5109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/077,939

FILING DATE: 18-JUN-1992

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 184328/1992

FILING DATE: 18-JUN-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 62997/1993

FILING DATE: 26-FEB-1993

ATTORNEY/AGENT INFORMATION:

NAME: BENT, Stephen A.

REGISTRATION NUMBER: 29,768

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TELEX: 904136

INFORMATION FOR SEQ ID NO: 19:

SEQUENCE CHARACTERISTICS:

LENGTH: 525 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-077-939-19

OY 4 LKSEWATHKF--ADCKA 18
|| | | | ||:
Db 337 LKFEMLDVFIADCRS 353

Search completed: December 19, 2001, 16:21:02
Job time: 407 sec

Query Match 29.5%; Score 41; DB 1; Length 525;
Best Local Similarity 52.9%; Pred. No. 90;
Matches 9; Conservative 2; Mismatches 4; Indels 2; Gaps 1;

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 19, 2001, 16:19:36 : Search time 170.68 Seconds
(without alignments)
6.510 Million cell updates/sec

Title: US-09-202-104A-9
Perfect score: 81
Sequence: 1 WVEAENALGKVTSDH 15

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 522463 seqs, 74073290 residues
Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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23: /SID88/gcgdata/geneseq/geneseq/AA2001.DAT:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	81	100.0	15	19	AAW52209	Interleukin-6 anta
2	81	100.0	24	22	AAW88836	Human Interleukin-
3	81	100.0	329	18	AAW17859	Rheumatoid arthrit
4	81	100.0	332	20	AAW70799	Human gp130-delta-
5	81	100.0	332	21	AAV92188	Human gp130-delta-
6	81	100.0	658	17	AAW94576	Human gp130 splice
7	81	100.0	708	14	AAW37804	Human gp130 N-term
8	81	100.0	708	17	AAW85911	gp130 N-terminal f
9	81	100.0	727	21	AAW92192	Human gp130-Kappa
10	81	100.0	738	21	AAV92194	Human gp130-U-kapp
11	81	100.0	859	20	AAW70796	Human gp130-Fc-His

12	81	100.0	859	21	AAV92184	Human gp130-Fc-His
13	81	100.0	918	12	AAW10545	Recombinant human
14	81	100.0	918	15	AAW46233	Human soluble glyc
15	81	100.0	918	17	AAW75368	Human gp130 protei
16	81	100.0	918	21	AAW44694	Human gp130 protei
17	81	100.0	951	21	AAW70798	Human gp130-C-gam
18	81	100.0	951	21	AAV92186	Human gp130-C-gam
19	81	100.0	961	21	AAV92187	Human gp130-J-C-ga
20	81	100.0	1158	21	AAV92205	Fusion polypeptide
21	81	100.0	1168	21	AAV92204	Fusion polypeptide
22	72	88.9	180	17	AAW0404	Interleukin-6 anta
23	65	80.2	917	13	AAW26334	gp130. Mus muscul
24	65	80.2	917	21	AAV5073	Mouse gp130 protei
25	57	70.4	24	22	AAW88837	Human interleukin-
26	47	58.0	278	22	AAW55014	Protein sequence o
27	47	58.0	278	22	AAW50823	Murine NR6 isoform
28	47	58.0	303	20	AAW70843	Human zcyto5 vari
29	47	58.0	303	20	AAW70845	Human zcyto5 vari
30	47	58.0	348	21	AAV32205	Human receptor mol
31	47	58.0	350	19	AAW55015	Amino acid sequenc
32	47	58.0	350	22	AAW08824	Human NR6 haemopo
33	47	58.0	383	20	AAV05783	Mouse type 1 cyto
34	47	58.0	385	20	AAW70841	Human zcyto5 vari
35	47	58.0	385	20	AAW70842	Human zcyto5 vari
36	47	58.0	388	20	AAW70839	Human zcyto5 vari
37	47	58.0	389	20	AAW70846	Human zcyto5 vari
38	47	58.0	389	20	AAW70847	Human zcyto5 vari
39	47	58.0	389	20	AAW70848	Human zcyto5 vari
40	47	58.0	389	20	AAW70850	Human zcyto5 vari
41	47	58.0	389	20	AAW70851	Human zcyto5 vari
42	47	58.0	389	20	AAW70852	Human zcyto5 vari
43	47	58.0	389	20	AAW70853	Human zcyto5 vari
44	47	58.0	389	20	AAW70844	Human zcyto5 vari
45	47	58.0	392	20	AAW70840	Human zcyto5 vari

ALIGNMENTS

RESULT	1	
AAW52209	AAW52209 standard; peptide; 15 AA.	
XX		
AC	AAW52209;	
XX		
DT	09-JUN-1998 (first entry)	
XX		
DE	Interleukin-6 antagonist peptide.	
XX		
KW	Interleukin-6; IL-6; antagonist; IL-6 related disease; multiple myeloma;	
KW	acquired immune deficiency syndrome-related lymphoma; immune response;	
KW	rheumatoid arthritis; psoriasis; sepsis; osteoporosis; therapy;	
KW	Alzheimer's disease.	
XX		
OS	Synthetic.	
XX		
PN	WO9748728-A1.	
XX		
PD	24-DEC-1997.	
XX		
PF	19-JUN-1997; 97MO-NL00345.	
XX		
PR	20-JUN-1996; 96EP-0201720.	
XX		
PA	(KOST/) KOSTER H W.	
XX		
PI	Hoebel KHN, Van Leengoed LAMG;	
XX		
DR	WPI; 1998-063080/06.	
XX		
PT	New peptide(s) with Interleukin-6 agonist or antagonist activity - useful for treatment, prevention and diagnosis of IL-6 associated	

PT diseases
 PS Claim 6; Page 17; 28pp; English.
 XX This sequence represents a interleukin-6 (IL-6) antagonist peptide. This
 XX sequence is a peptide of the invention, which are of 5-30 amino acids
 CC and have antagonistic activity against: (a) IL-6; (b) the alpha chain
 CC and/or beta chain of the IL-6 receptor (IL-6R); or (c) IL-6 activity. The
 CC antagonists are used to treat or prevent IL-6 related diseases (typical
 CC of many exemplified are multiple myeloma, acquired immune deficiency
 CC syndrome-related lymphoma, rheumatoid arthritis, psoriasis, sepsis,
 CC osteoporosis, Alzheimer's disease etc.), also to remove IL-6 or IL-6R
 CC from extracorporeal blood. They may also be used diagnostically for such
 CC diseases and IL-6 agonists are additives for cell cultures. Antibodies
 CC specific for the antagonists may be administered to subjects previously
 CC treated with the antagonists to counter their effects, also in
 CC extracorporeal dialysis and diagnosis. The antagonists are too small to
 CC induce an immune response and have minimal side effects (they are not
 CC lytic for erythrocytes nor toxic for polymorphonuclear cells or
 CC hepatocytes); contrast no-human anti-IL-6 antibodies. The mixtures, or
 CC multimers, have greater activity (acting on both IL-6 and its receptor)
 CC and the peptides can be engineered to increase half-life or to target
 CC organs by incorporating unnatural aa or altering the
 CC hydrophilic/lipophilic balance.
 CC
 CC Sequence 15 AA;
 SQ

Query Match 100.0%; Score 81; DB 19; Length 15;
 Best Local Similarity 100.0%; Pred. No. 6.5e-08;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WVEAENALGKVTSDH 15
 |||||||||
 Db 1 wveaenalgkvtscd 15

RESULT 2
 AAB88836
 ID AAB88836 standard; Peptide; 24 AA.
 XX
 AC AAB88836;
 XX
 DT 23-MAY-2001 (first entry)
 XX
 DE Human interleukin-6 receptor binding inhibitor #33.
 XX
 KW Interleukin-6; ligand; IL-6 receptor; antagonist; cancer; allergy;
 KW rheumatoid arthritis; diabetes; multiple sclerosis; infection;
 KW autoimmune disease; inflammatory disease.
 XX
 OS Synthetic.
 XX
 PN WO200116166-A2.
 XX
 PD 08-MAR-2001.
 XX
 PF 25-AUG-2000; 2000WO-US23490.
 XX
 PR 27-AUG-1999; 99US-0151277.
 XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Saxinger C;
 XX
 DR WPI; 2001-244395/25.
 XX
 PT Polypeptides which inhibit the binding of interleukin (IL)-6 ligand
 PT with the IL-6 receptor, and the nucleic acids that encode them, useful
 PT for treating e.g. inflammation and autoimmune diseases -
 XX
 PS Sample 5; Page 51; 98pp; English.
 XX

CC The present invention describes a number of peptides which are able to
 CC bind to the human interleukin-6 (IL-6) receptor and inhibit IL-6 binding.
 CC These are useful in the treatment of diseases associated with abnormal
 CC IL-6 expression, including multiple myeloma, plasmacytoma, haematological
 CC diseases such as plasma cell dyscrasias, leukaemia and lymphoma,
 CC mesangial proliferative glomerulonephritis, polyclonal B cell activation
 CC conditions, allergies, rheumatoid arthritis, diabetes, multiple
 CC sclerosis, septic shock, infections, post-menopausal osteoporosis,
 CC chronic immune deficiency, autoimmune diseases and inflammatory diseases.
 CC
 CC Sequence 24 AA;
 SQ

Query Match 100.0%; Score 81; DB 22; Length 24;
 Best Local Similarity 100.0%; Pred. No. 1.1e-07;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WVEAENALGKVTSDH 15
 |||||||||
 Db 7 wveaenalgkvtscd 21

RESULT 3
 AAM17859
 ID AAM17859 standard; Protein; 329 AA.
 XX
 AC AAM17859;
 XX
 DT 04-FEB-1998 (first entry)
 XX
 DE Rheumatoid arthritis auto-antigen clone A.
 XX
 KW Rheumatoid arthritis; auto-antigen; clone A; diagnosis;
 KW prediction; synovial cell.
 XX
 OS Homo sapiens.
 XX
 PN WO9717441-A1.
 XX
 PD 15-MAY-1997.
 XX
 PF 06-NOV-1996; 96WO-JP03250.
 XX
 PR 07-NOV-1995; 95JP-0288957.
 XX
 PA (KANF) KANEKA CORP.
 XX
 PI Kishimura M, Nakao K, Osakada F, Osaki S, Tanaka M;
 XX
 DR WPI; 1997-281030/25.
 XX
 DR N-PSDB; AAT68830.
 XX
 PT Auto-antigen from synovial cells of rheumatoid arthritis patients -
 PT binds to antibodies present in these patients, for diagnosis and
 PT prediction of the disease
 XX
 PS Claim 3; Pages 36-37; 61pp; Japanese.
 XX
 CC The present sequence is the rheumatoid arthritis (RA) auto-antigen
 CC clone A, which can be used to diagnose and predict the development
 CC of RA by reaction with antibodies in biological specimens, e.g.
 CC sera, from patients.
 CC RNA was isolated from synovial cells from a RA patient and used to
 CC construct a cDNA library. This was screened using 19g separated
 CC from the synovial fluid of a RA patient. Active clones were
 CC isolated in a cloning vector, and inserted into an expression
 CC vector for the transformation of E. coli NM522. Transformants on
 CC culture express clone A peptide and follistatin related protein
 CC into the culture medium.
 CC
 CC Sequence 329 AA;
 SQ

Query Match 100.0%; Score 81; DB 18; Length 329;
 Best Local Similarity 100.0%; Pred. No. 2.3e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WVEAENALGKVTSDH 15
 |||||||
 Db 197 wveaenalgkvtstdh 211

RESULT 4

AAW70799
 ID AAW70799 standard; protein; 332 AA.
 XX
 AC AAW70799;
 XX
 DT 03-FEB-1999 (first entry)
 XX
 DE Human gp130-delta-3fibro amino acid sequence.
 XX
 KW gp130: cytokine antagonist; interleukin; gamma-interferon;
 KM granulocyte macrophage colony-stimulating factor; J peptide;
 KM transforming growth factor-beta.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Protein 1..330
 FT /note= "human gp130"
 XX
 PN US844099-A.
 PD 01-DEC-1998.
 XX
 PF 27-NOV-1995; 95US-0563105.
 XX
 PR 27-NOV-1995; 95US-0563105.
 PR 20-OCT-1993; 93US-0140222.
 XX
 PA (REG-) REGENERON PHARM INC.
 XX
 PI Economides A, Stahl N, Yancopoulos GD;
 DR WPI; 1999-044669/04.
 XX
 PT Cytokine antagonists - comprising extracellular domains of
 PT specificity-determining and signal-transducing components of
 PT cytokine receptor
 XX
 PS Example 4; Fig 10; 46pp; English.

XX The present sequence represents the amino acid sequence of human
 CC gp130-delta-3fibro. The protein is used in the course of the invention.
 CC The specification describes cytokine antagonists comprising only the
 CC extracellular domain of the specificity-determining component of
 CC the cytokine receptor and the extracellular domain of a
 CC signal-transducing component of the cytokine receptor. The cytokine
 CC is an interleukin (IL-1, IL-2, IL-3, IL-4, IL-5 or IL-15),
 CC granulocyte macrophage colony-stimulating factor (GM-CSF),
 CC gamma-interferon or transforming growth factor-beta (TGF-beta). The
 CC antagonist is capable of binding the cytokine to form a nonfunctional
 CC complex. The compounds have therapeutic activity as cytokine antagonists
 CC and can also be used in assays for identifying novel agonists and
 CC antagonists of cytokines.
 XX

Sequence 332 AA;

Query Match 100.0%; Score 81; DB 20; Length 332;
 Best Local Similarity 100.0%; Pred. No. 2.3e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WVEAENALGKVTSDH 15

Db |||||||
 197 wveaenalgkvtstdh 211

RESULT 5

AA92188
 ID AA92188 standard; protein; 332 AA.
 XX
 AC AA92188;
 XX
 DT 01-AUG-2000 (first entry)
 XX
 DE Human gp130-delta-3fibro.
 XX
 KW gp130-delta-3fibro; cytokine; antagonist; CNTF; receptor; fusion protein;
 KM cytostatic; immunomodulator; osteopathic.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Protein 1..330
 FT /label= gp130
 FT Peptide 331..332
 FT /note= "Ser-Gly bridge"
 XX
 PN MO200018932-A2.
 PD 06-APR-2000.
 XX
 PF 22-SEP-1999; 99WO-US22045.
 XX
 PR 25-SEP-1998; 98US-0101858.
 PR 19-MAY-1999; 99US-0313942.
 XX
 PA (REG-) REGENERON PHARM INC.
 XX
 PI Stahl N, Yancopoulos GD;
 DR WPI; 2000-293165/25.
 XX
 PT Isolated nucleic acid molecule for treating cytokine-related diseases
 PT or disorders encodes a fusion polypeptide capable of binding a cytokine
 PT to form a nonfunctional complex
 XX
 PS Example 4; Fig 10; 152pp; English.

XX The invention concerns production of antagonists to any cytokine that
 CC utilizes an alpha specificity determining component, which when combined
 CC with the cytokine, binds to a first beta signal transducing component to
 CC form a non-functional intermediate which then binds to a second beta
 CC signal transducing component causing beta-receptor dimerization, the
 CC soluble alpha specificity determining component of the receptor
 CC (SR-alpha) and the extracellular domain of the first beta signal
 CC transducing component of the cytokine receptor (beta-1) are combined to
 CC form heterodimers (SR-alpha:beta-1) that act as antagonist to the
 CC cytokine by binding the cytokine to form a non-functional complex. The
 CC receptor components are shared by cytokines such as the CNTF (ciliary
 CC neurotrophic factor) family of cytokines. The invention provides the
 CC basis for the development of IL-6 antagonists, as they show that if, in
 CC the presence of a ligand, a non-functional intermediate complex,
 CC consisting of the ligand, its alpha receptor and its beta-1 receptor
 CC component, can be formed, it will effectively block the action of the
 CC ligand. Effective antagonists of IL-6 or CNTF consist of heterodimers
 CC of the extracellular domains of the alpha specificity determining
 CC components of their receptors and the extracellular domain of gp130.
 CC The resultant heterodimers, function as high-affinity traps, rendering
 CC the cytokine inaccessible to form a signal transducing complex with the
 CC native membrane-bound forms of their receptor. The nucleic acids and
 CC polypeptides are useful for treating cytokine-related diseases or
 CC disorders such as osteoporosis and primary and secondary effects of
 CC cancer including multiple myeloma or cachexia.

SQ Sequence 332 AA;

Query Match 100.0%; Score 81; DB 21; Length 332;

Best Local Similarity 100.0%; Pred. No. 2.3e-06; Mismatches 0; Indels 0; Gaps 0;

QY 1 WVEAENALGKVTSDH 15

Db 197 wveaenalgkvtstdh 211

RESULT 6

ID AAR94576 standard; Protein; 658 AA.

XX AAR94576;

XX 20-JUN-1996 (first entry)

XX Human gp130 splice variant.

XX Gp130: transmembrane domain; growth factor antagonist;

XX embryo preimplantation; in vitro fertilisation.

XX Homo sapiens.

XX MO9609382-A1.

XX 28-MAR-1996.

XX 21-SEP-1995; 95WO-GB02243.

XX 21-SEP-1994; 94GB-0019021.

XX (ISTF) ARS APPLIED RES SYST HOLDING NV.

XX Dellow KA, Sharkey A, Smith SK;

XX WPI; 1996-188444/19.

XX N-PSDB; AAT14602.

XX New splice variant of gp130 lacking the trans-membrane domain

XX useful as an antagonist for growth factors esp. for ensuring correct

XX development of pre-implantation embryos

XX Example 2; Fig 1; 33pp; English.

XX A novel, soluble splice variant (AAR94576) of human gp130 corresponds

XX to amino acids 1-613 of native gp130 (AAR75368) but has a novel

XX C-terminal sequence (AAR94575) from amino acid 614 onwards.

XX The splice variant lacks a transmembrane region. It was initially

XX detected during the motuila to blastocyst transition of human

XX embryos. The splice variant antagonises the action of growth

XX factors, e.g. interleukin-6, leukaemia inhibitory factor,

XX oncostatin M and interleukin-11, and can be used to ensure correct

XX development of preimplantation embryos, partic. for in vitro

SQ Sequence 658 AA;

Query Match 100.0%; Score 81; DB 17; Length 658;

Best Local Similarity 100.0%; Pred. No. 5e-06; Mismatches 0; Indels 0; Gaps 0;

QY 1 WVEAENALGKVTSDH 15

Db 197 wveaenalgkvtstdh 211

RESULT 7

AAR37804

ID AAR37804 standard; Protein; 708 AA.

XX AAR37804;

XX 01-OCT-1993 (first entry)

XX Human gp130 N-terminal fragment.

XX Oncostatin M; leukaemia inhibitory factor; receptor; PCR; fusion;

XX LIF-R; gp130; linker.

XX Synthetic.

XX Key

XX Peptide

XX Protein

XX Domain

XX Region

XX Domain

XX Misc-difference

XX 8

XX MO9310151-A.

XX 27-MAY-1993.

XX 20-NOV-1992; 92WO-US10272.

XX 22-NOV-1991; 91US-0797556.

XX (IMMV) IMMUNEX CORP.

XX Gearing DP;

XX WPI; 1993-182493/22.

XX N-PSDB; AAQ42588.

XX Receptor protein comprising gp130 covalently linked to LIF

XX Receptor - binds to oncostatin M and LIF useful for treating

XX Kaposi's sarcoma, atherosclerosis, obesity etc.

XX Disclosure; Page 48-53; 79pp; English.

XX A new receptor (R), able to bind oncostatin M and leukaemia

XX inhibitory factor (LIF), comprises a gp130 polypeptide (AAQ42588)

XX covalently coupled to LIF-receptor (LIF-R) (AAQ42590); for example

XX via a Fc region of an IgG1 antibody (AAQ42589).

XX Suitable gp130 polypeptides comprise amino acids 22-528, 22-320,

XX 120-320 etc., or lack all or part of the transmembrane region

XX and/or cytoplasmic domain.

XX Pref. both components of (R) are soluble proteins and are connected

XX by a polypeptide linker of 20-100 amino acids consisting of Gly, Asn,

SQ Sequence 708 AA;

Query Match 100.0%; Score 81; DB 14; Length 708;

Best Local Similarity 100.0%; Pred. No. 5.5e-06; Mismatches 0; Indels 0; Gaps 0;

QY 1 WVEAENALGKVTSDH 15

Db 197 wveaenalgkvtstdh 211

Db 197 wveaenalgkvrtsdh 211

RESULT 8
AAR85911
ID AAR85911 standard; Protein; 708 AA.
XX
XX AAR85911;
AC
XX
XX 03-JUL-1996 (first entry)
DT
XX
XX gp130 N-terminal fragment.
DE
XX
XX Human; gp130; inhibitor; oncostatin M; cytokine; antibody Fc region;
KW oncostatin M receptor-beta chain; antibody; tumour; growth factor;
KM therapy.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH Peptide 1..22 /note= "signal peptide"
FT 23..708
FT Peptide /note= "N-terminal fragment of mature gp130"
FT 21..23 /note= "glycosylation site"
FT Modified-site /note= "glycosylation site"
FT 61..63 /note= "glycosylation site"
FT 109..111 /note= "glycosylation site"
FT Modified-site /note= "glycosylation site"
FT 135..137 /note= "glycosylation site"
FT Modified-site /note= "glycosylation site"
FT 153..154 /note= "glycosylation site"
FT Cleavage-site 205..207 /note= "glycosylation site"
FT Modified-site 224..226 /note= "glycosylation site"
FT 357..359 /note= "glycosylation site"
FT Modified-site /note= "glycosylation site"
FT 361..363 /note= "glycosylation site"
FT Modified-site /note= "glycosylation site"
FT 368..370 /note= "glycosylation site"
FT Modified-site /note= "glycosylation site"
FT 531..533 /note= "glycosylation site"
FT Modified-site /note= "glycosylation site"
FT 542..544 /note= "glycosylation site"
FT Modified-site /note= "glycosylation site"
FT Cleavage-site 621..622
XX
XX W09533059-A2.
PN
XX
XX 07-DEC-1995.
PD
XX
XX 22-MAY-1995; 95WO-US06530.
PF
XX
XX 12-SEP-1994; 94US-0308881.
PR 26-MAY-1994; 94US-0249553..
PR
XX
XX (IMMV) IMMUNEX CORP.
PA
XX
XX Cosman DJ, Mosley B;
PI
XX
XX WPI: 1996-030570/03.
DR N-PSDB: AAO74081.
XX
XX Hetero: dimeric receptor proteins comprising OSM-R beta and gp 130 -
PT bind oncostatin M and are used in inhibiting biological activities
PT mediated by oncostatin M
XX
XX
XX Claim 1; Page 35-38; 60pp; English.
XX
XX This sequence represents an N-terminal fragment of gp130 obtained from
CC human placenta. gp130 binds to oncostatin M, which is a secreted single

CC chain polypeptide cytokine. Oncostatin M regulates the growth of
CC certain tumour derived and normal cell lines. This receptor protein, and
CC the oncostatin M receptor-beta chain (see AAR85912) sequence can be
CC covalently joined, to give a heterodimeric receptor protein capable of
CC binding to oncostatin M. The receptors can also comprise fusion
CC polypeptides, where an antibody Fc region is joined to the C-terminus of
CC each of the soluble proteins. In this case, the two fusion polypeptides
CC are joined by disulphide bonds between the two antibody Fc regions. The
CC heterodimeric receptors can be used to inhibit biological activities
CC mediated by oncostatin M. The advantage with using the heterodimeric
CC receptors is that they bind to oncostatin M at greater levels than gp130
CC does alone.
XX
XX SQ Sequence 708 AA;
XX
XX
XX Query Match 100.0%; Score 81; DB 17; Length 708;
XX Best Local Similarity 100.0%; Pred. No. 5.5e-06;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 WVEAENALGKVRSDH 15
XX |||||||||||||||
Db 197 wveaenalgkvrtsdh 211

RESULT 9
AAY92192
ID AAY92192 standard; protein; 727 AA.
XX
XX AAY92192;
AC
XX
XX 01-AUG-2000 (first entry)
DT
XX
XX Human gp130-kappa domain fusion protein.
DE
XX
XX gp130-kappa domain; cytokine; antagonist; CNTF; receptor; fusion protein;
KW Cytostatic; immunomodulator; osteopathic.
KM
XX
XX OS Synthetic.
OS Homo sapiens.
XX
XX FH Key Location/Qualifiers
FT Protein 1..619 /label= gp130
FT Peptide 620..621
FT /note= "Ser-Gly bridge"
FT Protein 622..727
FT /label= IgG1_Kappa_domain
XX
XX W0200018932-A2.
PN
XX
XX 06-APR-2000.
PD
XX
XX 22-SEP-1999; 99WO-US22045.
PF
XX
XX 25-SEP-1998; 98US-0101858.
PR 19-MAY-1999; 99US-0313942.
PR
XX
XX (REGG-) REGENERON PHARM INC.
PA
XX
XX Stahl N, Yancopoulos GD;
PI
XX
XX WPI: 2000-293165/25.
DR
XX
XX Isolated nucleic acid molecule for treating cytokine-related diseases
PT or disorders encodes a fusion polypeptide capable of binding a cytokine
PT to form a nonfunctional complex
XX
XX Example 4; Page -- 152pp; English.
XX
XX The invention concerns production of antagonists to any cytokine that
CC utilizes an alpha specificity determining component, which when combined
CC with the cytokine, binds to a first beta signal transducing component to

CC form a non-functional intermediate which then binds to a second beta
 CC signal transducing component causing beta-receptor dimerization, the
 CC soluble alpha specificity determining component of the receptor
 CC (SR-alpha) and the extracellular domain of the first beta signal
 CC transducing component of the cytokine receptor (beta-1) are combined to
 CC form heterodimers (SR-alpha:beta-1) that act as antagonist to the
 CC cytokine by binding the cytokine to form a non-functional complex. The
 CC receptor components are shared by cytokines such as the CNTF (ciliary
 CC neurotrophic factor) family of cytokines. The invention provides the
 CC basis for the development of IL-6 antagonists, as they show that if, in
 CC the presence of a ligand, a non-functional intermediate complex,
 CC consisting of the ligand, its alpha receptor and its beta-1 receptor
 CC component, can be formed, it will effectively block the action of the
 CC ligand. Effective antagonists of IL-6 or CNTF consist of heterodimers
 CC of the extracellular domains of the alpha specificity determining
 CC components of their receptors and the extracellular domain of gp130.
 CC The resultant heterodimers, function as high-affinity traps, rendering
 CC the cytokine inaccessible to form a signal transducing complex with the
 CC native membrane-bound forms of their receptor. The nucleic acids and
 CC polypeptides are useful for treating cytokine-related diseases or
 CC disorders such as osteoporosis and primary and secondary effects of
 CC cancer including multiple myeloma or cachexia.
 CC NB. This sequence was constructed from the gp130 and kappa domain
 CC sequences given in Figures 9 and 13 of the specification.

XX Sequence 727 AA:

QY 1 WVEAENALGKVTSDH 15
 |||||||
 Db 197 WVEAENALGKVTSDH 211

RESULT 10
 AAY92194
 ID AAY92194 standard; protein; 738 AA.
 AC AAY92194:
 XX 01-AUG-2000 (first entry)
 DT Human gp130-J-kappa fusion protein.
 DE
 XX
 KW gp130-J-kappa; cytokine; antagonist; CNTF; receptor; fusion protein;
 KW cytoskeletal; immunomodulator; osteopathic.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Protein 1..619
 FT Peptide /label= gp130
 FT Peptide 620..621
 FT Peptide /note= "Ser-gly bridge"
 FT Peptide 622..632
 FT Peptide /note= "J-peptide"
 FT Domain 633..738
 FT /label= Kappa-domain
 XX
 PN W0200018932-A2.
 PD 06-APR-2000.
 XX
 PF 22-SEP-1999; 99WO-US22045.
 XX
 PR 25-SEP-1998; 98US-0101858.
 PR 19-MAY-1999; 99US-0313942.
 XX
 PA (REG-) REGENERON PHARM INC.

XX Stahl N, Yancopoulos GD;
 PT
 XX
 DR WPI; 2000-293165/25.
 XX
 PT Isolated nucleic acid molecule for treating cytokine-related diseases
 PT or disorders encodes a fusion polypeptide capable of binding a cytokine
 PT to form a nonfunctional complex

XX
 PS Example 4; Page -: 152pp; English.

CC The invention concerns production of antagonists to any cytokine that
 CC utilizes an alpha specificity determining component, which when combined
 CC with the cytokine, binds to a first beta signal transducing component to
 CC form a non-functional intermediate which then binds to a second beta
 CC signal transducing component causing beta-receptor dimerization, the
 CC soluble alpha specificity determining component of the receptor
 CC (SR-alpha) and the extracellular domain of the first beta signal
 CC transducing component of the cytokine receptor (beta-1) are combined to
 CC form heterodimers (SR-alpha:beta-1) that act as antagonist to the
 CC cytokine by binding the cytokine to form a non-functional complex. The
 CC receptor components are shared by cytokines such as the CNTF (ciliary
 CC neurotrophic factor) family of cytokines. The invention provides the
 CC basis for the development of IL-6 antagonists, as they show that if, in
 CC the presence of a ligand, a non-functional intermediate complex,
 CC consisting of the ligand, its alpha receptor and its beta-1 receptor
 CC component, can be formed, it will effectively block the action of the
 CC ligand. Effective antagonists of IL-6 or CNTF consist of heterodimers
 CC of the extracellular domains of the alpha specificity determining
 CC components of their receptors and the extracellular domain of gp130.
 CC The resultant heterodimers, function as high-affinity traps, rendering
 CC the cytokine inaccessible to form a signal transducing complex with the
 CC native membrane-bound forms of their receptor. The nucleic acids and
 CC polypeptides are useful for treating cytokine-related diseases or
 CC disorders such as osteoporosis and primary and secondary effects of
 CC cancer including multiple myeloma or cachexia.

XX Sequence 738 AA:

QY 1 WVEAENALGKVTSDH 15
 |||||||
 Db 197 WVEAENALGKVTSDH 211

RESULT 11
 AAW70796
 ID AAW70796 standard; protein; 859 AA.
 AC AAW70796:
 XX 03-FEB-1999 (first entry)
 DT Human gp130-FC-His6 amino acid sequence.
 DE
 XX
 KW gp130; cytokine antagonist; interleukin; gamma-interferon;
 KW granulocyte macrophage colony-stimulating factor; J peptide;
 KW transforming growth factor-beta.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Protein 1..619
 FT Protein /note= "human gp130"
 FT Misc-difference 2 /label= LZV
 FT /note= "amino acid changed to accomodate a Kozak
 FT sequence"


```

FT Peptide 1..22
FT /note= "signal peptide"
FT Misc-difference 620..621
FT /note= "Ser-Gly bridge"
FT Protein 662..853
FT /note= "From the Fc domain of human IgG1"
FT Disulfide-bond 632..635
FT Peptide 854..859
FT /note= "hexahistidine tag"
PN US5844099-A.
XX 01-DEC-1998.
XX
XX 27-NOV-1995; 95US-0563105.
XX
XX 27-NOV-1995; 95US-0563105.
XX
XX 20-OCT-1993; 93US-0140222.
XX
XX (REG- ) REGENERON PHARM INC.
XX
XX Economidis A, Stahl N, Yancopoulos GD;
XX
XX WPI; 1999-044669/04.
XX
XX Cytokine antagonists - comprising extracellular domains of
XX specificity-determining and signal-transducing components of
XX cytokine receptor
XX
XX Example 3; Fig 4; 46pp; English.
XX
XX The present sequence represents the amino acid sequence of human
XX gp130-Fc-His6. The protein is used in the course of the invention. The
XX specification describes cytokine antagonists comprising only the
XX extracellular domain of the specificity-determining component of
XX the cytokine receptor and the extracellular domain of a
XX signal-transducing component of the cytokine receptor. The cytokine
XX is an Interleukin (IL-1, IL-2, IL-3, IL-4, IL-5 or IL-15),
XX granulocyte macrophage colony-stimulating factor (GM-CSF),
XX gamma-Interferon or transforming growth factor-beta (TGF-beta). The
XX antagonist is capable of binding the cytokine to form a nonfunctional
XX complex. The compounds have therapeutic activity as cytokine antagonists
XX and can also be used in assays for identifying novel agonists and
XX antagonists of cytokines.
XX
XX Sequence 859 AA:
SQ

```

Query Match 100.0%; Score 81; DB 20; Length 859;
Best Local Similarity 100.0%; Pred. No. 6.8e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 WVEAENALGKVTSDH 15
   |||
Db 197 wveaenalgkvtsh 211

```

RESULT 12
AA92184
ID AA92184 standard; protein; 859 AA.
XX
AC AA92184;
XX
DT 01-AUG-2000 (first entry)
DE Human gp130-Fc-His6.
XX
XX gp130-Fc-His6; cytokine; antagonist; CNTF; receptor; fusion protein;
KM cyostatic; immunomodulator; osteopathic.
XX
OS Synthetic.
XX Homo sapiens.
XX

```

FH Key Location/Qualifiers
FT Protein 1..619
FT /label= gp130
FT Peptide 1..22
FT /label= signal-peptide
FT Peptide 620..621
FT /note= "Ser-Gly bridge"
FT Disulfide-bond 632
FT /note= "forms inter-chain disulfide bridge that
FT link two Fc domains"
FT Disulfide-bond 635
FT /note= "forms inter-chain disulfide bridge that
FT link two Fc domains"
FT Protein 662..853
FT /label= IgG1_Fc_domain
FT Peptide 854..859
FT /label= histidine_tag
PN W0200018932-A2.
XX 06-APR-2000.
XX
XX 22-SEP-1999; 99WO-US22045.
XX
XX 25-SEP-1998; 98US-0101858.
XX
XX 19-MAY-1999; 99US-0313942.
XX
XX (REG- ) REGENERON PHARM INC.
XX
XX Stahl N, Yancopoulos GD;
XX
XX WPI; 2000-293165/25.
XX
XX Isolated nucleic acid molecule for treating cytokine-related diseases
XX or disorders encodes a fusion polypeptide capable of binding a cytokine
XX to form a nonfunctional complex
XX
XX Example 3; Fig 4; 152pp; English.
XX
XX The invention concerns production of antagonists to any cytokine that
XX utilizes an alpha specificity determining component, which when combined
XX with the cytokine, binds to a first beta signal transducing component to
XX form a non-functional intermediate which then binds to a second beta
XX signal transducing component causing beta-receptor dimerization, the
XX soluble alpha specificity determining component of the receptor
XX (SR-alpha) and the extracellular domain of the first beta signal
XX transducing component of the cytokine receptor (beta-1) are combined to
XX form heterodimers (SR-alpha:beta-1) that act as antagonist to the
XX cytokine by binding the cytokine to form a non-functional complex. The
XX receptor components are shared by cytokines such as the CNTF (ciliary
XX neurotrophic factor) family of cytokines. The invention provides the
XX basis for the development of IL-6 antagonists, as they show that if, in
XX the presence of a ligand, a non-functional intermediate complex,
XX consisting of the ligand, its alpha receptor and its beta-1 receptor
XX component, can be formed, it will effectively block the action of the
XX ligand. Effective antagonists of IL-6 or CNTF consist of heterodimers
XX of the extracellular domains of the alpha specificity determining
XX components of their receptors and the extracellular domain of gp130.
XX The resultant heterodimers, function as high-affinity traps, rendering
XX the cytokine inaccessible to form a signal transducing complex with the
XX native membrane-bound forms of their receptor. The nucleic acids and
XX polypeptides are useful for treating cytokine-related diseases or
XX disorders such as osteoporosis and primary and secondary effects of
XX cancer including multiple myeloma or cachexia.
XX
XX Sequence 859 AA:
SQ

```

Query Match 100.0%; Score 81; DB 21; Length 859;
Best Local Similarity 100.0%; Pred. No. 6.8e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 WVEAENALGKVTSDH 15

```

Db 197 wweaenalgkvtstdh 211

RESULT 13

AA10545 standard; Protein; 918 AA.

AA10545;

12-APR-1991 (first entry)

Recombinant human gp130 protein.

Recombinant human gp130; interleukin-6; interleukin-6 receptor; immunity; haematopoiesis; inflammation; therapy.

Homo sapiens.

EP411946-A.

06-FEB-1991.

02-AUG-1990; 90EP-0308530.

31-MAY-1990; 90JP-0140069.

03-AUG-1989; 89JP-0200230.

(KISH/) KISHIMOTO T.

Kishimoto T;

WPI; 1991-038820/06.

N-PSDB; AAQ10402.

Recombinant human gp130 protein - acts in the transmission of interleukin-6 signal for defence mechanisms

Disclosure; fig 7; 32pp; English.

This gp130 protein is produced using standard recombinant DNA methods (see AAQ10402), free from any other human protein. It participates in the transmission of the interleukin (IL)-6 signal, and therefore the proliferation and differentiation of an organism. It is important in an animals defence mechanisms, e.g. immunity, haematopoiesis and inflammation.

Sequence 918 AA:

Query Match 100.0%; Score 81; DB 12; Length 918;
Best Local Similarity 100.0%; Pred. No. 7.4e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WVEAENALGKVTSDH 15

Db 197 wweaenalgkvtstdh 211

RESULT 14
AA10545 standard; Protein; 918 AA.

AA10545;

15-SEP-1994 (first entry)

Human soluble glycoprotein (gp) 130.

Glycoprotein; soluble; gp; gp130; antibody production; assay;

Immunochemical assay; detection; immunogen; transmembrane domain.

Homo sapiens.

JP06022786-A.

01-FEB-1994.

02-AUG-1991; 91JP-0217924.

02-AUG-1991; 91JP-0217924.

(KISH/) KISHIMOTO C.

(TOYO) TOSOH CORP.

WPI; 1994-071006/09.

N-PSDB; AAQ56931.

Preparation of recombinant soluble human gp 130 deriv - for use in the production of anti-gp 130 antibody for immunochemical assay

Claim 1; Figure 7; 13pp; Japanese.

The soluble glycoprotein (gp) 130 can be used as an immunogen for the preparation of anti-gp130 antibody and as the standard substance for immunochemical assay of gp130. Soluble gp130 cDNA was prepared by inserting a termination codon prior to the extracellular domain or transmembrane domain of the gp130 coding sequence or simply by eliminating the transmembrane domain.

Sequence 918 AA:

Query Match 100.0%; Score 81; DB 15; Length 918;
Best Local Similarity 100.0%; Pred. No. 7.4e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WVEAENALGKVTSDH 15

Db 197 wweaenalgkvtstdh 211

RESULT 15
AA10545 standard; Protein; 918 AA.

AA10545;

20-JUN-1996 (first entry)

Human gp130 protein.

Gp130; transmembrane domain; growth factor antagonist;

embryo pre-implantation; in vitro fertilisation.

Homo sapiens.

Key Location/Qualifiers

Region 620..641

Label= Transmembrane_region

WO9609382-A1.

28-MAR-1996.

21-SEP-1995; 95WO-GB02243.

21-SEP-1994; 94GB-0019021.

(ISTF) ARS APPLIED RES SYST HOLDING NV.

Dellow KA, Sharkey A, Smith SK;

WPI; 1996-188444/19.

N-PSDB; AAT14603.

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 19, 2001, 16:22:40 ; Search time 88.82 seconds
(without alignments)
12.864 Million cell updates/sec

Title: US-09-202-104a-9
Perfect score: 81
Sequence: 1 WVEAENALGKVTSDH 15

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	81	100.0	918	2	A36337 membrane glycoprot
2	65	80.2	917	2	I49699 glycoprotein I30 -
3	60	74.1	918	2	A44257 interleukin-6 sign
4	46	56.8	771	2	B38252 granulocyte colony
5	46	56.8	783	2	JH0329 granulocyte colony
6	46	56.8	863	2	C38252 granulocyte colony
7	42	51.9	170	2	F85807 hypothetical prote
8	42	51.9	340	2	C85822 probable integrase
9	42	51.9	642	2	A81798 RNA polymerase sig
10	42	51.9	642	2	F81072 granulocyte colony
11	42	51.9	837	2	A34898 granulocyte colony
12	41	50.6	148	1	H71021 hypothetical prote
13	41	50.6	237	2	B55857 KlcB protein - pla
14	41	50.6	264	2	I46020 FC gamma 2 recepto
15	41	50.6	536	2	T16458 hypothetical prote
16	41	50.6	580	2	H82878 threonyl-tRNA synt
17	41	50.6	1032	2	T30270 major tegumental a
18	40	49.4	146	2	H75111 hypothetical prote
19	40	49.4	1462	1	DJH0AC DNA-directed DNA p
20	39.5	48.8	686	2	B75267 prolyl endopeptid
21	39	48.1	161	2	D82042 transcription elon
22	39	48.1	268	2	A70090 hypothetical prote
23	39	48.1	377	2	D81980 carboxyl-phosphat
24	39	48.1	377	2	F81034 catenoyl-phosphat
25	39	48.1	422	2	H69839 multidrug resistan
26	39	48.1	468	2	T08057 tubulin gamma chal
27	39	48.1	468	2	T07904 tubulin gamma chal
28	39	48.1	507	2	T08337 hypothetical prote
29	39	48.1	637	2	F83939 myo-inositol catab

30	39	48.1	952	2	E86147 hypothetical prote
31	38.5	47.5	240	2	T28659 transposase - Sp1r
32	38	46.9	113	2	C81525 conserved hypothet
33	38	46.9	113	2	E72013 CT809 hypothetical
34	38	46.9	113	2	F86610 CT809 hypothetical
35	38	46.9	211	2	C37491 hypothetical prote
36	38	46.9	220	2	T31184 hypothetical prote
37	38	46.9	264	2	G84152 hypothetical prote
38	38	46.9	426	2	T01790 DNA-directed DNA p
39	38	46.9	426	2	G75187 protoporphyrin IX
40	38	46.9	533	2	E86412 probable trehalose
41	38	46.9	630	2	I51086 hypothetical prote
42	38	46.9	680	2	S37955 prolactin receptor
43	38	46.9	704	2	S07512 protein kinase YPK
44	38	46.9	909	2	JN0665 DNA-directed DNA p
45	38	46.9	1109	2	C84545 nitrate reductase
					probable disease r

ALIGNMENTS

RESULT 1
A36337 membrane glycoprotein gp130 precursor - human
C:Species: Homo sapiens (man)
C>Date: 12-Apr-1991 #sequence_revision 12-Apr-1991 #text_change 28-Jul-2000
C:Accession: A36337
R:Hibi, M.; Murakami, M.; Salto, M.; Hirano, T.; Taga, T.; Kishimoto, T.
Cell 63, 1149-1157, 1990
A>Title: Molecular cloning and expression of an IL-6 signal transducer, gp130.
A:Reference number: A36337; MUID:91084844
A:Accession: A36337
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-918 <HIB>
A:Cross-references: GB:M57230; NID:9186353; PIDN:AAA59155.1; PID:9186354
C:Genetics:
A:Gene: GDB:IL6ST; GP130
A:Cross-references: GDB:126725; OMIM:600694
A:Map position: Sq11-Sq11
C:Superfamily: cytokine receptor homology
C:Keywords: glycoprotein; membrane protein
F:334-316/Domain: cytokine receptor homology <CRS>

Query Match 100.0%; Score 81; DB 2; Length 918;
Best Local Similarity 100.0%; Pred. No. 3.8e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WVEAENALGKVTSDH 15
DB 197 WVEAENALGKVTSDH 211
RESULT 2
I49699
glycoprotein I30 - mouse
C:Species: Mus musculus (house mouse)
C>Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 28-Jul-2000
C:Accession: I49699; I48370
R:Salto, M.; Yoshida, K.; Hibi, M.; Taga, T.; Kishimoto, T.
J. Immunol. 148, 4066-4071, 1992
A>Title: Molecular cloning of a murine IL-6 receptor-associated signal transducer, gp
A:Reference number: I48370; MUID:92291532
A:Accession: I49699
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-917 <RES>
A:Cross-references: GB:M83336; NID:9193591; PIDN:AAA37723.1; PID:9193592
A:Accession: I48370
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-917 <RES>

A:Cross-references: EMBL:X62646; NID:g840816; PIDN:CAA44515.1; PID:g840817
C:Genetics:
A:Gene: gp130
C:Superfamily: cytokine receptor homology
C:Keywords: glycoprotein
F:134-314/Domain: cytokine receptor homology <CRS>

Query Match 80.2%; Score 65; DB 2; Length 917;
Best Local Similarity 85.7%; Pred. No. 0.0027;
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 WVEAENALGKVTSD 14
|||
Db 195 WVEAENALGKVSSE 208

RESULT 3
A44257
Interleukin-6 signal transducing molecule gp130 - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 28-Jul-2000
C:Accession: A44257
R:Wang, Y.; Mesibit, J.E.; Fuentes, N.L.; Fuller, G.M.
A:Title: Molecular cloning and characterization of the rat liver IL-6 signal transducing
A:Reference number: A44257; MUID:93052397
A:Accession: A44257
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-918 <MAN>
A:Experimental source: liver
A:Note: sequence extracted from NCBI backbone (NCBIP:118488)
C:Superfamily: cytokine receptor homology
C:Keywords: transmembrane protein
F:134-315/Domain: cytokine receptor homology <CRS>

Query Match 74.1%; Score 60; DB 2; Length 918;
Best Local Similarity 78.6%; Pred. No. 0.021;
Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 WVEAENALGKVTSD 14
|||
Db 196 WVEAENALGNVSSE 209

RESULT 4
B38252
granulocyte colony-stimulating factor receptor precursor (clone pHQ2) - human
C:Species: Homo sapiens (man)
C:Date: 14-Jun-1991 #sequence_revision 14-Jun-1991 #text_change 05-Nov-1999
C:Accession: B38252
R:Fukunaga, R.; Seto, Y.; Mizushima, S.; Nagata, S.
Proc. Natl. Acad. Sci. U.S.A. 87, 8702-8706, 1990
A:Title: Three different mRNAs encoding human granulocyte colony-stimulating factor rece
A:Reference number: A38252; MUID:91062348
A:Accession: B38252
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-771 <PUK>
A:Cross-references: GB:M59819; GB:M38026; NID:g485363; PIDN:AAA63177.1; PID:g485364

Query Match 56.8%; Score 46; DB 2; Length 771;
Best Local Similarity 88.9%; Pred. No. 5.6;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 WVEAENALG 9
|||
Db 202 WVOAENALG 210

RESULT 5
JH0329
granulocyte colony-stimulating factor receptor D7 precursor - human

C:Species: Homo sapiens (man)
C:Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 05-Nov-1999
C:Accession: JH0329; S21608
R:Larsen, A.; Davis, T.; Curtis, B.M.; Gimpe, S.; Sims, J.E.; Cosman, D.; Park, L.;
J. Exp. Med. 172, 1559-1570, 1990
A:Title: Expression cloning of a human granulocyte colony-stimulating factor receptor
A:Reference number: JH0329; MUID:91079757
A:Accession: JH0329

A:Molecule type: mRNA
A:Residues: 1-783 <LAR>
A:Cross-references: GB:X55720; NID:g31698; PIDN:CAA39252.1; PID:g31699
A:Experimental source: placenta
C:Keywords: glycoprotein; transmembrane protein
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-783/Product: granulocyte colony-stimulating factor receptor D7 #status predicted
F:25-627/Domain: extracellular #status predicted <EXT>
F:628-653/Domain: transmembrane #status predicted <TRA>
F:654-783/Domain: intracellular #status predicted <INT>
F:93,128,134,389,474,579,610/Binding site: carbohydrate (Asn) (covalent) #status pred

Query Match 56.8%; Score 46; DB 2; Length 783;
Best Local Similarity 88.9%; Pred. No. 5.7;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 WVEAENALG 9
|||
Db 202 WVOAENALG 210

RESULT 6
C38252
granulocyte colony-stimulating factor receptor precursor, long form - human
N:Contains: granulocyte colony-stimulating factor, long form; granulocyte colony-stim
C:Species: Homo sapiens (man)
C:Date: 14-Jun-1991 #sequence_revision 30-Jan-1993 #text_change 05-Nov-1999
C:Accession: C38252; JH0330; A46486; S68332; S21607
R:Fukunaga, R.; Seto, Y.; Mizushima, S.; Nagata, S.
Proc. Natl. Acad. Sci. U.S.A. 87, 8702-8706, 1990
A:Title: Three different mRNAs encoding human granulocyte colony-stimulating factor r
A:Reference number: A38252; MUID:91062348
A:Accession: C38252
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-863 <PUK>
A:Cross-references: GB:M59820; GB:M38027; NID:g183048; PIDN:AAA63178.1; PID:g183049

A:Note: clones pHG11 and pHG5
A:Accession: A38252
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-680,708-863 <PU2>
A:Cross-references: GB:M59818; GB:M38025; NID:g183046; PIDN:AAA63176.1; PID:g183047
A:Note: clone pHQ3
R:Larsen, A.; Davis, T.; Curtis, B.M.; Gimpe, S.; Sims, J.E.; Cosman, D.; Park, L.;
J. Exp. Med. 172, 1559-1570, 1990
A:Title: Expression cloning of a human granulocyte colony-stimulating factor receptor
A:Reference number: JH0329; MUID:91079757
A:Accession: JH0329

A:Molecule type: mRNA
A:Residues: 1-680,708-863 <LAR>
A:Cross-references: GB:X55721; NID:g31696; PIDN:CAA39253.1; PID:g31697
A:Note: clone 25-1; placenta
R:Seto, Y.; Fukunaga, R.; Nagata, S.
J. Immunol. 146, 259-266, 1992
A:Title: Chromosomal gene organization of the human granulocyte colony-stimulating fa
A:Reference number: A46486; MUID:92091782
A:Accession: A46486
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 855-863 <SET>

A:Cross-references: GB:S71484; NID:g240883; PIDN:AA02060.1; PID:g240884
A:Experimental source: granulocyte
A:Note: sequence extracted from NCBI backbone (NCBIN:71484, NCBI:71485)
R:Hanlu, M.; Horan, T.; Arakawa, T.; Le, J.; Katta, V.; Rohde, M.F.
Arch. Biochem. Biophys. 324, 344-356, 1995
A:Title: Extracellular domain of granulocyte-colony stimulating factor receptor.
A:Reference number: S68331; MUID:96132662
A:Accession: S68332
A:Molecule type: protein
A:Residues: 234-269 <HAN>
C:Genetics:
A:Gene: GDB:CSF3R
A:Cross-references: GDB:126430; OMIM:138971
A:Map position: 1p35-1p34.3
C:Keywords: alternative splicing; glycoprotein; transmembrane protein
F:1-24/Domain: signal sequence #status predicted <SIC>
F:25-863/Product: granulocyte colony-stimulating factor receptor, long form #status pred
F:25-860,708-863/Product: granulocyte colony-stimulating factor receptor, short form #st
F:25-627/Domain: extracellular #status predicted <EXT>
F:628-653/Domain: transmembrane #status predicted <TM>
F:654-863/Domain: intracellular #status predicted <INT>
F:93,128,134,389,474,579,610/Binding site: carbohydrate (Asn) (covalent) #status predict

Query Match 56.8%; Score 46; DB 2; Length 863;
Best Local Similarity 88.9%; Pred. No. 6.3;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 WVEAENALGKVT 9
||:|||||
DB 202 WVEAENALG 210

RESULT 7
F85807
hypothetical protein z2990 [imported] - Escherichia coli (strain O157:H7)
C:Species: Escherichia coli
C>Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Mar-2001
C:Accession: F85807
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: AB5480; MUID:21074935; PMID:11206551
A:Accession: F85807
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-170 <STO>
A:Cross-references: GB:AE005174; NID:g12516002; PIDN:AA056922.1; GSPDB:GN00145; UWGP:z29
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: Z2990
C:Superfamily: pseudomonas aeruginosa hypothetical protein FTR2

Query Match 51.9%; Score 42; DB 2; Length 170;
Best Local Similarity 61.5%; Pred. No. 5.3;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 WVEAENALGKVT 13
||:|||||
DB 13 FVDEHNEVKVTS 25

RESULT 8
C85822
probable integrase for prophage CP-933U intv [imported] - Escherichia coli (strain O157:
C:Species: Escherichia coli
C>Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Mar-2001
C:Accession: C85822
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001

A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: AB5480; MUID:21074935; PMID:11206551
A:Accession: C85822
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-340 <STO>
A:Cross-references: GB:AE005174; NID:g12516149; PIDN:AA057039.1; GSPDB:GN00145; UWGP:
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: intv

Query Match 51.9%; Score 42; DB 2; Length 340;
Best Local Similarity 58.3%; Pred. No. 12;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 WVEAENALGKVT 12
|||||
DB 264 WVEARNHAKGIS 275

RESULT 9
AB1798
RNA polymerase sigma factor NMA1737 [imported] - Neisseria meningitidis (strain Z2491
C:Species: Neisseria meningitidis
C>Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
C:Accession: AB1798
R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Mo
; Holroyd, S.; Jagers, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandre
Nature 404, 502-506, 2000
A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491
A:Reference number: AB1775; MUID:20222556
A:Accession: AB1798
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-642 <PAR>
A:Cross-references: GB:AL162757; GB:AL157959; NID:g7380371; PIDN:CA084965.1; PID:g738
A:Experimental source: serogroup A, strain Z2491
C:Genetics:
A:Gene: rPOD; NMA1737
C:Superfamily: transcription initiation factor sigma 70; transcription initiation fac

Query Match 51.9%; Score 42; DB 2; Length 642;
Best Local Similarity 57.1%; Pred. No. 24;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 WVEAENALGKVTSD 14
|||||
DB 339 WIEBEIAKGRVMSD 352

RESULT 10
F81072
RNA polymerase sigma factor RPOD NMB1538 [imported] - Neisseria meningitidis (strain
C:Species: Neisseria meningitidis
C>Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
C:Accession: F81072
R:Petelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen,
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.
ri, H.; Qin, H.; Vamathavan, J.; Gill, J.; Scarlato, V.; Mastignani, V.; Pizza, M.
Science 287, 1809-1815, 2000
A:Authors: Grandt, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappelli, R.;
A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A:Reference number: AB1000; MUID:20175755
A:Accession: F81072
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-642 <RET>
A:Cross-references: GB:AE002503; GB:AE002096; NID:g7226775; PIDN:AA041893.1; PID:g722
A:Experimental source: serogroup B, strain MC58
C:Genetics:
A:Gene: NMB1538

C:Superfamily: transcription initiation factor sigma 70; transcription initiation factor

Query Match 51.9%; Score 42; DB 2; Length 642;

Best Local Similarity 57.1%; Pred. No. 24;

Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 WVEAENALGKVTSD 14

||| | | | | |

Db 339 WVEEIAKGRVMSD 352

RESULT 11

A34898 granulocyte colony-stimulating factor precursor - mouse

C:Species: Mus musculus (house mouse)

C>Date: 20-Jul-1990 #sequence_revision 20-Jul-1990 #text_change 05-Nov-1999

C:Accession: A34898

R:Fukunaga, R.; Ishizaka-Ikeda, E.; Seto, Y.; Nagata, S.

Cell 61, 341-350, 1990

A:Title: Expression cloning of a receptor for murine granulocyte colony-stimulating factor

A:Reference number: A34898; MUID:90235283

A:Accession: A34898

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-837 <FEUK>

A:Cross-references: GB:M58288; NID:g193454; PIDN:AAA37673.1; PID:g193455; GB:M32699

C:Keywords: transmembrane protein

Query Match 51.9%; Score 42; DB 2; Length 837;

Best Local Similarity 61.5%; Pred. No. 32;

Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 WVEAENALGKVTSD 13

||| | | | | |

Db 203 WVOAENMLGSSSES 215

RESULT 12

H71021

hypothetical protein PH1469 - Pyrococcus horikoshii

C:Species: Pyrococcus horikoshii

C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000

C:Accession: H71021

R:Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Halkawa, Y.; Hino, Y.; Yamamoto, S.; Sekin

M.; Ohnuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi

DNA Res. 5, 55-76, 1998

A:Title: Complete sequence and gene organization of the genome of a hyper-thermophilic

A:Reference number: A71000; MUID:98344137

A:Accession: H71021

A>Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-148 <KKA>

A:Cross-references: GB:AP000006; NID:g3236133; PIDN:BAA30576.1; PID:g3257893

A:Experimental source: strain OT3

A>Note: this accession replaces an interim accession for a sequence replaced by GenBank

C:Genetics:

A:Gene: PH1469

C:Superfamily: Escherichia coli hypothetical protein b3356

Query Match 50.6%; Score 41; DB 1; Length 148;

Best Local Similarity 42.9%; Pred. No. 6.9;

Matches 6; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 WVEAENALGKVTSD 14

||| | | | | |

Db 15 WVEGEQFIGRIECD 28

RESULT 13

B55957

k1cB protein - plasmid RK2

C:Species: plasmid RK2

C>Date: 17-Nov-1995 #sequence_revision 17-Nov-1995 #text_change 08-Oct-1999

C:Accession: B55857

R:Larsen, M.H.; Figurski, D.H.

J. Bacteriol. 176, 5022-5032, 1994

A:Title: Structure, expression, and regulation of the k1cB operon of promiscuous IncP

A:Reference number: A55857; MUID:9437471

A:Accession: B55857

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-237 <LAR>

A:Cross-references: GB:U05773; NID:g529756; PIDN:AAA57449.1; PID:g603901

C:Genetics:

A:Genome: plasmid

Query Match 50.6%; Score 41; DB 2; Length 237;

Best Local Similarity 46.7%; Pred. No. 12;

Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 WVEAENALGKVTSDH 15

||| | | | | |

Db 211 WVEVESGYGLTVAH 225

RESULT 14

I46020

FC gamma 2 receptor precursor - bovine

C:Species: Bos primigenius taurus (cattle)

C>Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 05-Nov-1999

C:Accession: I46020; S53115

R:Zhang, G.; Young, J.R.; Iregaske, C.A.; Sopp, P.; Howard, C.J.

J. Immunol. 155, 1534-1541, 1995

A:Title: Identification of a novel class of mammalian FC gamma receptor.

A:Reference number: I46020; MUID:95363119

A:Accession: I46020

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-264 <ZHA>

A:Cross-references: EMBL:Z37506; NID:g732571; PIDN:CAA85736.1; PID:g732572

C:Keywords: immunoglobulin receptor

Query Match 50.6%; Score 41; DB 2; Length 264;

Best Local Similarity 53.3%; Pred. No. 13;

Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 WVEAENALGKVTSDH 15

||| | | | | |

Db 181 WVOEFSLPVTSAH 195

RESULT 15

T16458

hypothetical protein F55D10.5 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 04-Mar-2000

C:Accession: T16458

R:Leimbach, D.

submitted to the EMBL Data Library, November 1995

A:Description: The sequence of C. elegans cosmid F55D10.

A:Reference number: Z18516

A:Accession: T16458

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-536 <LEI>

A:Cross-references: EMBL:U40948; NID:g1072223; PID:g1072227; PIDN:AAA81730.1; CESP:F5

A:Genetics: CESP:F55D10.5

A:Introns: 36/3; 54/3; 143/3; 220/3; 256/3; 278/2; 340/1; 446/1; 501/3

C:Superfamily: acetylcholine receptor

Query Match 50.6%; Score 41; DB 2; Length 536;
Best Local Similarity 42.9%; Pred. No. 29;
Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 1 WVEAENALGKVTSD 14
||:|:|:|:|
Db 97 WVOEVNSVNEITSD 110

Search completed: December 19, 2001, 16:22:41
Job time: 461 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 19, 2001, 16:26:18 ; Search time 48.45 Seconds
(without alignments)
11.351 Million cell updates/sec

Title: US-09-202-104a-9

Perfect score: 81

Sequence: 1 WVEAENLCKVTSDH 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

100059

Total number of hits satisfying chosen parameters:

100059

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	81	100.0	918	1 IL6B_HUMAN	P40189 homo sapien
2	65	80.2	917	1 IL6B_MOUSE	Q00560 mus musculu
3	60	74.1	918	1 IL6B_RAT	P40190 rattus norv
4	46	56.8	836	1 GCSR_HUMAN	O99062 homo sapien
5	42	51.9	837	1 GCSR_MOUSE	P40223 mus musculu
6	41	50.6	461	1 KLB2_ECOLI	P52605 escherichia
7	41	50.6	580	1 SYT_UREPA	Q9PVP6 ureaplasma
8	40	49.4	1462	1 DPOA_HUMAN	P09884 homo sapien
9	39	48.1	468	1 TBG_CHURE	O39582 chlamydomon
10	38	46.9	211	1 YOR3_SOYU3	O04550 southampton
11	38	46.9	426	1 CHIL_TOBAC	O22436 nicotiana t
12	38	46.9	630	1 PRUR_ORENT	O91513 oreochromis
13	38	46.9	680	1 YPR1_YEAST	P12688 saccharomyc
14	38	46.9	704	1 DPOL_BPT3	P20311 bacteriopho
15	38	46.9	909	1 N1A_PETHY	P36859 petunia hyb
16	37	45.7	92	1 NODE_RHILV	P04685 rhizobium l
17	37	45.7	186	1 YALD_TRYPB	P17962 trypanosoma
18	37	45.7	234	1 OP65_NEIGO	Q04885 neisseria g
19	37	45.7	321	1 VG16_BPB03	Q37897 bacteriopho
20	37	45.7	642	1 FIMB_YEAST	P32599 saccharomyc
21	37	45.7	642	1 RPSD_NEIGO	P52225 neisseria g
22	37	45.7	825	1 BISC_HAETN	P44798 haemophilus
23	37	45.7	889	1 N1A3_MAI2E	P49102 zea mays (m
24	37	45.7	1053	1 CAPP_SYNP6	P06516 synechococc
25	37	45.7	1192	1 LMG2_MOUSE	Q61092 mus musculu
26	37	45.7	1301	1 SACS_YEAST	P46674 saccharomyc
27	37	45.7	1316	1 RPOC_MYCLE	P30761 mycobacteri
28	37	45.7	2514	1 POLN_SINDO	P27283 sindbis vir
29	36	44.4	21	1 CSPS_STRTR	P81622 streptococc
30	36	44.4	68	1 CYC3_DESAC	P00137 desulfurmo
31	36	44.4	102	1 HVR4_RHOCA	P42805 rhodobacter
32	36	44.4	164	1 GCSH_CHICK	P11183 gallus gall
33	36	44.4	173	1 GCSH_HUMAN	P23434 homo sapien

34	36	44.4	299	1	YV13_MYCTU	O50713 mycobacteri
35	36	44.4	384	1	MEFK_HAETN	P43762 haemophilus
36	36	44.4	384	1	POE_METEX	P71517 methylobact
37	36	44.4	687	1	CIKC_RABIT	P51803 oryctolagus
38	36	44.4	756	1	NRG2_MOUSE	P56974 mus musculu
39	36	44.4	767	1	ACES_CHICK	P36196 gallus gall
40	36	44.4	778	1	ACON_YEAST	P19414 saccharomyc
41	36	44.4	814	1	CADF_HUMAN	P55291 homo sapien
42	36	44.4	850	1	NRG2_HUMAN	O14511 homo sapien
43	36	44.4	868	1	NRG2_RAT	O35369 rattus norv
44	36	44.4	879	1	MANB_CAPRI	O95327 capra hircu
45	36	44.4	882	1	ALKS_PSEOL	P17051 pseudomonas

ALIGNMENTS

```

RESULT 1
ID IL6B_HUMAN STANDARD: PRT: 918 AA.
AC P40189; Q9UQ41;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE INTERLEUKIN-6 RECEPTOR BETA CHAIN PRECURSOR (IL-6R-BETA) (INTERLEUKIN
DE 6 SIGNAL TRANSDUCER) (MEMBRANE GLYCOPROTEIN 130) (GP130) (ONCOSTATIN M
DE RECEPTOR) (CDW130) (CD130 ANTIGEN).
GN IL6ST.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID:9606;
[1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Myeloma, and Placenta;
RA MEDLINE=91084844; PubMed=2261637;
RA Hibi M., Murakami M., Saito M., Hirano T., Taga T., Kishimoto T.;
RT "Molecular cloning and expression of an IL-6 signal transducer,
RT gp130."
RT Cell 63:1149-1157(1990).
[2]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Synovium;
RA PubMed=10880057;
RA Tanaka M., Kishimura M., Ozaki S., Osakada F., Hashimoto H., Okubo M.,
RA Murakami M., Nakao K.;
RT "Cloning of novel soluble gp130 and detection of its neutralizing
RT autoantibodies in rheumatoid arthritis."
RT J. Clin. Invest. 106:137-144(2000).
[3]
RP PARTIAL SEQUENCE, DISULFIDE BONDS, AND CARBOHYDRATE-LINKAGE SITES.
RP PubMed=11098061;
RA Moritz R.L., Hall N.E., Connolly L.M., Simpson R.J.;
RT "Determination of the disulfide structure and N-glycosylation sites of
RT the extracellular domain of the human signal transducer gp130."
RT J. Biol. Chem. 276:8244-8253(2001).
[4]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 122-325.
RP MEDLINE=98169383; PubMed=9501088;
RA Bravo J., Staunton D., Heath J.K., Jones E.Y.;
RT "Crystal structure of a cytokine-binding region of gp130."
RT EMBO J. 17:1665-1674(1998).
-1- FUNCTION: SIGNAL-TRANSDUCING MOLECULE. THE RECEPTOR SYSTEMS FOR
IL-6, LIF, OSM, CNTF, IL-11 AND CT-1 CAN UTILIZE GP130 FOR
INITIATING SIGNAL TRANSMISSION. BINDS TO IL-6/IL-6-R (ALPHA CHAIN)
COMPLEX, RESULTING IN THE FORMATION OF HIGH-AFFINITY IL-6 BINDING
SITES, AND TRANSDUCES THE SIGNAL. DOES NOT BIND IL-6. MAY HAVE A
ROLE IN EMBRYONIC DEVELOPMENT (BY SIMILARITY).
-1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
-1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (ISOFORM 1) AND
SECRETED (ISOFORM 2).
-1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 (SHOWN HERE) AND 2/GP130-
RAPs; ARE PRODUCED BY ALTERNATIVE SPLICING.

```

CC	-	TISSUE SPECIFICITY: FOUND IN ALL THE TISSUES AND CELL LINES	
CC	EXAMINED.	EXPRESSION NOT RESTRICTED TO IL-6 RESPONSIVE CELLS.	
CC	-	DISEASE: GP130-RAPS IS AN AUTOANTIGEN FOUND IN RHEUMATOID	
CC	ARTHRITIS (RA)	BUT IT IS NOT SPECIFIC TO PATIENTS WITH RA.	
CC	-	SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.	
CC	-	SIMILARITY: CONTAINS 5 FIBRONECTIN TYPE III-LIKE DOMAINS.	
CC	-	SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.	
CC	-	DATABASE: NAME-PROX; NOTE=CD guide CD130 entry;	
CC	WWW=	http://www.ncbi.nlm.nih.gov/prov/cd/cd130.htm"	
CC	-	-----	
CC	THIS	SWISS-PROT entry is copyright. It is produced through a collaboration	
CC	CC	between the Swiss Institute of Bioinformatics and the EMBL outstation	
CC	CC	the European Bioinformatics Institute. There are no restrictions on its	
CC	CC	use by non-profit institutions as long as its content is in no way	
CC	CC	modified and this statement is not removed. Usage by and for commercial	
CC	CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/	
CC	CC	or send an email to license@isb-sib.ch).	
CC	-	-----	
DR	EMBL:	M57230; AAA59155.1; -	
DR	EMBL:	AB015706; BAA78112.1; -	
DR	PIR:	A36337; A36337.	
DR	PDB:	1BOU; 26-AUG-98.	
DR	MIM:	600694; -	
DR	InterPro:	IPR002996; CRLA	
DR	InterPro:	IPR001777; FN_III.	
DR	InterPro:	IPR003529; Hematopo_receptor_L_F2.	
DR	Pfam:	PF00041; fn3; 3.	
DR	PRINTS:	PRO0014; FNTPEIII.	
DR	SMART:	SM00060; FN3; 3.	
DR	PROSITE:	PS01353; HEMATOPO_REC_L_F2; 1.	
KW	Receptor;	Transmembrane; Glycoprotein; Immunoglobulin domain; Signal;	
KW	Repeat:	3d-structure; Alternative splicing.	
FT	SIGNAL	1 22	
FT	CHAIN	23 918	INTERLEUKIN-6 RECEPTOR BETA CHAIN.
FT	DOMAIN	23 619	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	620 641	POTENTIAL.
FT	DOMAIN	642 918	CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	26 120	IG-LIKE C2-TYPE DOMAIN.
FT	DOMAIN	124 222	FIBRONECTIN TYPE-III 1.
FT	DOMAIN	223 324	FIBRONECTIN TYPE-III 2.
FT	DOMAIN	325 423	FIBRONECTIN TYPE-III 3.
FT	DOMAIN	424 517	FIBRONECTIN TYPE-III 4.
FT	DOMAIN	518 613	FIBRONECTIN TYPE-III 5.
FT	DOMAIN	725 755	SER-RICH.
FT	DISULFID	28 54	
FT	DISULFID	48 103	
FT	DISULFID	134 144	
FT	DISULFID	172 182	
FT	DISULFID	458 466	
FT	CARBOHYD	43 43	N-LINKED (GLCNAC. . .).
FT	CARBOHYD	83 83	N-LINKED (GLCNAC. . .).
FT	CARBOHYD	131 131	N-LINKED (GLCNAC. . .).
FT	CARBOHYD	157 157	N-LINKED (GLCNAC. . .).
FT	CARBOHYD	227 227	N-LINKED (GLCNAC. . .).
FT	CARBOHYD	379 379	N-LINKED (GLCNAC. . .).
FT	CARBOHYD	383 383	N-LINKED (GLCNAC. . .).
FT	CARBOHYD	553 553	N-LINKED (GLCNAC. . .).
FT	CARBOHYD	564 564	N-LINKED (GLCNAC. . .).
FT	VARSPLIC	325 329	RPSKA -> N1ASF (IN GP130-RAPS).
FT	VARSPLIC	330 918	MISSING (IN GP130-RAPS).
SEQ	SEQUENCE	918 AA: 103522 MW: 813672DD10D53 CAC64:	

```

Query Match          100.0%; Score 81; DB 1; Length 918;
Best Local Similarity 100.0%; Pred. No. 1.1e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY      1 WVEAENALGKVTSDH 15
      |||
Db      197 WVEAENALGKVTSDH 211

RESULT : 2

```

ID	IL6B_MOUSE	STANDARD;	PRT;	917 AA.
AC	000560:			
DT	01-FEB-1995 (Rel. 31, Created)			
DT	01-FEB-1995 (Rel. 31, Last sequence update)			
DT	20-AUG-2001 (Rel. 40, Last annotation update)			
DE	INTERLEUKIN-6 RECEPTOR BETA CHAIN PRECURSOR (IL-6R-BETA) (INTERLEUKIN-6 SIGNAL TRANSDUCER) (MEMBRANE GLYCOPROTEIN 130) (gp130).			
GN	IL6ST.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=ICR; TISSUE=Macrophage;			
RX	MEDLINE=92291532; PubMed=1602143;			
RA	Saito M., Yoshida K., Hibl M., Tsga T., Kishimoto T.;			
RT	"Molecular cloning of a murine IL-6 receptor-associated signal transducer, gp130, and its regulated expression in vivo."			
RL	J. Immunol. 148:4066-4071(1992).			
CC	-1- FUNCTION: SIGNAL-TRANSDUCING MOLECULE. THE RECEPTOR SYSTEMS FOR IL-6, ILF, OSM, CMF, AND IL-11 CAN UTILIZE GP130 FOR INITIATING SIGNAL TRANSMISSION. BINDS TO IL-6/IL-6-R (ALPHA CHAIN) COMPLEX, RESULTING IN THE FORMATION OF HIGH-AFFINITY IL-6 BINDING SITES, AND TRANSDUCES THE SIGNAL. DOES NOT BIND IL-6. MAY HAVE A ROLE IN EMBRYONIC DEVELOPMENT.			
CC	-1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.			
CC	-1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.			
CC	-1- TISSUE SPECIFICITY: FOUND IN TISSUES SUCH AS BRAIN, HEART, THYMUS, SPLEEN, KIDNEY, LUNG AND LIVER. FOUND IN ALL THE CELL LINES TESTED EXCEPT BAF-B03. EXPRESSION NOT RESTRICTED TO IL-6-RESPONSIVE CELLS.			
CC	-1- DEVELOPMENTAL STAGE: IN EMBRYONIC STEM CELLS IT IS FOUND FROM DAY 6 OF GESTATION. IT REACHES A PEAK ON DAY 8 AND GRADUALLY DECLINES DURING THE REST OF EMBRYOGENESIS.			
CC	-1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.			
CC	-1- SIMILARITY: CONTAINS 5 FIBRONECTIN TYPE III-LIKE DOMAINS.			
CC	-1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.			
CC	THIS SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/ or send an email to license@sib-sib.ch).			
CC	EMBL: X62646; CAA44515.1; -			
DR	EMBL: M83336; AAA37723.1; -			
DR	HSSP: PA0189; 1BOU.			
DR	MCD: MG1:96560; 1I6ST.			
DR	InterPro: IPR002996; CRIA.			
DR	InterPro: IPR001777; FN_111.			
DR	InterPro: IPR003529; Hematopo_rcptor_L_F2.			
DR	Pfam: PF00041; fn3; 4.			
DR	PRINTS: PR00014; ENTPEP11.			
DR	SMART: SM00060; FN3; 2.			
DR	PROSITE: PS01353; HEMATOPO_REC_L_F2; 1.			
KW	Receptor; Transmembrane; Glycoprotein; Immunoglobulin domain; Signal;			
KW	Repeat.			
FT	SIGNAL	1	22	POTENTIAL.
FT	CHAIN	23	917	INTERLEUKIN-6 RECEPTOR BETA CHAIN.
FT	DOMAIN	23	617	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	618	639	POTENTIAL.
FT	DOMAIN	640	917	CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	26	120	IG-LIKE C2-TYPE DOMAIN.
FT	DOMAIN	124	220	FIBRONECTIN TYPE-III 1.
FT	DOMAIN	221	322	FIBRONECTIN TYPE-III 2.
FT	DOMAIN	323	420	FIBRONECTIN TYPE-III 3.
FT	DOMAIN	422	515	FIBRONECTIN TYPE-III 4.
FT	DOMAIN	516	611	FIBRONECTIN TYPE-III 5.
FT	DOMAIN	723	741	SER-RICH.

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FT DISULFID 28 54 BY SIMILARITY.
FT DISULFID 48 103 BY SIMILARITY.
FT DISULFID 134 144 BY SIMILARITY.
FT DISULFID 172 180 BY SIMILARITY.
FT DISULFID 456 464 BY SIMILARITY.
FT CARBOHYD 43 43 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 61 61 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 83 83 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 131 131 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 157 157 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 225 225 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 388 388 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 476 476 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 551 551 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 917 AA; 102452 MW; FCFD220BC2466F4 CRC64;

Query Match 80.2%; Score 65; DB 1; Length 917;
Best Local Similarity 85.7%; Pred. No. 0.00088;
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 WEAENALGKVTSD 14
Db 195 WEAENALGKVSSE 208

RESULT 3
ID IL6B_RAT STANDARD; PRT; 918 AA.
AC P40190;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE INTERLEUKIN-6 RECEPTOR BETA CHAIN PRECURSOR (IL-6R-BETA) (INTERLEUKIN
DE 6 SIGNAL-TRANSDUCER (MEMBRANE GLYCOPROTEIN 130) (GP130).
GN IL6ST.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=93052397; PubMed=1427893;
RA Wang Y., Nesbitt J.E., Fuentes N.L., Fuller G.M.;
RT Molecular cloning and characterization of the rat liver IL-6 signal
RT transducing molecule, gp130."
RL Genomics 14:666-672(1992).
CC - FUNCTION: SIGNAL-TRANSDUCING MOLECULE. THE RECEPTOR SYSTEMS FOR
CC IL-6, LIF, OSM, CNTF, AND IL-11 CAN UTILIZE GP130 FOR INITIATING
CC SIGNAL TRANSMISSION. BINDS TO IL-6/IL-6-R (ALPHA CHAIN) COMPLEX,
CC RESULTING IN THE FORMATION OF HIGH-AFFINITY IL-6 BINDING SITES,
CC AND TRANSDUCES THE SIGNAL. DOES NOT BIND IL-6. MAY HAVE A ROLE IN
CC EMBRYONIC DEVELOPMENT (BY SIMILARITY).
CC - SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
CC - SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC - TISSUE SPECIFICITY: FOUND IN HEPATOCYTES, ASTROCYTES, FIBROBLASTS
CC AND ENDOTHELIAL CELLS.
CC - SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC - SIMILARITY: CONTAINS 5 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC - SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -----
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CC -----
CC EMBL: M92340; ; NOT_ANNOTATED_CDS.
CC PIR: A44257; A44257.
CC HSSP: P40189; 1BDU.

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DR InterPro: IPR002996; CRIA.
DR InterPro: IPR001777; FN_III.
DR InterPro: IPR003529; Hematopo_receptor_L_F2.
DR Pfam: PF00041; Irb3_3.
DR SMART: SM00060; FN3_3.
DR PROSITE: PS01353; HEMATOPO_REC_L_F2; 1.
KV Receptor; Transmembrane; Glycoprotein; Immunoglobulin domain; Signal;
KW Repeat.
FT SIGNAL. 1 22
FT CHAIN 23 918
FT DOMAIN 23 618
FT TRANSMEM 619 640
FT DOMAIN 641 918
FT DOMAIN 26 120
FT DOMAIN 124 221
FT DOMAIN 222 323
FT DOMAIN 324 422
FT DOMAIN 423 516
FT DOMAIN 517 612
FT DOMAIN 724 754
FT DISULFID 28 54
FT DISULFID 48 103
FT DISULFID 134 144
FT DISULFID 172 181
FT DISULFID 457 465
FT CARBOHYD 43 43
FT CARBOHYD 61 61
FT CARBOHYD 83 83
FT CARBOHYD 131 131
FT CARBOHYD 157 157
FT CARBOHYD 205 205
FT CARBOHYD 226 226
FT CARBOHYD 382 382
FT CARBOHYD 389 389
FT CARBOHYD 477 552
FT CARBOHYD 552 552
SQ SEQUENCE 918 AA; 102450 MW; 9E1B6FECEFF087F7 CRC64;

Query Match 74.1%; Score 60; DB 1; Length 918;
Best Local Similarity 78.6%; Pred. No. 0.007;
Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 WEAENALGKVTSD 14
Db 196 WEAENALGKVSSE 209

RESULT 4
ID GCSR_HUMAN STANDARD; PRT; 836 AA.
AC Q99062;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE GRANULOCYTE COLONY STIMULATING FACTOR RECEPTOR PRECURSOR (G-CSF-R)
DE (CD114 ANTIGEN).
GN CSF3R OR GCSFR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=91079757; PubMed=2147944;
RA Larsen A., Davis F., Curtis B.M., Gimpel S., Sims J.E., Cosman D.,
RA Park L., Sorensen E., March C.J., Smith C.A.;
RT Expression cloning of a human granulocyte colony-stimulating factor
RT receptor: a structural mosaic of hematopoietin receptor,
RT immunoglobulin, and fibronectin domains."
RL J. Exp. Med. 172:1559-1570(1990).
RN [2]

```

RP SEQUENCE FROM N.A.
 RC TISSUE-Placenta:
 RX MEDLINE-91062348; PubMed-1701053;
 RA Fukunaga R., Seto Y., Mizushima S., Nagata S.;
 RT "Three different mRNAs encoding human granulocyte colony-stimulating
 factor receptor.";
 RT Proc. Natl. Acad. Sci. U.S.A. 87:8702-8706(1990).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-92091782; PubMed-1530796;
 RA Seto Y., Fukunaga R., Nagata S.;
 RT "Chromosomal gene organization of the human granulocyte colony-
 stimulating factor receptor.";
 RT J. Immunol. 148:259-266(1992).
 RN [4]
 RP DOMAINS STRUCTURE.
 RX MEDLINE-92007729; PubMed-1717255;
 RA Fukunaga R., Ishizaka-Ikeda E., Pan C.-X., Seto Y., Nagata S.;
 RT "Functional domains of the granulocyte colony-stimulating factor
 receptor.";
 RT EMBO J. 10:2855-2865(1991).
 RN [5]
 RP STRUCTURE BY NMR OF 227-334.
 RX MEDLINE-97331327; PubMed-9187659;
 RA Yamasaki K., Naito S., Anaguchi H., Ohkubo T., Ota Y.;
 RT "Solution structure of an extracellular domain containing the MSXMS
 motif of the granulocyte colony-stimulating factor receptor and its
 interaction with ligand.";
 RT Nat. Struct. Biol. 4:498-503(1997).
 RN [6]
 RP 3D-STRUCTURE MODELING OF 125-331.
 RX MEDLINE-98037802; PubMed-9368043;
 RA Layton J.E., Iatia J., Smith D.K., Treutlein H.R.;
 RT "Identification of a ligand-binding site on the granulocyte colony-
 stimulating factor receptor by molecular modeling and mutagenesis.";
 RT J. Biol. Chem. 272:29735-29741(1997).
 CC -1- FUNCTION: RECEPTOR FOR GRANULOCYTE COLONY-STIMULATING FACTOR (G-
 CSF). IN ADDITION IT MAY FUNCTION IN SOME ADHESION OR RECOGNITION
 EVENTS AT THE CELL SURFACE.
 CC -1- SUBUNIT: DIMER (PROBABLE).
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. THE GCSF-2 FORM,
 WHICH LACKS THE TRANSMEMBRANE DOMAIN, MAY REPRESENT A SOLUBLE FORM
 OF THE RECEPTOR.
 CC -1- ALTERNATIVE PRODUCTS: AT LEAST 4 ISOFORMS: GCSF-1 (SHOWN HERE),
 GCSF-2, GCSF-3 AND GCSF-4/D7; SEEM TO BE PRODUCED BY
 ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: ONE OR SEVERAL FORMS HAVE BEEN FOUND IN
 MYELOGENOUS LEUKEMIA CELL LINE KG-1, LEUKEMIA U937 CELL LINE, IN
 BONE MARROW CELLS, PLACENTA, AND PERIPHERAL BLOOD GRANULOCYTES.
 CC THE GCSF-2 FORM HAS BEEN FOUND ONLY IN LEUKEMIA U937 CELLS. THE
 GCSF-3 FORM IS HIGHLY EXPRESSED IN PLACENTA.
 CC -1- DISEASE: DEFECTS IN GCSF3 ARE A CAUSE OF KOSTMANN SYNDROME;
 ALSO KNOWN AS SEVERE CONGENITAL NEUTROPENIA (SCN).
 CC -1- SIMILARITY: CONTAINS 5 FIBROBLAST TYPE III-LIKE DOMAINS.
 CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 CC -1- DATABASE: NAME=PRO; NOTE=CD guide CD114 entry;
 WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd114.htm".
 CC -----
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 or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; X55721; CAA39253.1; -;
 DR EMBL; X55720; CAA39252.1; -;
 DR EMBL; S71484; AAB20660.1; -;
 DR EMBL; M59818; AAA63176.1; -;
 DR EMBL; M59819; AAA63177.1; -;
 DR EMBL; M59820; AAA63178.1; -;

[illegible]


```
OX NCBI_TaxID=3055;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=21GR;
RA Sliflow C.D., Liu B., Lavoie M., Palevitz B.A.;
RT "Gamma-tubulin in Chlamydomonas: characterization of the gene and
  localization of the gene product in cells."
RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=137C;
RA Trabucco E.C., Dutcher S.K.;
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: TUBULIN IS THE MAJOR CONSTITUENT OF MICROTUBULES.
CC GAMMA TUBULIN IS FOUND AT MICROTUBULE ORGANIZING CENTERS (MTOC)
CC SUCH AS THE SPINDLE POLES OR THE CENTROSOME, SUGGESTING THAT IT
CC IS INVOLVED IN THE MINUS-END NUCLEATION OF MICROTUBULE ASSEMBLY.
CC -1- SIMILARITY: BELONGS TO THE TUBULIN FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U31545; AAA82610.1; -
DR EMBL: AF013109; AAB71841.1; -
DR Mendel; 7652; Chlre;TUBC;7652.
DR Mendel; 26346; Chlre;TUBC;26346.
DR InterPro: IPR000217; Tubulin.
DR InterPro: IPR003008; Tubulin_FtsZ.
DR Pfam: PF00091; tubulin.1.
DR PRINTS: PR01161; TUBULIN.
DR PRINTS: PR01164; GAMMAMTUBULIN.
DR PROSITE: PS00227; TUBULIN; 1.
KW Microtubules; GTP-binding.
FT NP_BIND 142 148 GTP (POTENTIAL).
FT CONFLICT 411 411 R->A (IN REF. 2).
SQ SEQUENCE 468 AA; 52158 MW; DA4BFC3C03AD1C4 CRC64;

Query Match 48.1%; Score 39; DB 1; Length 468;
Best Local Similarity 72.7%; Pred. No. 21;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 4 AENALGKVTSD 14
DB 278 AENAGQVTSN 288
|||||:||||
YOR3_SOUV3 STANDARD; PRT; 211 AA.
AC 004550;
DT 01-OCT-1994 (Rel. 30; Created)
DT 01-OCT-1994 (Rel. 30; Last sequence update)
DT 20-AUG-2001 (Rel. 40; Last annotation update)
DE HYPOTHETICAL 22.3 KDA PROTEIN IN COAT PROTEIN GENE 3' REGION (ORF3).
OS Southampton virus (serotype 3).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Caliciviridae;
OC Norwalk-like viruses.
OX NCBI_TaxID=37129;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=93142023; PubMed=8380940;
RA Lamden P.R., Caul E.O., Ashley C.R., Clarke I.N.;
RT "Sequence and genome organization of a human small round-structured
  (Norwalk-like) virus."
RL Science 259:516-519(1993).
CC -----
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CC -----
DR EMBL: L07418; AAA92985.1; -
DR PIR: C37491; C37491.
KW Hypothetical protein.
SQ SEQUENCE 211 AA; 22257 MW; 3D6D1B51CC3C27B4 CRC64;

Query Match 46.9%; Score 38; DB 1; Length 211;
Best Local Similarity 40.0%; Pred. No. 14;
Matches 6; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

OY 1 WYEENALGKVTSDH 15
DB 156 WYQSONLSRVSPPH 170
|||||:|1:-|
CHL1_TOBAC STANDARD; PRT; 426 AA.
AC 022436;
DT 15-JUL-1998 (Rel. 36; Created)
DT 15-JUL-1998 (Rel. 36; Last sequence update)
DT 30-MAY-2000 (Rel. 39; Last annotation update)
DE MAGNESIUM-CHELATASE SUBUNIT CHL1 PRECURSOR (MG-PROTOPORPHYRIN IX
  CHELATASE).
DE CHL1.
GN Nicotiana tabacum (Common tobacco).
OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. SRL;
RA Kruse E., Mock H.-P., Grimm B.;
RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: INVOLVED IN CHLOROPLAST PIGMENT BIOSYNTHESIS; INTRODUCES
  A MAGNESIUM ION INTO PROTOPORPHYRIN IX TO YIELD MG-
  PROTOPORPHYRIN IX.
CC -1- PATHWAY: CHLOROPHYLL BIOSYNTHESIS.
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST STROMA.
CC -1- SIMILARITY: BELONGS TO THE MG-CHELATASE SUBUNITS D/I FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AF014053; AAB97153.1; -
DR InterPro: IPR003593; AAA.
DR InterPro: IPR000523; Mg_chelatase_chl1.
DR Pfam: PF01078; Mg_chelatase; 1.
DR SMART: SM00382; AAA; 1.
KW Photosynthesis; Chlorophyll biosynthesis; Chloroplast;
KW Transit peptide; ATP-binding.
KW TRANSIT 1 ?
FT CHAIN 121 426 CHLOROPLAST (POTENTIAL).
FT NP_BIND 121 128 MAGNESIUM-CHELATASE SUBUNIT CHL1.
FT NP_BIND 121 128 ATP (POTENTIAL).
SQ SEQUENCE 426 AA; 46627 MW; 42B7A6F04E1G3274 CRC64;

Query Match 46.9%; Score 38; DB 1; Length 426;
Best Local Similarity 66.7%; Pred. No. 29;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

OY 4 AENALGKVTSDH 15
 DB 335 ARNALSAVTIDH 346

RESULT 12

PRLR_ORENI STANDARD; PRT; 630 AA.

AC 091513;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 15-JUL-1998 (Rel. 36, Last annotation update)

DE PROLACTIN RECEPTOR PRECURSOR (PRL-R).

PRLR.

OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

OC Acanthomorpha; Acanthopterygii; Perciformes; Labroidae;

OC Cichlidae; Oreochromis.

NCBI_TaxID=8128;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Kidney;

MDLINE=9530210; PubMed=7597076;

RA Sandra O., Sohm F., de Luze A., Prunet P., Edey M., Kelly P.A.;

RT "Expression cloning of a cDNA encoding a fish prolactin receptor.";

Proc. Natl. Acad. Sci. U.S.A. 92:6037-6041(1995).

- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE

PROLACTIN.

- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.

- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.

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CC EMBL; L34783; AAA98997.1; -

DR HSSP; P16471; 1BP3.

DR InterPro: IPR002996; CRA.

DR InterPro: IPR001777; FN.III.

DR InterPro: IPR005528; Hematopo_receptor_L.FI.

DR Pfam; PF00041; Fn3; 2.

DR SMART; SM00060; Fn3; 2.

DR PROSITE; PS01352; HEMATOPO_REC_L.FI. 1.

KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat.

FT SIGNAL 1 23 BY SIMILARITY.

FT CHAIN 24 630 PROLACTIN RECEPTOR.

FT DOMAIN 24 234 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 235 258 POTENTIAL.

FT DOMAIN 259 630 CYTOPLASMIC (POTENTIAL).

FT DOMAIN 24 123 FIBRONECTIN TYPE-III 1.

FT DOMAIN 124 228 FIBRONECTIN TYPE-III 2.

FT DISULFID 37 47 BY SIMILARITY.

FT DISULFID 76 87 BY SIMILARITY.

FT CARBOHYD 92 92 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 101 101 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT SEQUENCE 630 AA; 70810 MW; A451563FD12979D CRC64;

Query Match 46.9%; Score 38; DB 1; Length 630;

Best Local Similarity 69.2%; Pred. No. 44;

Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 2 VEENALGKVTSD 14

DB 104 VVATNALGKVTSD 116

RESULT 13
 YPK1_YEAST STANDARD; PRT; 680 AA.

ID YPK1_YEAST

AC P12688;

DT 01-OCT-1989 (Rel. 12, Created)

DT 01-JUN-1994 (Rel. 29, Last sequence update)

DT 20-AUG-2001 (Rel. 40, Last annotation update)

DE SERINE/THREONINE-PROTEIN KINASE YPK1 (EC 2.7.1.1.-).

GN YPK1 OR YKL126W.

OS Saccharomyces cerevisiae (Baker's yeast).

OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.

NCBI_TaxID=4932;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=89090805; PubMed=2850145;

RA Maurer R.A.;

RT "Isolation of a yeast protein kinase gene by screening with a

RT mammalian protein kinase cDNA.";

RT DNA 7:469-474(1988).

RN [2]

RP SEQUENCE FROM N.A.

RA Red M.R., Xu G., Kirchbach L., Fritz C., Keuchel H., Hollenberg C.P.;

RL Submitted (MAR-1994) to the EMBL/GenBank/DBJ databases.

RN [3]

RP DISCUSSION OF SEQUENCE.

RX MEDLINE=93173125; PubMed=8437590;

RA Chen P.C., Lee K.S., Levin D.E.;

RT "A pair of putative protein kinase genes (YPK1 and YPK2) is required

RT for cell growth in Saccharomyces cerevisiae.";

RT Mol. Gen. Genet. 236:443-447(1993).

- FUNCTION: PLAYS AN ESSENTIAL ROLE IN THE PROLIFERATION OF YEAST

CELLS.

- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

- RAC SUBFAMILY. STRONGEST TO YPK2.

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CC EMBL; M21307; AAA3480.1; -

DR EMBL; Z28126; CAA81967.1; -

DR PIR; S37955; S37955.

DR HSSP; P05132; ICTP.

DR SGD; S0001609; YPK1.

DR InterPro: IPR000719; Euk_pkinase.

DR InterPro: IPR000961; Pkinase_C.

DR InterPro: IPR002290; Ser_thr_kin_actsite.

DR Pfam; PF00069; Pkinase; 1.

DR Pfam; PF00433; Pkinase_C; 1.

DR SMART; SM00220; S_TKc; 1.

DR SMART; SM00133; S_TK_X; 1.

DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.

KW transferase; Serine/threonine-protein kinase; ATP-binding.

FT DOMAIN 347 602 PROTEIN KINASE.

FT NP_BIND 353 361 ATP (BY SIMILARITY).

FT BINDING 376 376 ATP (BY SIMILARITY).

FT ACT SITE 470 470 BY SIMILARITY.

FT CONFLICT 201 201 P -> I (IN REF. 2).

FT CONFLICT 553 553 M -> I (IN REF. 2).

FT SEQUENCE 680 AA; 76479 MW; 00112BB8649CD2B5 CRC64;

Query Match 46.9%; Score 38; DB 1; Length 680;

Best Local Similarity 45.5%; Pred. No. 48;

Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Oy 1 WVEAENALGKV 11
 Db 318 WITLNGLEKI 328

RESULT 14
 ID DPOL_BPT3 STANDARD: PRT: 704 AA.

AC 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE DNA POLYMERASE (EC 2.7.7.7).

OS Bacteriophage T3.
 OC Viruses: dsDNA viruses, no RNA stage; Tailed phages; Podoviridae;
 OC T7-like phages.
 OX NCBI_TaxID=10759;

RP SEQUENCE FROM N.A.

RC STRAIN-LURIA:
 RX MEDLINE=90133923; PubMed=2614843;

RA Beck P.J., Gonzalez S., Ward C.L., Molineux I.J.;
 RT "Sequence of bacteriophage T3 DNA from gene 2.5 through gene 9.";

RL J. Mol. Biol. 210:687-701(1989).

CC -1- FUNCTION: IN ADDITION TO POLYMERASE ACTIVITY, THIS DNA POLYMERASE
 EXHIBITS A 3' TO 5' EXONUCLEASE ACTIVITY.

CC -1- CATALYTIC ACTIVITY: N DEOXYNUCLEOSIDE TRIPHOSPHATE -
 N PYROPHOSPHATE + DNA(N).

CC -1- SUBUNIT: COMPOSED OF TWO SUBUNITS. ONE IS ENCODED BY THE PHAGE AND
 THE OTHER IS ENCODED BY THE HOST THIOREDOXIN.

CC -1- SIMILARITY: BELONGS TO DNA POLYMERASE TYPE-A FAMILY.

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 or send an email to license@isb-sib.ch).

DR EMBL: X17255; CAA35140.1; -
 DR PIR: S07512; S07512.

DR HSSP: P00581; 177P.

DR InterPro: IPR001098; DNA_pol_A.

DR Pfam: PF00476; DNA_pol_A.1.

DR SMART: SM00482; POLAC.1.

DR PROSITE: PS00447; DNA_POLYMERASE_A.1.

KW Transferase: DNA-directed DNA polymerase; DNA replication;
 KW DNA-binding; Hydrolase: Exonuclease

SEQUENCE 704 AA; 79985 MW; D65DFBD99AE31234 CRC64;

Query Match 46.9%; Score 38; DB 1; Length 704;
 Best Local Similarity 57.1%; Pred. No. 50;

Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Oy 2 VEAENALGKVTSDH 15
 Db 6 IEANNLEKVKF 19

RESULT 15

ID NIA_PETHY STANDARD: PRT: 909 AA.

AC P36859;

DT 01-JUN-1994 (Rel. 29, Created)

DT 01-JUN-1994 (Rel. 29, Last sequence update)

DT 01-OCT-1994 (Rel. 30, Last annotation update)

DE NITRATE REDUCTASE (EC 1.6.6.1) (NR).

GN NIA.
 OS Petunia hybrida (Petunia).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; euasterids I; Solanales; Solanaceae; Petunia.

OX NCBI_TaxID=4102;

RP SEQUENCE FROM N.A.

RC STRAIN-CV. TURL13; TISSUE=Leaf;

RX MEDLINE=93292981; PubMed=8514183;

RA Salanoubat M., Ha D.B.D.;

RT "Analysis of the petunia nitrate reductase apoenzyme-encoding gene: a
 first step for sequence modification analysis.";

RL Gene 128:147-154(1993).

CC -1- FUNCTION: NITRATE REDUCTASE IS A KEY ENZYME INVOLVED IN THE FIRST
 STEP OF NITRATE ASSIMILATION IN PLANTS, FUNGI AND BACTERIA.

CC -1- CATALYTIC ACTIVITY: NADH + NITRATE -> NAD(+) + NITRITE + H(2)O.

CC -1- COFACTOR: EACH SUBUNIT OF THE ENZYME CONTAINS 1 EQUIVALENT OF FAD,
 HEME IRON, AND MOLYBDENUM-PTERIN AS PROSTHETIC GROUPS. THE HEME

CC GROUP IS CALLED CYTOCHROME B-557.

CC -1- ENZYME REGULATION: REGULATED BY THE NITROGEN SOURCE AND CONTROLLED
 BY THE CIRCADIAN RHYTHM.

CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).

CC -1- DEVELOPMENTAL STAGE: MAXIMUM EXPRESSION 2 HOURS AFTER SUNRISE. LOW
 EXPRESSION FOUND 2 HOURS BEFORE AND 8 HOURS AFTER SUNRISE.

CC -1- SIMILARITY: TO EUKARYOTIC MOLYBDOPTERIN OXIDOREDUCTASES IN THE
 N-TERMINAL DOMAIN.

CC -1- SIMILARITY: CONTAINS A CYTOCHROME B5 FAMILY, HEME-BINDING DOMAIN.
 C-TERMINAL DOMAIN.

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DR EMBL: L13691; AAA33713.1; -
 DR PIR: JN0665; JN0665.

DR HSSP: P17371; 2CND.

DR InterPro: IPR001199; Cyt_B5.

DR Pfam: PF001834; Cyt_B5_reductase.

DR InterPro: IPR000572; Euk_oxidored_molyb.

DR InterPro: IPR001709; Flavyrid_cyt_redctse.

DR InterPro: IPR001433; Oxidored_FAD.

DR Pfam: PF00970; Cyt_reductase.1.

DR Pfam: PF00173; heme_1.1.

DR Pfam: PF00175; oxidored_fad.1.

DR PRINTS: PR00363; CYTOCHROME5.

DR PRINTS: PR00371; FPNCR.

DR PRINTS: PR00406; CYTB5RDPASE.

DR PRINTS: PR00407; EUMOPTERIN.

DR PROSITE: PS00191; CYTOCHROME_B5_1.1.

DR PROSITE: PS00255; CYTOCHROME_B5_2.1.

DR PROSITE: PS00559; MOLYBDOPTERIN_EUK.1.

KW Oxidoreductase; Flavoprotein; FAD; NAD; Heme; Molybdenum;
 KW Nitrate assimilation; Multigene family.

FT METAL 187 187

FT METAL 241 241

FT DISULFID 426 426

FT BINDING 570 570

FT BINDING 593 593

SEQUENCE 909 AA; 102376 MW; 502C706FE6E3E706 CRC64;

Query Match 46.9%; Score 38; DB 1; Length 909;
 Best Local Similarity 33.3%; Pred. No. 65;

Matches 5; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Oy 1 WVEAENALGKVTSDH 15

Db 100 WIERNNSMITRLCKH 114

Search completed: December 19, 2001, 16:26:19
Job time: 574 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: December 19, 2001, 16:25:26 ; Search time 157.32 seconds
(without alignments)
13.947 Million cell updates/sec

Title: US-09-202-104A-9
Perfect score: 81
Sequence: 1 WVEAENALGKVTSDH 15

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: SPREMBL_17.*
2: sp_archaea:*
3: sp_bacteria:*
4: sp_fungi:*
5: sp_human:*
6: sp_invertebrate:*
7: sp_mammal:*
8: sp_mhc:*
9: sp_organelle:*
10: sp_phage:*
11: sp_plant:*
12: sp_rodent:*
13: sp_virus:*
14: sp_vertebrate:*
14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	81	100.0	329	4	Q9U041
2	65	80.2	918	13	Q9W609
3	47	58.0	422	4	Q75462
4	47	58.0	422	4	Q9U0H5
5	47	58.0	425	11	Q9JM58
6	44	54.3	1066	5	Q9VXL6
7	43	53.1	538	13	Q9DPU0
8	43	53.1	665	5	Q16793
9	42	51.9	642	2	Q9UTK7
10	42	51.9	642	2	Q9UTK6
11	41	50.6	148	1	Q59138
12	41	50.6	264	6	Q28109
13	41	50.6	536	5	Q20828
14	41	50.6	1032	5	Q05645
15	40	49.4	146	1	Q9V0U4
16	40	49.4	255	2	Q9E030
17	40	49.4	280	12	Q89642
18	40	49.4	552	5	Q96579
19	40	49.4	615	2	Q9ZB96

20	39.5	48.8	686	2	Q9RR17	Q9RR17 deinooccus
21	39	48.1	161	2	Q9DXL7	Q9DXL7 vibrio chol
22	39	48.1	235	12	Q9DXE1	Q9DXE1 cucurbit ye
23	39	48.1	235	12	Q9DXE0	Q9DXE0 cucurbit ye
24	39	48.1	235	12	Q9DXD9	Q9DXD9 cucurbit ye
25	39	48.1	235	12	Q9DXD8	Q9DXD8 cucurbit ye
26	39	48.1	235	12	Q9DXD7	Q9DXD7 cucurbit ye
27	39	48.1	235	12	Q9DXD6	Q9DXD6 cucurbit ye
28	39	48.1	235	12	Q9DXD5	Q9DXD5 cucurbit ye
29	39	48.1	235	12	Q9DXD4	Q9DXD4 cucurbit ye
30	39	48.1	235	12	Q9DXD3	Q9DXD3 cucurbit ye
31	39	48.1	235	12	Q9DXD2	Q9DXD2 cucurbit ye
32	39	48.1	235	12	Q9DXD1	Q9DXD1 cucurbit ye
33	39	48.1	235	12	Q9DXD0	Q9DXD0 cucurbit ye
34	39	48.1	235	12	Q9DXC9	Q9DXC9 cucurbit ye
35	39	48.1	235	12	Q9DXC8	Q9DXC8 cucurbit ye
36	39	48.1	235	12	Q9DXC7	Q9DXC7 cucurbit ye
37	39	48.1	235	12	Q9DXC6	Q9DXC6 cucurbit ye
38	39	48.1	235	12	Q9DXC5	Q9DXC5 cucurbit ye
39	39	48.1	235	12	Q9DXC4	Q9DXC4 cucurbit ye
40	39	48.1	235	12	Q9DXC3	Q9DXC3 cucurbit ye
41	39	48.1	235	12	Q9DXC2	Q9DXC2 cucurbit ye
42	39	48.1	235	12	Q9DXC1	Q9DXC1 cucurbit ye
43	39	48.1	235	12	Q9DXC0	Q9DXC0 cucurbit ye
44	39	48.1	235	12	Q9DXB9	Q9DXB9 cucurbit ye
45	39	48.1	235	12	Q9DXB8	Q9DXB8 cucurbit ye

ALIGNMENTS

RESULT	ID	Q9U041	PRELIMINARY;	PRT;	329 AA.
AC	Q9U041	01-MAY-2000 (TREMBLrel. 13, Created)			
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)				
DT	01-JUN-2001 (TREMBLrel. 17, Last annotation update)				
DE	GP130 OF THE RHEUMATOID ARTHRITIS ANTIGENIC PEPTIDE-BEARING SOLUBLE FORM (GP130-RAPS).				
GN	GP130.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=SYNOVIUM;				
RA	Tanaka M., Kishimura M., Ozaki S., Hashimoto H., Osakada F., Okubo M., Murakami M., Nakao K.,				
RT	*Cloning of novel soluble gp130 and detection of its neutralizing autoantibodies in rheumatoid arthritis.*;				
RL	Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.				
DR	EMBL; AB015706; BAA78112.1; -				
DR	HSSP; P40189; 1BOU.				
DR	InterPro; IPR002996; CRLA.				
DR	InterPro; IPR003962; FN1L-repeat.				
DR	InterPro; IPR003961; FN_III.				
DR	Pfam; PF00041; fn3; 1.				
DR	PRINTS; PRO0014; FNTYPEP11.				
DR	SMART; SM00060; FN3; 1.				
KW	Repeat.				
SQ	SEQUENCE	329 AA;	37484 MW;	D9776576B34FC596 CRC64;	

Query Match 100.0%; Score 81; DB 4; Length 329;
Best local Similarity 100.0%; Pred. No. 3e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WVEAENALGKVTSDH 15
DB 197 WVEAENALGKVTSDH 211

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RESULT 2
ID 09W609 PRELIMINARY; PRT; 918 AA.
AC 09W609;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE GLYCOPROTEIN 130 PRECURSOR.
GN GP130.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_Taxid=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-EMBRYONIC HEART PRIMARY CULTURE (E7, E8);
RX MEDLINE-99026068; PubMed-9806927;
RA Geissen M., Heller S., Pennica D., Ernberger U., Rohrer H.;
RT "The specification of sympathetic neurotransmitter phenotype depends
RT on gp130 cytokine receptor signaling."
RL Development 125:4791-4801(1998).
DR EMBL: A0111688; CAB42084.1; -.
DR HSSP: P40189; IBOU.
DR InterPro: IPR002996; CRIA.
DR InterPro: IPR003961; FN_III.
DR InterPro: IPR003529; Hematopo_receptor_L_F2.
DR Pfam: PF00041; fn3; 4.
DR SMART: SM00060; FN3; 3.
DR POSITIVE; PS01353; HEMATOPO_REC_L_F2; UNKNOWN_1.
KM Signal.
KW SIGNAL.
SQ SEQUENCE 918 AA; 102495 MW; FE7625FF3E3613EF CRC64;

Query Match 80.2%; Score 65; DB 13; Length 918;
Best Local Similarity 80.0%; Pred. No. 0.0067;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 WVEAENALGKVTSDH 15
Db 202 WVEAENALGKVESDH 216

RESULT 3
ID 075462 PRELIMINARY; PRT; 422 AA.
AC 075462;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE CYTOKINE-LIKE FACTOR-1 PRECURSOR.
GN CLF-1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Elson G.C.A., Grader P., Losberger P., Herren S., Gretener D.,
RA Menoud L.N., Wells T.N.C., Kosco-Vilbois M.H., Gauchat J.F.;
RT "Clf-1, a Novel Soluble Protein Shares Homology With Members of the
RT Cytokine Type-I Receptor Family."
RL J. Immunol. 0:0-0(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Magrangaes F., Jacques Y., Minvielle S.;
RT "Cloning and expression of a novel soluble protein containing
RT hematopoietic cytokine receptor domains."
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF059293; AAC28335.1; -.
DR EMBL: AF073515; AAD39681.1; -.

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DR HSSP: P40189; IBOU.
DR InterPro: IPR002996; CRIA.
DR InterPro: IPR003961; FN_III.
DR Pfam: PF00041; fn3; 2.
DR SMART: SM00060; FN3; 2.
KM Signal; Receptor.
FT SIGNAL
FT CHAIN 38 422 CYTOKINE-LIKE FACTOR-1
FT SEQUENCE 422 AA; 46301 MW; AD9DFCB01B84228 CRC64;

Query Match 58.0%; Score 47; DB 4; Length 422;
Best Local Similarity 64.3%; Pred. No. 4.4;
Matches 9; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 WVEAENALGKVTSD 14
Db 210 WVEATNRLGSARSD 223

RESULT 4
ID 09UHH5 PRELIMINARY; PRT; 422 AA.
AC 09UHH5;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE CLASS I CYTOKINE RECEPTOR.
GN ZCYTOR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Lok S., Presnell S.R., Jelmberg A.C., Gilbert T., Whitmore T.E.,
RA Foster D.C., Adams R.L., Lehner J.M., O'Hara P.J.;
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF178684; AAD34385.1; -.
DR HSSP: P40189; IBOU.
DR InterPro: IPR002996; CRIA.
DR InterPro: IPR003961; FN_III.
DR Pfam: PF00041; fn3; 2.
DR SMART: SM00060; FN3; 2.
KM Receptor.
KW RECEPTOR.
SQ SEQUENCE 422 AA; 46315 MW; 0D2C5F7A01B942EE CRC64;

Query Match 58.0%; Score 47; DB 4; Length 422;
Best Local Similarity 64.3%; Pred. No. 4.4;
Matches 9; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 WVEAENALGKVTSD 14
Db 210 WVEATNRLGSARSD 223

RESULT 5
ID 09JMS8 PRELIMINARY; PRT; 425 AA.
AC 09JMS8;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE CYTOKINE RECEPTOR LIKE MOLECULE 3 PRECURSOR.
GN CRFL1 OR CRIM3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathii; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Hitoiyama T., Iwama A., Nakamura Y., Nakauchi H.;

```

RT *cytokine receptor like molecule 3.*;
 RL Submitted (MAR-2000) to the EMBL/Genbank/DBJ databases.
 RA EMBL: AB040038; BAA92777.1; -
 DR MGD: MGI:1340030; Crfl1.
 DR InterPro: IPR002996; CR1A.
 DR InterPro: IPR003961; FN_III.
 DR Pfam: PF00041; fn3; 2.
 DR SMART: SM00060; FN3; 1.
 KW Signal; Receptor.
 FT SIGNAL 1 34 POTENTIAL.
 SQ SEQUENCE 425 AA; 46662 MW; 910535C629CA7056 CRC64;

Query Match 58.0%; Score 47; DB 11; Length 425;
 Best Local Similarity 64.3%; Pred. No. 4.5;
 Matches 9; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 WVEANALGKVTSD 14
 DB 213 WVEATNRIGSARSD 226

RESULT 6
 ID Q9VXL6 PRELIMINARY; PRT; 1066 AA.
 AC Q9VXL6:
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE CG9126 PROTEIN.
 GN RANBP16 OR CG9126.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Ceiniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Adamatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Mortan J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Milos G.L.G.,
 RA Abiri J.F., Agbayani A., An H.-J., Andrews-Pfankoch C., Baldwin D.,
 RA Balles R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borova D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,
 RA Burtis K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos R., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck C.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.F., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Laslo P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Modarity C., Morris J., Mostrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muniz D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazozo M., Pitman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svitskas R., Tector R., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,

RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT *The genome sequence of Drosophila melanogaster.*;
 RL Science 287:2185-2195(2000).
 DR EMBL: AE003500; AAF48542.1; -
 DR Flybase: FBgn0030709; Rnbp16.
 DR InterPro: IPR001660; SAM.
 DR SMART: SM00454; SAM; 1.
 SQ SEQUENCE 1066 AA; 121171 MW; 6512FF71F132FF12 CRC64;

Query Match 54.3%; Score 44; DB 5; Length 1066;
 Best Local Similarity 69.2%; Pred. No. 4.3;
 Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 2 VEARNALGVTNE 14
 DB 476 VEARNALGVTNE 488

RESULT 7
 ID Q9DFU0 PRELIMINARY; PRT; 538 AA.
 AC Q9DFU0:
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE PROLACTIN RECEPTOR.
 OS Sparus aurata (Gilthead sea bream).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidae;
 OC Sparidae; Sparus.
 OX NCBI_TaxID=8175;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Santos C.R.A., Ingleton P.M., Cavaco J.E.B., Kelly P.A., Edery M.,
 RA Power D.M.;
 RT "Cloning, characterization and tissue distribution of prolactin
 RT receptor in the sea bream (Sparus aurata).";
 RL Submitted (APR-2000) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AF253527; AAG17629.1; -
 DR InterPro: IPR002996; CR1A.
 DR InterPro: IPR003961; FN_III.
 DR Pfam: PF00041; fn3; 2.
 DR SMART: SM00060; FN3; 2.
 KW Receptor.
 SQ SEQUENCE 538 AA; 60677 MW; D9EBCCFE4890E83 CRC64;

Query Match 53.1%; Score 43; DB 13; Length 538;
 Best Local Similarity 50.0%; Pred. No. 30;
 Matches 10; Conservative 1; Mismatches 3; Indels 6; Gaps 1;

OY 1 WVE-----AENALGKVTSD 14
 DB 93 WVDYITLVASNALGNATSD 112

RESULT 8
 ID O16793 PRELIMINARY; PRT; 666 AA.
 AC O16793:
 DT 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
 DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
 DE F18A12.7 PROTEIN.
 GN F18A12.7.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2.
 RX MEDLINE-94150718: PubMed-7906398;
 RA Wilson R., Almscough R., Anderson K., Baynes C., Barks M.,
 Bonfield J., Burton J., Connell M., Copesey T., Cooper J., Coulson A.,
 Craxton M., Dear S., Du Z., Durbin R., Favell A., Fulton L.,
 Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
 Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
 Lightning J., Lloyd C., Murray A., Mortimore B., O'Callaghan M.,
 Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Showkeen R.,
 Smaldon N., Smith A., Sonnenhammer E., Staden R., Sulston J.,
 Thierly-Mieg J., Thomas K., Vaadin M., Vaughan K., Waterston R.,
 Watson A., Welnsstock L., Wilkinson-Sproat J., Wohlman P.,
 RT *2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 RL elegans.*
 RN Nature 368:32-38(1994).
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2.
 RX Le T., Waterston R., Ozersky P.,
 RA Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF016688; AAB66073.1;
 SQ SEQUENCE 666 AA; 76112 MW; 73E1FA18F4C8BA10 CRC64;
 Query Match 53.1%; Score 43; DB 5; Length 666;
 Best Local Similarity 46.7%; Pred. No. 38;
 Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
 OY 1 WVEAENALGKVTSDH 15
 Db 264 WIEENSGDRTDDH 278
 ID Q9JTK7 PRELIMINARY; PRT; 642 AA.
 AC Q9JTK7;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE RNA POLYMERASE SIGMA FACTOR.
 GN NMB1538.
 OS Neisseria meningitidis (serogroup B).
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
 OX NCBI_TaxID=491;
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-MC58 / SEROGROUP B;
 RX MEDLINE-20175755; PubMed-10710307;
 RA Tetteijn H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E.,
 Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J.,
 Nelson W.C., Gwinn M.L., Deboy R., Peterson J.D., Hickey E.K.,
 Hatt D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A.,
 Mason T., Clecko A., Parksey D.S., Blair E., Clifton H., Clark E.B.,
 Cotton M.D., utterback T.R., Khouri H., Qin H., Yamathayan J.,
 Gill J., Scarlato V., Maignani V., Pizsa M., Grandi G., Sun L.,
 Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.;
 RA *Complete genome sequence of Neisseria meningitidis serogroup B strain
 RT MC58.*
 RL Science 287:1809-1815(2000).
 CC -1- FUNCTION: THE SIGMA FACTOR IS AN INITIATION FACTOR THAT PROMOTES
 ATTACHMENT OF THE RNA POLYMERASE TO SPECIFIC INITIATION SITES AND
 THEN IS RELEASED (BY SIMILARITY).
 CC -1- SIMILARITY: TO THE SIGMA-70 FACTOR FAMILY.
 CC EMBL: AE002503; AAF1893.1;
 CC TIGR: NMB1538;
 DR InterPro: IPR000943; Sigma_70.
 DR Pfam: PF00140; sigma70.1.
 DR PRINTS: PR00046; SIGMA70FCT.1.
 DR PROSITE: PS00715; SIGMA70_1; 1.
 DR PROSITE: PS00716; SIGMA70_2; 1.

KW Complete proteome: DNA-binding; DNA-directed RNA polymerase;
 KW Sigma factor; Transcription regulation;
 SQ SEQUENCE 642 AA; 73831 MW; 113BFF516B894039 CRC64;
 Query Match 51.9%; Score 42; DB 2; Length 642;
 Best Local Similarity 57.1%; Pred. No. 55;
 Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 OY 1 WVEAENALGKVTSD 14
 Db 339 WIEEIAKGRVSD 352
 ID Q9JTK6 PRELIMINARY; PRT; 642 AA.
 AC Q9JTK6;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE RNA POLYMERASE SIGMA FACTOR.
 GN RPOD OR NMA1737.
 OS Neisseria meningitidis (serogroup A).
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
 OX NCBI_TaxID=65699;
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-22491 / SEROGROUP A / SEROTYPE 4A;
 RX MEDLINE-20222556; PubMed-10761919;
 RA Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.,
 Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
 Davies R.M., Davis P., Devlin K., Feltham T., Hamlin N., Holroyd S.,
 Jagsels K., Leather S., Moule S., Mungall K., Quail M.A.,
 RA Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
 RA Whitehead S., Spratt B.G., Barrall B.G.;
 RT *Complete DNA sequence of a serogroup A strain of Neisseria
 RL meningitidis 22491.*
 RL Nature 404:502-506(2000).
 CC -1- FUNCTION: THE SIGMA FACTOR IS AN INITIATION FACTOR THAT PROMOTES
 ATTACHMENT OF THE RNA POLYMERASE TO SPECIFIC INITIATION SITES AND
 THEN IS RELEASED (BY SIMILARITY).
 CC -1- SIMILARITY: TO THE SIGMA-70 FACTOR FAMILY.
 CC EMBL: AL162757; CAB84965.1;
 DR InterPro: IPR000943; Sigma_70.
 DR Pfam: PF00140; sigma70.1.
 DR PRINTS: PR00046; SIGMA70FCT.1.
 DR PROSITE: PS00715; SIGMA70_1; 1.
 DR PROSITE: PS00716; SIGMA70_2; 1.
 KW Complete proteome: DNA-binding; DNA-directed RNA polymerase;
 KW Sigma factor; Transcription regulation;
 SQ SEQUENCE 642 AA; 73787 MW; 7796E947FC057458 CRC64;
 Query Match 51.9%; Score 42; DB 2; Length 642;
 Best Local Similarity 57.1%; Pred. No. 55;
 Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 OY 1 WVEAENALGKVTSD 14
 Db 339 WIEEIAKGRVSD 352
 ID Q59138 PRELIMINARY; PRT; 148 AA.
 AC Q59138;
 DT 01-AUG-1998 (TREMBlrel. 07, Created)
 DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
 DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
 DE HYPOTHETICAL 16.7 KDA PROTEIN PH1469.
 GN PH1469.
 OS Pyrococcus horikoshii.


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OC Archaea; Euryarchaeota; Thermococcales; Thermococcaceae; Pyrococcus.
OX NCBI_TaxID=53953;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OT3;
RX MEDLINE=98344137; PubMed=9679194;
RA Kawarabayashi Y., Sawada M., Horikawa H., Hino Y.,
RA Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Horoyama A., Nagai Y.,
RA Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,
RA Fuhashi T., Tanaka T., Kudo Y., Yamazaki J., Kushiida N., Oguchi A.,
RA Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
RA Masuchi Y., Shizuya H., Kikuchi H.;
RT *Complete sequence and gene organization of the genome of a hyper-
RT thermophilic archaeobacterium, Pyrococcus horikoshii OT3.;
RL DNA Res. 5:55-76(1998);
DR EMBL; AF000006; BAA30576.1;
KW Hypothetical protein: Complete proteome;
SQ SEQUENCE 148 AA; 16690 MW; 7CF5DB328D1B7C1E CRC64;

Query Match 50.6%; Score 41; DB 1; Length 148;
Best Local Similarity 42.9%; Pred. No. 16;
Matches 6; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

OY 1 WYEAEENALGKVTSD 14
   ||| |::| |
DB 15 WYEGFGFGRIGSD 28

RESULT 12
O28109 PRELIMINARY; PRT; 264 AA.
AC O28109;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE FC GAMMA 2 RECEPTOR.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95363119; PubMed=7636215;
RA Zhang G.P., Young J.R., Tregaskes C.A., Sopp P., Howard C.J.;
RT *Identification of a novel class of mammalian Fc gamma receptor.;
RL J. Immunol. 155:1534-1541(1995).
CC -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL; Z37506; CAA85736.1;
DR HSRP; P43626; INKR.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003600; Ig_1like.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig_2.
DR SMART; SM00409; Ig_1.
DR SMART; SM00410; Ig_1like; 1.
FT CHAIN 20
FT 264
SQ SEQUENCE 264 AA; 28693 MW; A8BC251A69782B7C CRC64;

Query Match 50.6%; Score 41; DB 6; Length 264;
Best Local Similarity 53.3%; Pred. No. 30;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

OY 1 WYEAEENALGKVTSD 15
   ||| |::| |
DB 181 WYQAFSLSPVSAH 195

RESULT 13
O20828

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ID O20828 PRELIMINARY; PRT; 536 AA.
AC O20828;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE COSMID F55D10.
GN F55D10.5.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Pelodietinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94150718; PubMed=7906398;
RA Wilson R., Alnsough R., Anderson K., Baynes C., Berks M.,
RA Bonfield J., Burton J., Connell M., Copey T., Cooper J., Coulson A.,
RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Rifkin L., Roopra A., Saunders D., Showkneen R.,
RA Smaiden N., Smith A., Sonnenhammer B., Staden R., Sulston J.,
RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
RA Watson A., Weinstock L., Wilkinson-Sproat J., Wohlman P.;
RT *2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans.;
RL Nature 368:32-38(1994).
RN [2]
RP SEQUENCE FROM N.A.
RA Leimbach D.;
RL Submitted (NOV-1995) to the EMBL/Genbank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Waterston R.;
RL Submitted (NOV-1995) to the EMBL/Genbank/DBJ databases.
DR EMBL; U40948; AAA81730.1;
DR InterPro; IPR001175; Neur_channel.
DR Pfam; PF00065; neur_chan; 3.
DR PROSITE; PS00236; NEURORR_ION_CHANNEL; UNKNOWN_1.
SQ SEQUENCE 536 AA; 61299 MW; 1F0686B867FBAAZE CRC64;

Query Match 50.6%; Score 41; DB 5; Length 536;
Best Local Similarity 42.9%; Pred. No. 68;
Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

OY 1 WYEAEENALGKVTSD 14
   ||| |::| |
DB 97 WYQEVNSVNEITS 110

RESULT 14
O05645 PRELIMINARY; PRT; 1032 AA.
AC O05645;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE MAJOR TEGUMENTAL ANTIGEN SM15 PRECURSOR (SM15).
GN GSM70.
OS Schistosoma mansoni (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Rhabditophora; Neodermata;
OC Trematoda; Digenea; Strigoidae; Schistosomatidae; Schistosomatidae;
OC Schistosoma.
OX NCBI_TaxID=6183;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PUERTO RICAN;
RX MEDLINE=93376023; PubMed=8366897;
RA Abach F.G., Hagan P., Holder A.A., Simpson A.J.;
RT *Structure of the gene encoding a putative Schistosoma mansoni
RL Mol. Biochem. Parasitol. 60:81-91(1993).

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: December 19, 2001, 16:21:02 ; Search time 78.52 Seconds
(without alignments)
4.299 Million cell updates/sec

Title: US-09-202-104A-9

Sequence: 1 WVEAENALGKVTSDH 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

- Issued Patents_AA:*
- 1: /cgcn2_6/ptodata/2/1aa/5A.COMB.pep:*
 - 2: /cgcn2_6/ptodata/2/1aa/5B.COMB.pep:*
 - 3: /cgcn2_6/ptodata/2/1aa/6A.COMB.pep:*
 - 4: /cgcn2_6/ptodata/2/1aa/6B.COMB.pep:*
 - 5: /cgcn2_6/ptodata/2/1aa/PTC05.COMB.pep:*
 - 6: /cgcn2_6/ptodata/2/1aa/Backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	81	100.0	488	2	US-08-599-455B-5
2	81	100.0	488	4	US-09-069-781B-5
3	81	100.0	572	2	US-08-419-652-5
4	81	100.0	658	2	US-08-825-558-4
5	81	100.0	708	1	US-07-797-556-2
6	81	100.0	708	1	US-08-308-881-2
7	81	100.0	708	2	US-09-058-263-2
8	81	100.0	708	2	US-09-059-099-2
9	81	100.0	708	3	US-09-058-264-2
10	81	100.0	708	5	PTC-US95-06530-2
11	81	100.0	918	2	US-08-825-558-6
12	47	58.0	303	4	US-09-071-224-21
13	47	58.0	303	4	US-09-071-224-23
14	47	58.0	385	4	US-09-071-224-19
15	47	58.0	385	4	US-09-071-224-20
16	47	58.0	388	4	US-09-071-224-17
17	47	58.0	389	4	US-09-071-224-22
18	47	58.0	389	4	US-09-071-224-24
19	47	58.0	389	4	US-09-071-224-25
20	47	58.0	389	4	US-09-071-224-26
21	47	58.0	389	4	US-09-071-224-28
22	47	58.0	389	4	US-09-071-224-29
23	47	58.0	389	4	US-09-071-224-30
24	47	58.0	389	4	US-09-071-224-31
25	47	58.0	392	4	US-09-071-224-18
26	47	58.0	405	3	US-09-012-072-2
27	47	58.0	405	4	US-09-120-601-2

28	47	58.0	422	4	US-09-071-224-2	Sequence 2, Appl1
29	47	58.0	425	4	US-09-071-224-4	Sequence 4, Appl1
30	47	58.0	425	4	US-09-071-224-6	Sequence 6, Appl1
31	47	58.0	434	3	US-09-012-072-4	Sequence 4, Appl1
32	47	58.0	434	4	US-09-120-601-4	Sequence 4, Appl1
33	47	58.0	448	4	US-09-120-601-6	Sequence 6, Appl1
34	46	56.8	602	2	US-08-419-652-6	Sequence 6, Appl1
35	46	56.8	771	1	US-07-923-976-6	Sequence 6, Appl1
36	46	56.8	783	6	5422248-2	Patent No. 5422248
37	46	56.8	836	1	US-07-923-976-4	Sequence 4, Appl1
38	46	56.8	863	1	US-07-923-976-8	Sequence 8, Appl1
39	45	55.6	389	4	US-09-071-224-27	Sequence 27, Appl1
40	44.5	54.9	151	2	US-08-815-175-1	Sequence 1, Appl1
41	42	51.9	837	1	US-07-923-976-2	Sequence 2, Appl1
42	40	49.4	1462	3	US-07-792-600-31	Sequence 31, Appl1
43	40	49.4	1462	3	US-09-157-021-31	Sequence 31, Appl1
44	40	49.4	1462	3	US-09-156-842-31	Sequence 31, Appl1
45	36	44.4	35	4	US-08-810-009-19	Sequence 19, Appl1

ALIGNMENTS

RESULT 1
US-08-599-455B-5
Sequence 5, Application US/08599455B
Patent No. 5972621
GENERAL INFORMATION:
APPLICANT: Tartaglia, Louis A.
APPLICANT: Tepper, Robert I.
TITLE OF INVENTION: METHODS OF IDENTIFYING COMPOUNDS THAT
MODULATE BODY WEIGHT USING THE OB RECEPTOR
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/599,455B
FILING DATE: 22-JAN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/583,153
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: 08/570,142
FILING DATE: 11-DEC-1995
APPLICATION NUMBER: 08/569,485
FILING DATE: 08-DEC-1995
APPLICATION NUMBER: 08/566,622
FILING DATE: 04-DEC-1995
APPLICATION NUMBER: 08/562,663
FILING DATE: 27-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: Melkielejohn, Ph.D., Anita L.
REGISTRATION NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 07334/017001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 488 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: protein
US-08-599-455B-5

Query Match 100.0%; Score 81; DB 2; Length 488;
Best Local Similarity 100.0%; Pred. No. 9.9e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WVEAENALGKVTSDH 15
|||||
DB 168 WVEAENALGKVTSDH 182

RESULT 2
US-09-069-781B-5
; Sequence 5, Application US/09069781B
; Patent No. 6287782
; GENERAL INFORMATION:
; APPLICANT: Tataqila, Louis A.
; APPLICANT: Tepper, Robert I.
; APPLICANT: Culpepper, Janice A.
; APPLICANT: White, David W.
; TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR
; TITLE OF INVENTION: THE DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS,
; TITLE OF INVENTION: INCLUDING OBESITY AND CACHEXIA
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: Windows95
; SOFTWARE: FASTED for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/069,781B
; FILING DATE: 29-APRIL-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/864,564
; FILING DATE: 28-MAY-1997
; APPLICATION NUMBER: US 08/708,123
; FILING DATE: 03-SEP-1996
; APPLICATION NUMBER: US 08/638,524
; FILING DATE: 26-APR-1996
; APPLICATION NUMBER: US 08/599,455
; FILING DATE: 22-JAN-1996
; APPLICATION NUMBER: US 08/583,153
; FILING DATE: 28-DEC-1995
; APPLICATION NUMBER: US 08/570,142
; FILING DATE: 11-DEC-1995
; APPLICATION NUMBER: US 08/569,485
; FILING DATE: 08-DEC-1995
; APPLICATION NUMBER: US 08/566,622
; FILING DATE: 04-DEC-1995
; APPLICATION NUMBER: US 08/562,663
; FILING DATE: 27-NOV-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Melkiesohn, P.D., Anita L.
; REGISTRATION NUMBER: 35,283
; REFERENCE/DOCKET NUMBER: 07334/082001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELER: 200154
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 488 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown

MOLECULE TYPE: protein
US-09-069-781B-5

Query Match 100.0%; Score 81; DB 4; Length 488;
Best Local Similarity 100.0%; Pred. No. 9.9e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WVEAENALGKVTSDH 15
|||||
DB 168 WVEAENALGKVTSDH 182

RESULT 3
US-08-419-652-5
; Sequence 5, Application US/08419652
; Patent No. 5831007
; GENERAL INFORMATION:
; APPLICANT: Chua, Anne O
; APPLICANT: Gubler, Ulrich A
; TITLE OF INVENTION: INTERLEUKIN-12 RECEPTOR
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: New Jersey
; COUNTRY: United States of America
; ZIP: 07110-1199
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: PC compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/419,652
; FILING DATE: 11-APR-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/248,532
; FILING DATE: 31-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/094,713
; FILING DATE: 19-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Kass, Alan P
; REGISTRATION NUMBER: 32142
; REFERENCE/DOCKET NUMBER: CD 9174
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (201) 235-4205
; TELEFAX: (201) 235-3500
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 572 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Region
; LOCATION: 1..572
; OTHER INFORMATION:
; OTHER INFORMATION: 742 of human gp130."
US-08-419-652-5

Query Match 100.0%; Score 81; DB 2; Length 572;
Best Local Similarity 100.0%; Pred. No. 1.2e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WVEAENALGKVTSDH 15
|||||
DB 74 WVEAENALGKVTSDH 88

RESULT 4
US-08-825-558-4
; Sequence 4, Application US/08825558
; Patent No. 5965724
; GENERAL INFORMATION:
; APPLICANT: SHARKEY, ANDREW
; APPLICANT: SMITH, STEPHEN K.
; APPLICANT: DELLOW, KIMBERLEY A.
; TITLE OF INVENTION: Gp 130 Lacking the Transmembrane Domain
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX
; STREET: 1100 NEW YORK AVENUE
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/825,558
; FILING DATE: 19-MAR-1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: ESMOND, ROBERT W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 0623.0530001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)371-2600
; TELEFAX: (202)371-2540
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 658 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-825-558-4

Query Match 100.0%; Score 81; DB 2; Length 658;
Best Local Similarity 100.0%; Pred. No. 1.4e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WVEAENALGKVTSDH 15
DB 197 WVEAENALGKVTSDH 211

RESULT 5
US-07-797-556-2
; Sequence 2, Application US/07797556
; Patent No. 5262522
; GENERAL INFORMATION:
; APPLICANT: Gearing, David P.
; TITLE OF INVENTION: Receptor for Oncostatin M and Leukemia
; TITLE OF INVENTION: Inhibitory Factor
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/797,556
; FILING DATE: 19911122
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Seese, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2607
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-587-0430
; TELEFAX: 206-587-0606
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 708 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-797-556-2

Query Match 100.0%; Score 81; DB 1; Length 708;
Best Local Similarity 100.0%; Pred. No. 1.5e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WVEAENALGKVTSDH 15
DB 197 WVEAENALGKVTSDH 211

RESULT 6
US-08-308-881-2
; Sequence 2, Application US/08308881
; Patent No. 5783672
; GENERAL INFORMATION:
; APPLICANT: Mosley, Bruce
; APPLICANT: Cosman, David J.
; TITLE OF INVENTION: Receptor for Oncostatin M
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: Apple Macintosh
; SOFTWARE: Microsoft Word, Version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/308,881
; FILING DATE: 12-SEP-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/249,553
; FILING DATE: 26-MAY-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Seese, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2614-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 708 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-308-881-2

Query Match 100.0%; Score 81; DB 1; Length 708;
Best Local Similarity 100.0%; Pred. No. 1.5e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WVEAENALGKVTSDH 15
Db 197 WVEAENALGKVTSDH 211

RESULT 7

US-09-058-263-2
; Sequence 2, Application US/09058263
; Patent No. 5891997
; GENERAL INFORMATION:
; APPLICANT: Mosley, Bruce
; APPLICANT: Cosman, David J.
; TITLE OF INVENTION: Receptor for Oncostatin M
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple 7.1
; SOFTWARE: Microsoft Word, Version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/058,263
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/308,881
; FILING DATE: 12-SEP-1994
; APPLICATION NUMBER: US 08/249,553
; FILING DATE: 26-MAY-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Seese, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2614-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; TELEX: 756822
; INFORMATION FOR SEQ. ID NO.: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 708 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-058-263-2

Query Match 100.0%; Score 81; DB 2; Length 708;
Best Local Similarity 100.0%; Pred. No. 1.5e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WVEAENALGKVTSDH 15
Db 197 WVEAENALGKVTSDH 211

RESULT 8

US-09-059-099-2
; Sequence 2, Application US/09059099
; Patent No. 5925740
; GENERAL INFORMATION:
; APPLICANT: Mosley, Bruce
; APPLICANT: Cosman, David J.

; TITLE OF INVENTION: Receptor for Oncostatin M
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple 7.1
; SOFTWARE: Microsoft Word, Version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/059,099
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/308,881
; FILING DATE: 12-SEP-1994
; APPLICATION NUMBER: US 08/249,553
; FILING DATE: 26-MAY-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Seese, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2614-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; TELEX: 756822
; INFORMATION FOR SEQ. ID NO.: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 708 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-059-099-2

Query Match 100.0%; Score 81; DB 2; Length 708;
Best Local Similarity 100.0%; Pred. No. 1.5e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WVEAENALGKVTSDH 15
Db 197 WVEAENALGKVTSDH 211

RESULT 9

US-09-058-264-2
; Sequence 2, Application US/09058264
; Patent No. 6010886
; GENERAL INFORMATION:
; APPLICANT: Mosley, Bruce
; APPLICANT: Cosman, David J.
; TITLE OF INVENTION: Receptor for Oncostatin M
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple 7.1
; SOFTWARE: Microsoft Word, Version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/058,264
; FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/308,881
FILING DATE: 12-SEP-1994
APPLICATION NUMBER: US 08/249,553
FILING DATE: 26-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Seese, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2614-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 708 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-058-264-2

Query Match 100.0%; Score 81; DB 3; Length 708;
Best Local Similarity 100.0%; Pred. No. 1.5e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WVEAENALGKVTSDH 15
|||||
DB 197 WVEAENALGKVTSDH 211

RESULT 10
PCT-US95-06530-2
Sequence 2, Application PC/TUS9506530
GENERAL INFORMATION:
APPLICANT: Mosley, Bruce
APPLICANT: Cosman, David J.
TITLE OF INVENTION: Receptor for Oncostatin M
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/06530
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/308,881
FILING DATE: 09-SEP-1994
APPLICATION NUMBER: US 08/249,553
FILING DATE: 26-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Anderson, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2614-MO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 708 amino acids
TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-06530-2

Query Match 100.0%; Score 81; DB 5; Length 708;
Best Local Similarity 100.0%; Pred. No. 1.5e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WVEAENALGKVTSDH 15
|||||
DB 197 WVEAENALGKVTSDH 211

RESULT 11
US-08-825-558-6
Sequence 6, Application US/08825558
Patent No. 5965724
GENERAL INFORMATION:
APPLICANT: SHARKEY, ANDREW
APPLICANT: SMITH, STEPHEN K.
APPLICANT: DELLOW, KIMBERLEY A.
TITLE OF INVENTION: Gp 130 Lacking the Transmembrane Domain
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX
STREET: 1100 NEW YORK AVENUE
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/825,558
FILING DATE: 19-MAR-1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: ESMOND, ROBERT W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 0623.0530001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)371-2540
TELEFAX: (202)371-2540
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 918 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-825-558-6

Query Match 100.0%; Score 81; DB 2; Length 918;
Best Local Similarity 100.0%; Pred. No. 2e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WVEAENALGKVTSDH 15
|||||
DB 197 WVEAENALGKVTSDH 211

RESULT 12
US-09-071-224-21
Sequence 21, Application US/09071224
Patent No. 6271343
GENERAL INFORMATION:
APPLICANT: Lok, Si
APPLICANT: Presnell, Scott R.
APPLICANT: Jelmberg, Anna C.

APPLICANT: Gilbert, Teresa
APPLICANT: Foster, Donald C.
APPLICANT: Adams, Robyn L.
APPLICANT: Lehner, Joyce M.
TITLE OF INVENTION: MAMMALIAN ZCYTORS
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Zymogenetics
STREET: 1201 Eastlake Ave East
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98102
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071,224
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Lunn, Paul G
REGISTRATION NUMBER: 32,743
REFERENCE/DOCKET NUMBER: 96-22
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6627
TELEFAX: 206-442-6678
TELEX:
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 303 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-071-224-21

Query Match 58.0%; Score 47; DB 4; Length 303;
Best Local Similarity 64.3%; Pred. No. 0.74;
Matches 9; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 WVEAENALGKVTSD 14
DB 173 WVEATNRLGSARSD 186

RESULT 13
US-09-071-224-23
Sequence 23, Application US/09071224
Patent No. 6271343
GENERAL INFORMATION:
APPLICANT: Lok, Si
APPLICANT: Presnell, Scott R.
APPLICANT: Jelmeberg, Anna C.
APPLICANT: Gilbert, Teresa
APPLICANT: Foster, Donald C.
APPLICANT: Adams, Robyn L.
APPLICANT: Lehner, Joyce M.
TITLE OF INVENTION: MAMMALIAN ZCYTORS
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Zymogenetics
STREET: 1201 Eastlake Ave East
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98102

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071,224
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Lunn, Paul G
REGISTRATION NUMBER: 32,743
REFERENCE/DOCKET NUMBER: 96-22
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6627
TELEFAX: 206-442-6678
TELEX:
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 303 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-071-224-23

Query Match 58.0%; Score 47; DB 4; Length 303;
Best Local Similarity 64.3%; Pred. No. 0.74;
Matches 9; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 WVEAENALGKVTSD 14
DB 173 WVEATNRLGSARSD 186

RESULT 14
US-09-071-224-19
Sequence 19, Application US/09071224
Patent No. 6271343
GENERAL INFORMATION:
APPLICANT: Lok, Si
APPLICANT: Presnell, Scott R.
APPLICANT: Jelmeberg, Anna C.
APPLICANT: Gilbert, Teresa
APPLICANT: Foster, Donald C.
APPLICANT: Adams, Robyn L.
APPLICANT: Lehner, Joyce M.
TITLE OF INVENTION: MAMMALIAN ZCYTORS
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Zymogenetics
STREET: 1201 Eastlake Ave East
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98102
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071,224
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:

NAME: Lunn, Paul G
REGISTRATION NUMBER: 32,743
REFERENCE/DOCKET NUMBER: 96-22
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6627
TELEFAX: 206-442-6678
TELEX:
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 385 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-071-224-19

Query Match 58.0%; Score 47; DB 4; Length 385;
Best local Similarity 64.3%; Pred. No. 0.96;
Matches 9; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 WVEAENALGKVTSD 14
||| | | |
Db 173 WEATNRLGARSAD 186

RESULT 15

US-09-071-224-20
Sequence 20, Application US/09071224
Patent No. 6271343
GENERAL INFORMATION:
APPLICANT: Lok, SI
APPLICANT: Presnell, Scott R.
APPLICANT: Jelmberg, Anna C.
APPLICANT: Gilbert, Teresa
APPLICANT: Foster, Donald C.
APPLICANT: Adams, Robyn L.
APPLICANT: Lehner, Joyce M.
TITLE OF INVENTION: MAMMALIAN ZCYTORS
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: ZymoGenetics
STREET: 1201 Eastlake Ave East
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98102
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071,224
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Lunn, Paul G
REGISTRATION NUMBER: 32,743
REFERENCE/DOCKET NUMBER: 96-22
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6627
TELEFAX: 206-442-6678
TELEX:
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 385 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: protein
US-09-071-224-20

Query Match 58.0%; Score 47; DB 4; Length 385;
Best local Similarity 64.3%; Pred. No. 0.96;
Matches 9; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 WVEAENALGKVTSD 14
||| | | |
Db 173 WEATNRLGARSAD 186

Search completed: December 19, 2001, 16:21:02
Job time: 407 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 19, 2001, 16:19:36 ; Search time 170.68 seconds
(without alignments)
7.378 Million cell updates/sec

Title: US-09-202-104A-10

Perfect score: 95
Sequence: 1 PVYKVKPNPNNLSVIN 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: _Geneseq_1101.*
2: /SIDS8/gcgdata/geneseq/geneseqp/AA1980.DAT:*
3: /SIDS8/gcgdata/geneseq/geneseqp/AA1981.DAT:*
4: /SIDS8/gcgdata/geneseq/geneseqp/AA1982.DAT:*
5: /SIDS8/gcgdata/geneseq/geneseqp/AA1983.DAT:*
6: /SIDS8/gcgdata/geneseq/geneseqp/AA1984.DAT:*
7: /SIDS8/gcgdata/geneseq/geneseqp/AA1985.DAT:*
8: /SIDS8/gcgdata/geneseq/geneseqp/AA1987.DAT:*
9: /SIDS8/gcgdata/geneseq/geneseqp/AA1988.DAT:*
10: /SIDS8/gcgdata/geneseq/geneseqp/AA1989.DAT:*
11: /SIDS8/gcgdata/geneseq/geneseqp/AA1990.DAT:*
12: /SIDS8/gcgdata/geneseq/geneseqp/AA1991.DAT:*
13: /SIDS8/gcgdata/geneseq/geneseqp/AA1992.DAT:*
14: /SIDS8/gcgdata/geneseq/geneseqp/AA1993.DAT:*
15: /SIDS8/gcgdata/geneseq/geneseqp/AA1994.DAT:*
16: /SIDS8/gcgdata/geneseq/geneseqp/AA1995.DAT:*
17: /SIDS8/gcgdata/geneseq/geneseqp/AA1996.DAT:*
18: /SIDS8/gcgdata/geneseq/geneseqp/AA1997.DAT:*
19: /SIDS8/gcgdata/geneseq/geneseqp/AA1998.DAT:*
20: /SIDS8/gcgdata/geneseq/geneseqp/AA1999.DAT:*
21: /SIDS8/gcgdata/geneseq/geneseqp/AA2000.DAT:*
22: /SIDS8/gcgdata/geneseq/geneseqp/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	95	100.0	17	AAW52210	Interleukin-6 anta
2	95	100.0	24	AAB88838	Human Interleukin-
3	95	100.0	180	AAW00404	Interleukin-6 anta
4	95	100.0	329	AAW17859	Rheumatoid arthrit
5	95	100.0	332	AAW70799	Human gpi330-delta-
6	95	100.0	332	AAW92188	Human gpi330-delta-
7	95	100.0	638	AAW94576	Human gpi330 splice
8	95	100.0	708	AAW37804	Human gpi330 N-term
9	95	100.0	727	AAW85911	gpi330 N-terminal f
10	95	100.0	727	AAW92192	Human gpi330-kappa
11	95	100.0	738	AAW92194	Human gpi330-J-kapp

12	95	100.0	859	20	AAW70796
13	95	100.0	859	21	AAW92184
14	95	100.0	918	12	AAW10545
15	95	100.0	918	15	AAW46233
16	95	100.0	918	17	AAW75368
17	95	100.0	918	21	AAW44694
18	95	100.0	951	20	AAW70798
19	95	100.0	951	21	AAW92186
20	95	100.0	961	21	AAW92187
21	95	100.0	1158	21	AAW92205
22	95	100.0	1168	21	AAW92204
23	68	71.6	24	22	AAB88839
24	68	71.6	917	13	AAW26334
25	68	71.6	917	22	AAW55073
26	52	54.7	24	22	AAB88837
27	48.5	51.1	361	22	AAW81533
28	47	49.5	400	16	AAW71932
29	47	49.5	400	17	AAW92474
30	47	49.5	400	19	AAW56628
31	47	49.5	400	19	AAW47184
32	46	48.4	177	19	AAW58987
33	46	48.4	286	22	AAB90678
34	46	48.4	426	18	AAW09822
35	46	48.4	427	18	AAW24973
36	46	48.4	427	22	AAB19807
37	46	48.4	427	22	AAB19808
38	46	48.4	784	21	AAW92207
39	46	48.4	793	21	AAW92208
40	45	47.4	69	22	AAU14200
41	45	47.4	69	22	AAU1436
42	45	47.4	5701	22	AAW05328
43	45	47.4	26926	22	AAU05396
44	44	46.3	626	18	AAW16398
45	43	45.3	18	19	AAW65395

ALIGNMENTS

RESULT 1	
ID	AAW52210 standard; peptide; 17 AA.
XX	
AC	AAW52210;
XX	
DT	09-JUN-1998 (first entry)
XX	
DE	Interleukin-6 antagonist peptide.
XX	
KW	Interleukin-6; IL-6; antagonist; IL-6 related disease; multiple myeloma;
KW	acquired immune deficiency syndrome-related lymphoma; immune response;
KW	rheumatoid arthritis; psoriasis; sepsis; osteoporosis; therapy;
KW	Alzheimer's disease.
XX	
OS	Synthetic.
XX	
PN	Homo sapiens.
XX	
PN	WO9748728-A1.
XX	
PD	24-DEC-1997.
XX	
PF	19-JUN-1997; 97WO-NL00345.
XX	
PR	20-JUN-1996; 96EP-0201720.
XX	
PA	(KOST/) KOSTER H W.
XX	
PI	Hoebe KHN, Van Leengoed LAMG;
XX	
DR	WPI, 1998-063080/06.
XX	
PT	New peptide(s) with Interleukin-6 agonist or antagonist activity -
PT	useful for treatment, prevention and diagnosis of IL-6 associated


```

RESULT 4
AAW17859
ID AAW17859 standard; Protein; 329 AA.
XX
AC AAW17859;
XX
DT 04-FEB-1998 (first entry)
XX
DE Rheumatoid arthritis auto-antigen clone A.
XX
KM Rheumatoid arthritis; auto-antigen; clone A; diagnosis;
XX prediction; synovial cell.
XX
OS Homo sapiens.
XX
PN W09717441-A1.
XX
PD 15-MAY-1997.
XX
PF 06-NOV-1996; 96MO-JP03250.
XX
PR 07-NOV-1995; 95JP-0288957.
XX
PA (KANF) KANEKA CORP.
XX
PI Kishimura M, Nakao K, Osakada F, Osaki S, Tanaka M;
XX WPT. 1997-281030/25.
XX N-PSDB; AAT68830.
XX
DR Auto-antigen from synovial cells of rheumatoid arthritis patients -
XX binds to antibodies present in these patients, for diagnosis and
XX prediction of the disease
XX
PS Claim 3; Pages 36-37; 61pp; Japanese.
XX
XX The present sequence is the rheumatoid arthritis (RA) auto-antigen
XX clone A, which can be used to diagnose and predict the development
XX of RA by reaction with antibodies in biological specimens, e.g.
XX sera, from patients.
XX CC RNA was isolated from synovial cells from a RA patient and used to
XX construct a cDNA library. This was screened using Igg separated
XX from the synovial fluid of a RA patient. Active clones were
XX isolated in a cloning vector, and inserted into an expression
XX vector for the transformation of E. coli NM522. Transformants on
XX culture express clone A peptide and folistatin related protein
XX into the culture medium.
XX
SQ Sequence 329 AA:

```

```

Query Match 100.0%; Score 95; DB 18; Length 329;
Best Local Similarity 100.0%; Pred. No. 2.5e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

OY 1 PYYKVKPNPPHNLSTVN 17
    |||
DB 216 PYYKVKPNPPHNLSTVN 232

```

```

RESULT 5
AAW70799
ID AAW70799 standard; protein; 332 AA.
XX
AC AAW70799;
XX
DT 03-FEB-1999 (first entry)
XX
DE Human gp130-delta-3fibro amino acid sequence.
XX
KW gp130; cytokine antagonist; interleukin; gamma-interferon;
XX

```

```

KM granulocyte macrophage colony-stimulating factor; J peptide;
KW transforming growth factor-beta.
XX
OS Synthetic.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX FT 1..350
XX FT Protein /note="human gp130"
XX
XX PN US584409-A.
XX
XX PD 01-DEC-1998.
XX
XX PF 27-NOV-1995; 95US-0563105.
XX
XX PR 27-NOV-1995; 95US-0563105.
XX PR 20-OCT-1993; 93US-0140222.
XX
XX PA (REGG-) REGENERON PHARM INC.
XX
XX PI Economides A, Stahl N, Yancopoulos GD;
XX WPT. 1999-044669/04.
XX
XX PS Example 4; Fig 10; 46pp; English.
XX
XX CC The present sequence represents the amino acid sequence of human
XX gp130-delta-3fibro. The protein is used in the course of the invention.
XX CC The specification describes cytokine antagonists comprising only the
XX extracellular domain of the specificity-determining component of
XX the cytokine receptor and the extracellular domain of a
XX signal-transducing component of the cytokine receptor. The cytokine
XX is an interleukin (IL-1, IL-2, IL-3, IL-4, IL-5 or IL-15),
XX CC granulocyte macrophage colony-stimulating factor (GM-CSF),
XX gamma-interferon or transforming growth factor-beta (TGF-beta). The
XX CC antagonist is capable of binding the cytokine to form a nonfunctional
XX complex. The compounds have therapeutic activity as cytokine antagonists
XX and can also be used in assays for identifying novel agonists and
XX antagonists of cytokines.
XX
SQ Sequence 332 AA:

```

```

Query Match 100.0%; Score 95; DB 20; Length 332;
Best Local Similarity 100.0%; Pred. No. 2.5e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

OY 1 PYYKVKPNPPHNLSTVN 17
    |||
DB 216 PYYKVKPNPPHNLSTVN 232

```

```

RESULT 6
AA92188
ID AA92188 standard; protein; 332 AA.
XX
AC AA92188;
XX
DT 01-AUG-2000 (first entry)
XX
DE Human gp130-delta-3fibro.
XX
KW gp130-delta-3fibro; cytokine; antagonist; CNTF; receptor; fusion protein;
XX cytosolic; immunomodulator; osteopathic.
XX
OS Synthetic.
XX
XX Homo sapiens.
XX

```

```

FH Key Location/Qualifiers
FT Protein 1..330
FT /label= gp130
FT Peptide 331..332
FT /note= "Ser-gly bridge"
XX
XX MO200018932-A2.
XX
XX 06-APR-2000.
XX
XX 22-SEP-1999; 99MO-US22045.
XX
XX 25-SEP-1998; 98US-0101858.
XX 19-MAY-1999; 99US-0313942.
XX
XX (REGG-) REGENERON PHARM INC.
XX
XX Stahl N, Vancopoulos GD;
XX
XX WPI; 2000-293165/25.
XX
XX Isolated nucleic acid molecule for treating cytokine-related diseases
XX or disorders encodes a fusion polypeptide capable of binding a cytokine
XX to form a nonfunctional complex
XX
XX Example 4; Fig 10; 152pp: English.
XX
XX The invention concerns production of antagonists to any cytokine that
XX utilizes an alpha specificity determining component, which when combined
XX with the cytokine, binds to a first beta signal transducing component to
XX form a nonfunctional intermediate which then binds to a second beta
XX signal transducing component causing beta-receptor dimerization, the
XX soluble alpha specificity determining component of the receptor
XX (SR-alpha) and the extracellular domain of the first beta signal
XX transducing component of the cytokine receptor (beta-1) are combined to
XX form heterodimers (SR-alpha:beta-1) that act as antagonist to the
XX cytokine by binding the cytokine to form a non-functional complex. The
XX receptor components are shared by cytokines such as the CNTF (ciliary
XX neurotrophic factor) family of cytokines. The invention provides the
XX basis for the development of IL-6 antagonists, as they show that if, in
XX the presence of a ligand, a non-functional intermediate complex,
XX consisting of the ligand, its alpha receptor and its beta-1 receptor
XX component, can be formed, it will effectively block the action of the
XX ligand. Effective antagonists of IL-6 or CNTF consist of heterodimers
XX of the extracellular domains of the alpha specificity determining
XX components of their receptors and the extracellular domain of gp130.
XX The resultant heterodimers, function as high-affinity traps, rendering
XX the cytokine inaccessible to form a signal transducing complex with the
XX native membrane-bound forms of their receptor. The nucleic acids and
XX polypeptides are useful for treating cytokine-related diseases or
XX disorders such as osteoporosis and primary and secondary effects of
XX cancer including multiple myeloma or cachexia.
XX
XX Sequence 332 AA:
SQ

```

```

Query Match 100.0%; Score 95; DB 21; Length 332;
Best Local Similarity 100.0%; Pred. No. 2.5e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 PYVVKRPNPNNLSVIN 17
   |||||
Db 216 pyvkvknpnpnnlsvin 232

```

```

RESULT 7
AAR94576 standard; Protein: 658 AA.
XX
AC AAR94576;
XX
XX 20-JUN-1996 (first entry)
XX

```

```

DE Human gp130 splice variant.
XX
XX Gp130; transmembrane domain; growth factor antagonist;
XX embryo preimplantation; in vitro fertilisation.
XX
XX Homo sapiens.
XX
XX WO9609382-A1.
XX
XX 28-MAR-1996.
XX
XX 21-SEP-1995; 95MO-GB02243.
XX
XX 21-SEP-1994; 94GB-0019021.
XX
XX (ISTF ) ARS APPLIED RES SYST HOLDING NV.
XX
XX Dellow KA, Sharkey A, Smith SK;
XX
XX WPI; 1996-188444/19.
XX
XX N-PSDB; AAT14602.
XX
XX New splice variant of gp130 lacking the trans-membrane domain
XX useful as an antagonist for growth factors esp. for ensuring correct
XX development of pre-implantation embryos
XX
XX Example 2; Fig 1; 33pp: English.
XX
XX A novel, soluble splice variant (AAR94576) of human gp130 corresponds
XX to amino acids 1-613 of native gp130 (AAR75368) but has a novel
XX C-terminal sequence (AAR94575) from amino acid 614 onwards.
XX The splice variant lacks a transmembrane region. It was initially
XX detected during the morula to blastocyst transition of human
XX embryos. The splice variant antagonises the action of growth
XX factors, e.g. interleukin-6, leukaemia inhibitory factor,
XX oncostatin M and interleukin-11, and can be used to ensure correct
XX development of preimplantation embryos, partic. for in vitro
XX fertilisation.
XX
XX Sequence 658 AA:
SQ

```

```

Query Match 100.0%; Score 95; DB 17; Length 658;
Best Local Similarity 100.0%; Pred. No. 5.3e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 PYVVKRPNPNNLSVIN 17
   |||||
Db 216 pyvkvknpnpnnlsvin 232

```

```

RESULT 8
AAR37804 standard; Protein: 708 AA.
XX
AC AAR37804;
XX
XX 01-OCT-1993 (first entry)
XX
XX Human gp130 N-terminal fragment.
XX
XX Oncostatin M; leukaemia inhibitory factor; receptor; PCR; fusion;
XX LIF-R; gp130; linker.
XX
XX Synthetic.
XX
XX
XX
XX Key Location/Qualifiers
XX Peptide 1..22
XX Protein /label= sig-peptide
XX Domain /label= mat_protein
XX /label= extracellular_domain

```


FT	Region	620
FT	/label- transmembrane_region	
FT	/note- "beginning with amino acid 620"	
FT	Domain	643..708
FT	/label- cytoplasmic_domain	
FT	/note- "partial cytoplasmic domain"	
FT	Misc-difference	8
FT	/note-	"differs from the equiv. portion of the Hbl et al. Cell 63:1149 (1990) protein in that the eighth amino acid of the signal sequence is Leu rather than Val"
FT		
PD		
XX		
XX	27-MAY-1993.	
XX		
PE	20-NOV-1992;	92MO-US10272.
XX		
PR	22-NOV-1991;	9IUS-0797556.
XX		
PA	(IMMV) IMMUNEX CORP.	
XX		
PI	Gearing DP;	
XX		
DR	WPI; 1993-182493/22.	
XX	N-PSDB; AAQ42588.	
PT	Receptor protein comprising gp130 covalently linked to LIF	
PT	receptor - binds to oncostatin M and LIF useful for treating	
PT	kaposi sarcoma, atherosclerosis, obesity etc.	
PS	Disclosure; Page 48-53; 79pp; English.	
XX		
CC	A new receptor (R), able to bind oncostatin M and leukaemia	
CC	inhibitory factor (LIF), comprises a gp130 polypeptide (AAQ42588)	
CC	covalently coupled to LIF-receptor (LIF-R) (AAQ42590); for example	
CC	via a Fc region of an IgG1 antibody (AAQ42589).	
CC	Suitable gp130 polypeptides comprise amino acids 22-528, 22-320,	
CC	120-320 etc., or lack all or part of the transmembrane region	
CC	and/or cytoplasmic domain.	
CC	Pref. both components of (R) are soluble proteins and are connected	
CC	by a polypeptide linker of 20-100 amino acids consisting of Gly, Asn,	
XX	Ser, Thr or Ala.	
XX		
SO	Sequence	708 AA;
Query Match		100.0%; Score 95; DB 14; Length 708;
Best Local Similarity		100.0%; Pred. NO. 5; Fe-06;
Matches 17; Conservative		0; Mismatches 0; Indels 0; Gaps 0.
OY	1 PYYKKVPNPPHNLASYIN 17 	
Db	216 PYKVKVPNPPHNLASYIN 232	
RESULT	9	
ID	AAAR85911	
XX	AAAR85911 standard; Protein; 708 AA.	
XX	AAAR85911;	
XX		
DT	03-JUL-1996 (first entry)	
XX		
DE	gp130 N-terminal fragment.	
XX		
KW	Human; gp130; inhibitor; oncostatin M; cytokine; antibody Fc region; oncostatin M receptor-beta chain; antibody; tumour; growth factor; therapy.	
XX		
OS	Homo sapiens.	
XX		
TH	key	Location/Qualifiers

FT	Peptide	1..22
FT	Peptide	/note= "signal peptide"
FT	Peptide	23..708
FT	Modified-site	/note= "N-terminal fragment of mature gp130"
FT	Modified-site	21..23
FT	Modified-site	/note= "glycosylation site"
FT	Modified-site	61..63
FT	Modified-site	/note= "glycosylation site"
FT	Modified-site	109..111
FT	Modified-site	/note= "glycosylation site"
FT	Modified-site	135..137
FT	Cleavage-site	/note= "glycosylation site"
FT	Modified-site	153..154
FT	Modified-site	205..207
FT	Modified-site	/note= "glycosylation site"
FT	Modified-site	224..226
FT	Modified-site	/note= "glycosylation site"
FT	Modified-site	357..359
FT	Modified-site	/note= "glycosylation site"
FT	Modified-site	361..363
FT	Modified-site	/note= "glycosylation site"
FT	Modified-site	368..370
FT	Modified-site	/note= "glycosylation site"
FT	Modified-site	531..533
FT	Modified-site	/note= "glycosylation site"
FT	Modified-site	542..544
FT	Cleavage-site	/note= "glycosylation site"
FT	Cleavage-site	621..622
XX	WO9533059-A2.	
PN	07-DEC-1995.	
PD	22-MAY-1995;	95WO-US06530.
XX	12-SEP-1994;	94US-0308881.
PR	26-MAY-1994;	94US-0249535.
XX	(IMMV) IMMUNEX CORP.	
PA	Cosman DJ, Mosley B;	
XX	WPI: 1996-030570/03.	
DR	N-PSDB; AA074081.	
XX	Hetero: dimeric receptor proteins comprising OSM-R beta and gp 130	
PT	bind oncostatin M and are used in inhibiting biological activities	
PT	mediated by oncostatin M	
XX	Clalm 1; Page 35-38; 60pp; English.	
PS	This sequence represents an N-terminal fragment of gp130 obtained from	
XX	human placenta. gp130 binds to oncostatin M, which is a secreted single	
CC	chain polypeptide cytokine. Oncostatin M regulates the growth of	
CC	certain tumour derived and normal cell lines. This receptor protein, and	
CC	the oncostatin M receptor-beta chain (see AAR85912) sequence can be	
CC	covalently joined, to give a heterodimeric receptor protein capable of	
CC	binding to oncostatin M. The receptors can also comprise fusion	
CC	polypeptides, where an antibody Fc region is joined to the C-terminus of	
CC	each of the soluble proteins. In this case, the two fusion polypeptides	
CC	are joined by disulphide bonds between the two antibody Fc regions. The	
CC	heterodimeric receptors can be used to inhibit biological activities	
CC	mediated by oncostatin M. The advantage with using the heterodimeric	
CC	receptors is that they bind to oncostatin M at greater levels than gp130	
CC	does alone.	
XX	Sequence 708 AA;	
SQ	Query Match 100.0%; Score 95; DB 17; Length 708;	
	Best Local Similarity 100.0%; Pred. No. 5,7e-06;	
	Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	

QY 1 PVKVKRPNNLSVIN 17
 |||
 DB 216 PVKVKRPNNLSVIN 232

RESULT 10

AAV92192
 ID AAV92192 standard; protein; 727 AA.

XX AAV92192;

DT 01-AUG-2000 (first entry)

XX Human gp130-kappa domain fusion protein.

XX gp130-kappa domain; cytokine; antagonist; CNTF; receptor; fusion protein;

KM cytoskeletal; immunomodulator; osteopathic.

XX Synthetic.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Protein 1..619 /label= gp130

FT Peptide 620..621 /note= "Ser-Gly bridge"

FT Protein 622..727 /label= IgG1_kappa_domain

XX MO200018932-A2.

XX 06-APR-2000.

XX 22-SEP-1999; 99MO-US22045.

XX 25-SEP-1998; 98US-0101858.

PR 19-MAY-1999; 99US-0313942.

XX (REG-) REGENERON PHARM INC.

PI Stahl N, Yancopoulos GD;

XX WPI; 2000-293165/25.

XX Isolated nucleic acid molecule for treating cytokine-related diseases

PT or disorders encodes a fusion polypeptide capable of binding a cytokine

PT to form a nonfunctional complex

XX Example 4; Page -: 152pp; English.

XX The invention concerns production of antagonists to any cytokine that

CC utilizes an alpha specificity determining component, which when combined

CC with the cytokine, binds to a first beta signal transducing component to

CC form a non-functional intermediate which then binds to a second beta

CC signal transducing component causing beta-receptor dimerization, the

CC soluble alpha specificity determining component of the receptor

CC (SR-alpha) and the extracellular domain of the first beta signal

CC transducing component of the cytokine receptor (beta-1) are combined to

CC form heterodimers (SR-alpha:beta-1) that act as antagonist to the

CC cytokine by binding the cytokine to form a non-functional complex. The

CC receptor components are shared by cytokines such as the CNTF (ciliary

CC neurotrophic factor) family of cytokines. The invention provides the

CC basis for the development of IL-6 antagonists, as they show that if, in

CC the presence of a ligand, a non-functional intermediate complex,

CC consisting of the ligand, its alpha receptor and its beta-1 receptor

CC component, can be formed, it will effectively block the action of the

CC ligand. Effective antagonists of IL-6 or CNTF consist of heterodimers

CC of the extracellular domains of the alpha specificity determining

CC components of their receptors and the extracellular domain of gp130.

CC The resultant heterodimers, function as high-affinity traps, rendering

CC the cytokine inaccessible to form a signal transducing complex with the

CC native membrane-bound forms of their receptor. The nucleic acids and

CC polypeptides are useful for treating cytokine-related diseases or

CC disorders such as osteoporosis and primary and secondary effects of

CC cancer including multiple myeloma or cachexia.

CC NB. This sequence was constructed from the gp130 and kappa domain

CC sequences given in Figures 9 and 13 of the specification.

XX

QY 1 PVKVKRPNNLSVIN 17

DB 216 PVKVKRPNNLSVIN 232

RESULT 11

AAV92194
 ID AAV92194 standard; protein; 738 AA.

XX AAV92194;

DT 01-AUG-2000 (first entry)

XX Human gp130-J-kappa fusion protein.

XX gp130-J-kappa; cytokine; antagonist; CNTF; receptor; fusion protein;

KM cytoskeletal; immunomodulator; osteopathic.

XX Synthetic.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Protein 1..619 /label= gp130

FT Peptide 620..621 /note= "Ser-Gly bridge"

FT Peptide 622..632 /note= "J-peptide"

FT Domain 633..738 /label= kappa_domain

XX MO200018932-A2.

XX 06-APR-2000.

XX 22-SEP-1999; 99MO-US22045.

XX 25-SEP-1998; 98US-0101858.

PR 19-MAY-1999; 99US-0313942.

XX (REG-) REGENERON PHARM INC.

PI Stahl N, Yancopoulos GD;

XX WPI; 2000-293165/25.

XX Isolated nucleic acid molecule for treating cytokine-related diseases

PT or disorders encodes a fusion polypeptide capable of binding a cytokine

PT to form a nonfunctional complex

XX Example 4; Page -: 152pp; English.

XX The invention concerns production of antagonists to any cytokine that

CC utilizes an alpha specificity determining component, which when combined

CC with the cytokine, binds to a first beta signal transducing component to

CC form a non-functional intermediate which then binds to a second beta

CC signal transducing component causing beta-receptor dimerization, the

CC soluble alpha specificity determining component of the receptor

CC (SR-alpha) and the extracellular domain of the first beta signal

CC transducing component of the cytokine receptor (beta-1) are combined to

CC form heterodimers (SR-alpha:beta-1) that act as antagonist to the

CC cytokine by binding the cytokien to form a non-functional complex. The
 CC receptor components are shared by cytokines such as the CMF (ciliary
 CC neurotrophic factor) family of cytokines. The invention provides the
 CC basis for the development of IL-6 antagonists, as they show that if, in
 CC the presence of a ligand, a non-functional intermediate complex,
 CC consisting of the ligand, its alpha receptor and its beta-1 receptor
 CC component, can be formed, it will effectively block the action of the
 CC ligand. Effective antagonists of IL-6 or CMF consist of heterodimers
 CC of the extracellular domains of the alpha specificity determining
 CC components of their receptors and the extracellular domain of gp130.
 CC The resultant heterodimers, function as high-affinity traps, rendering
 CC the cytokine inaccessible to form a signal transducing complex with the
 CC native membrane-bound forms of their receptor. The nucleic acids and
 CC polypeptides are useful for treating cytokine-related diseases or
 CC disorders such as osteoporosis and primary and secondary effects of
 CC cancer including multiple myeloma or cachexia.

CC Sequence 738 AA:

Query Match 100.0%; Score 95; DB 21; Length 738;

Best Local Similarity 100.0%; Pred. No. 6e-06; Mismatches 0; Gaps 0;

Matches 17; Conservative 0; Indels 0; Gaps 0;

OY 1 PVYKVKPNPNNLSVIN 17
 |||||
 DB 216 PVYKVKPNPNNLSVIN 232

RESULT 12

AAW70796
 ID AAW70796 standard; protein; 859 AA.

AC AAW70796;

DT 03-FEB-1999 (first entry)

DE Human gp130-Fc-His6 amino acid sequence.

XX gp130; cytokine antagonist; interleukin; gamma-interferon;
 KW granulocyte macrophage colony-stimulating factor; J peptide;
 KW transforming growth factor-beta.

XX Synthetic.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Protein 1..619 /note= "human gp130"

FT Misc-difference 2 /label= L2V

FT /note= "amino acid changed to accomodate a Kozak
 sequence"

FT Peptide 1..22 /note= "signal peptide"

FT Misc-difference 620..621 /note= "Ser-Gly bridge"

FT Protein 662..853 /note= "from the Fc domain of human IgG1"

FT Disulfide-bond 632..635 /note= "Ser-Gly bridge"

FT Peptide 854..859 /note= "hexahistidine tag"

XX US5844099-A.

XX 01-DEC-1998.

XX 27-NOV-1995; 9505-0563105.

XX 27-NOV-1995; 9505-0563105.

XX 20-OCT-1993; 9305-0140222.

XX (REG-) REGENERON PHARM INC.

XX Economides A, Stahl N, Yancopoulos GD;

XX WPI; 1999-044669/04.

XX Cytokine antagonists - comprising extracellular domains of
 PY specificity-determining and signal-transducing components of
 PY cytokine receptor

XX Example 3; Fig 4; 46pp; English.

PS The present sequence represents the amino acid sequence of human
 CC gp130-Fc-His6. The protein is used in the course of the invention. The
 CC specification describes cytokine antagonists comprising only the
 CC extracellular domain of the specificity-determining component of
 CC the cytokine receptor and the extracellular domain of a
 CC signal-transducing component of the cytokine receptor. The cytokine
 CC is an interleukin (IL-1, IL-2, IL-3, IL-4, IL-5 or IL-15),
 CC granulocyte macrophage colony-stimulating factor (GM-CSF),
 CC gamma-interferon or transforming growth factor-beta (TGF-beta). The
 CC antagonist is capable of binding the cytokine to form a nonfunctional
 CC complex. The compounds have therapeutic activity as cytokine antagonists
 CC and can also be used in assays for identifying novel agonists and
 CC antagonists of cytokines.

CC Sequence 859 AA:

Query Match 100.0%; Score 95; DB 20; Length 859;

Best Local Similarity 100.0%; Pred. No. 7e-06; Mismatches 0; Gaps 0;

Matches 17; Conservative 0; Indels 0; Gaps 0;

OY 1 PVYKVKPNPNNLSVIN 17
 |||||
 DB 216 PVYKVKPNPNNLSVIN 232

RESULT 13

AA92184
 ID AA92184 standard; protein; 859 AA.

AC AA92184;

DT 01-AUG-2000 (first entry)

DE Human gp130-Fc-His6.

XX gp130-Fc-His6; cytokine antagonist; CMF; receptor; fusion protein;
 KW cytostatic; immunomodulator; osteopathic.

XX Synthetic.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Protein 1..619 /label= gp130

FT Peptide 1..22 /label= signal_peptide

FT Peptide 620..621 /note= "Ser-Gly bridge"

FT Disulfide-bond 632 /note= "forms inter-chain disulfide bridge that
 link two Fc domains"

FT Disulfide-bond 635 /note= "forms inter-chain disulfide bridge that
 link two Fc domains"

FT Protein 662..853 /label= IgG1_Fc-domain

FT Peptide 854..859 /label= histidine_tag

XX WO200018932-A2.

XX The soluble glycoprotein (gp) 130 can be used as an immunogen for
 CC the preparation of anti-gp130 antibody and as the standard substance
 CC for immunochemical assay of gp130. Soluble gp130 cDNA was prepared
 CC by inserting a termination codon prior to the extracellular domain
 CC or transmembrane domain of the gp130 coding sequence or simply by
 CC eliminating the transmembrane domain.
 XX

SQ Sequence 918 AA;

Query Match 100.0%; Score 95; DB 15; Length 918;
 Best Local Similarity 100.0%; Pred. No. 7.6e-06;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PYKXKPNPPHNLSTYN 17
 |||
 Db 216 PYKXKPNPPHNLSTYN 232

Search completed: December 19, 2001, 16:19:37
 Job time: 362 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 19, 2001, 16:22:41 ; Search time 88.82 Seconds
(without alignments)
14.580 Million cell updates/sec

Title: US-09-202-104a-10

Perfect score: 95

Sequence: 1 PYYKVKPNPNNLSVIN 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	95	100.0	918	2	A36337 membrane glycoprot
2	75	78.9	918	2	A44257 interleukin-6 sign
3	68	71.6	917	2	I49699 glycoprotein 130 -
4	47	49.5	225	2	T09964 extensin CYC15 pre
5	47	49.5	400	2	A46297 beta-1,6-N-acetylgl
6	47	49.5	491	2	T07598 proline-rich prote
7	45	47.4	693	2	S64904 probable membrane
8	45	47.4	26926	1	I38344 titin, cardiac mus
9	44	46.3	517	2	T28630 Y4CC protein - Rhl
10	44	46.3	625	2	S71930 neuron-derived rec
11	44	46.3	867	2	T27136 hypothetical prote
12	44	46.3	871	2	T27135 hypothetical prote
13	43.5	45.8	199	2	T07622 extensin homolog -
14	43	45.3	26	2	S06675 apidaecin 1b precu
15	43	45.3	144	2	S35331 apidaecin 14 precu
16	43	45.3	168	2	S35330 apidaecin 22 precu
17	43	45.3	259	2	T26484 hypothetical prote
18	43	45.3	281	2	D83383 hypothetical prote
19	43	45.3	283	2	S35332 apidaecin 73 precu
20	43	45.3	363	2	UC4186 fructose-bisphosph
21	43	45.3	630	2	I51086 prolactin receptor
22	43	45.3	2248	1	D42088 adenylate cyclase
23	42	44.2	121	2	D72712 hypothetical prote
24	42	44.2	150	2	B34631 lactogen receptor
25	42	44.2	292	2	I77525 prolactin receptor
26	42	44.2	303	2	I77524 prolactin receptor
27	42	44.2	310	2	A29884 prolactin-rich prote
28	42	44.2	313	2	T48057 proline-rich prote
29	42	44.2	313	2	T52077

30	42	44.2	412	2	A41070 prolactin receptor
31	42	44.2	492	2	S49147 ERF-2 protein - hu
32	42	44.2	513	2	C84447 probable WRKY DNA-
33	42	44.2	531	2	S20900 titin - mouse (fra
34	42	44.2	540	2	E64446 CTP synthase (EC 6
35	42	44.2	608	2	I53269 prolactin receptor
36	42	44.2	610	2	A34631 lactogen receptor
37	42	44.2	610	2	A36116 prolactin receptor
38	42	44.2	656	2	B96649 hypothetical prote
39	42	44.2	1049	2	T43020 hypothetical prote
40	42	44.2	1187	2	T26283 probable reverse t
41	42	44.2	6805	2	S20901 hypothetical prote
42	41.5	43.7	337	2	T29474 titin - rabbit (fr
43	41.5	43.7	499	2	T49630 phenylalanyl-tRNA
44	41	43.2	74	2	S19708 hypothetical prote
45	41	43.2	150	2	T12868 hypothetical prote

ALIGNMENTS

```
RESULT 1
A36337
membrane glycoprotein gp130 precursor - human
C:Species: Homo sapiens (man)
C:Date: 12-Apr-1991 #sequence_revision 12-Apr-1991 #text_change 28-Jul-2000
C:Accession: A36337
R:HiBi, M.; Murakami, M.; Saito, M.; Hirano, T.; Taga, T.; Kishimoto, T.
Cell 63, 1149-1157, 1990
A:Title: Molecular cloning and expression of an IL-6 signal transducer, gp130.
A:Reference number: A36337; MUID:91084844
A:Accession: A36337
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-918 <HIB>
A:Cross-references: GB:M57230; NID:9186353; PIDN:AAA59155.1; PID:9186354
C:Genetics:
A:Gene: GDB:1165T; GP130
A:Cross-references: GDB:126725; OMIM:600694
A:Map position: 5q11-5q11
C:Superfamily: cytokine receptor homology
C:Keywords: glycoprotein; membrane protein
P:134-316/Domain: cytokine receptor homology <CRS>

Query Match 100.0%; Score 95; DB 2; Length 918;
Best Local Similarity 100.0%; Pred. No. 6,2e+07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PYYKVKPNPNNLSVIN 17
DB 216 PYYKVKPNPNNLSVIN 232
|||||
A44257
interleukin-6 signal transducing molecule gp130 - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 28-Jul-2000
C:Accession: A44257
R:Wang, Y.; Nesbitt, J.E.; Fuentes, N.L.; Fuller, G.M.
Genomics 14, 666-672, 1992
A:Title: Molecular cloning and characterization of the rat liver IL-6 signal transduc
A:Reference number: A44257; MUID:93052397
A:Accession: A44257
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-918 <MAN>
A:Experimental source: liver
A>Note: sequence extracted from NCBI backbone (NCBIP:118488)
C:Superfamily: cytokine receptor homology
C:Keywords: transmembrane protein
P:134-315/Domain: cytokine receptor homology <CRS>
```

Query Match 78.9%; Score 75; DB 2; Length 918;
 Best Local Similarity 82.4%; Pred. No. 0.00087;
 Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 PVYKVKPNPNHLSVIN 17
 |||||
 DB 215 PVDKVKPPNHLSTVN 231

RESULT 3

I49699

glycoprotein 130 - mouse

C:Species: Mus musculus (house mouse)

C>Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 28-Jul-2000

C:Accession: I49699; I48370

R:Salto, M.; Yoshida, K.; Hibi, M.; Taga, T.; Kishimoto, T.

J. Immunol. 148, 4066-4071, 1992

A>Title: Molecular cloning of a murine IL-6 receptor-associated signal transducer, gp130

A:Reference number: I48370; MUID:92291532

A:Accession: I49699

A>Status: translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-917 <RES>

A:Cross-references: GB:M83336; NID:g193591; PIDN:AAA37723.1; PID:g193592

A:Accession: I48370

A>Status: translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-917 <RES>

A:Cross-references: EMBL:X62646; NID:g840816; PIDN:CAA44515.1; PID:g840817

C:Genetics:

A:Gene: gp130

C:Superfamily: cytokine receptor homology

C:Keywords: glycoprotein

F:134-314/Domain: cytokine receptor homology <CRS>

Query Match 71.6%; Score 68; DB 2; Length 917;
 Best Local Similarity 76.5%; Pred. No. 0.011;
 Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 PVYKVKPNPNHLSVIN 17
 |||||
 DB 214 PVDKVKPPNHLSTVN 230

RESULT 4

T09964

extensin cyc15 precursor - Madagascar periwinkle

C:Species: Catharanthus roseus (Madagascar periwinkle)

C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000

C:Accession: T09964

R:Itô, M.; Kodama, H.; Komamine, A.; Watanabe, A.

Plant Mol. Biol. 36, 343-351, 1998

A>Title: Expression of extensin genes is dependent on the stage of the cell cycle and ce

A:Reference number: Z16907; MUID:98145469

A:Accession: T09964

A>Status: translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-225 <IT0>

A:Cross-references: EMBL:D86853; NID:g1486262; PIDN:BA13175.1; PID:g1486263

C:Genetics:

A:Gene: cyc15

C:Function:

A:Description: structural component of cell wall

C:Superfamily: proline-rich protein 3

C:Keywords: cell wall; glycoprotein; hydroxyproline

Query Match 49.5%; Score 47; DB 2; Length 225;
 Best Local Similarity 72.7%; Pred. No. 4.77;
 Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 PVYKVKPNPPH 11
 |||||
 DB 91 PVYKSPPPPH 101

RESULT 5

A46297

beta-1,6-N-acetylglucosaminyltransferase (EC 2.4.1.-) - human

C:Species: Homo sapiens (man)

C>Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jul-2000

C:Accession: A46297

R:Biernizien, M.F.; Mattei, M.G.; Fukuda, M.

Genes Dev. 7, 468-478, 1993

A>Title: Expression of the developmental I antigen by a cloned human cDNA encoding a

A:Reference number: A46297; MUID:93194065

A:Accession: A46297

A>Status: preliminary

A:Molecule type: nucleic acid

A:Residues: 1-400 <BI>

A:Cross-references: GB:Z19550; NID:g296531; PIDN:CAA79610.1; PID:g296532

A>Note: sequence extracted from NCBI backbone (NCBIN:127166, NCBI:P:127167)

C:Keywords: glycosyltransferase; hexosyltransferase; transmembrane protein

Query Match 49.5%; Score 47; DB 2; Length 400;
 Best Local Similarity 63.6%; Pred. No. 8.8;
 Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 5 VKPNPNHLSV 15
 |||||
 DB 248 LKPPPHNLTI 258

RESULT 6

T07598

proline-rich protein GP1 - potato

C:Species: Solanum tuberosum (potato)

C>Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 08-Oct-1999

C:Accession: T07598

R:Menke, U.

submitted to the EMBL data library, August 1997

A:Reference number: Z16040

A:Accession: T07598

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-491 <MEN>

A:Cross-references: EMBL:A1000997; NID:e1314336; PIDN:CAA04449.1; PID:e1314337

A:Experimental source: cv. Desiree

C:Genetics:

A:Gene: gp1

Query Match 49.5%; Score 47; DB 2; Length 491;
 Best Local Similarity 80.0%; Pred. No. 11;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 PVYKVKPNPP 10
 |||||
 DB 259 PVYKPKRPP 268

RESULT 7

S64904

probable membrane protein YLR072w - yeast (Saccharomyces cerevisiae)

N:Alternate names: hypothetical protein U3321

C:Species: Saccharomyces cerevisiae

C>Date: 01-Aug-1995 #sequence_revision 24-May-1996 #text_change 05-Nov-1999

C:Accession: S64904

R:Pohl, T.M.

submitted to the Protein Sequence Database, May 1996

A:Reference number: S64899

A:Accession: S64904

A:Molecule type: DNA
A:Residues: 1-693 <POH>
A:Cross-references: EMBL:Z73244; NID:g1360427; PID:e245792; PDB:g1360428; GSPDB:GN00012;
A:Experimental source: strain S288C
A:Genetics:
C:Gene: MIPS:YLR072w
A:Map position: 12R
C:Keywords: transmembrane protein
F:634-650/Domain: transmembrane #status predicted <TM>

Query Match 47.4%; Score 45; DB 2; Length 693;
Best Local Similarity 70.0%; Pred. No. 34;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 PYKVKPNPP 10
| | | | | | | | | |
DB 371 PYKRLKPNAP 380

RESULT 8
138344
titin, cardiac muscle [validated] - human
N:Alternate names: connectin
N:Contains: serine/threonine-specific protein kinase (EC 2.7.1.-)
C:Species: Homo sapiens (man)
C>Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 15-Sep-2000
C:Accession: 138344; 138345; S20898; S20899; S63665; 537393
R:Labelit, S.; Kolmerer, B.
Science 270, 293-296, 1995
A:Title: Tiltins: giant proteins in charge of muscle ultrastructure and elasticity.
A:Reference number: A57430; MUID:96026330
A:Accession: 138344
A:Status: nucleic acid sequence not shown; translation not shown; translated from GB/EMBL
A:Molecule type: mRNA
A:Residues: 1-26926 <LAB1>
A:Cross-references: EMBL:X90568; NID:g1017424; PID:g1017425
R:Musco, G.; Tlatziros, C.; Schuck, P.; Pastore, A.
Biochemistry 34, 553-561, 1995
A:Title: Dissecting titin into its structural motifs: identification of an alpha-helix
A:Reference number: 138345; MUID:95119041
A:Accession: 138345
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1977-2014 <MUS>
A:Cross-references: EMBL:X83270; NID:9602579; PIDN:CAA58243.1; PID:9602580
A:Note: conformation and properties are reported for a synthetic peptide corresponding to
R:Labelit, S.; Gautel, M.; Lakey, A.; Trinick, J.
EMBO J. 11, 1711-1716, 1992
A:Title: Towards a molecular understanding of titin.
A:Reference number: S20897; MUID:92258380
A:Accession: S20896
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 13597-14200, 'I', 14202-14696 <LAB2>
A:Cross-references: EMBL:X64698; NID:g37192; PIDN:CAA45939.1; PID:g37193
A:Accession: S20897
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: mRNA
A:Residues: 16330-16382, 'S', 16384-16756, 'F', 16758-16860 <LAB3>
A:Cross-references: EMBL:X64699; NID:g37190; PIDN:CAA45940.1; PID:g37191
A:Accession: S20899
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: mRNA
A:Residues: 'P', 22278-22431, 'R', 22433-22448, 'G', 22450-22453, 'Q', 22455-22480, 'TR', 22483-2
A:Cross-references: EMBL:X64697; NID:g37190; PIDN:CAA45938.1; PID:g37195
R:Kolmerer, B.; Olivieri, N.; Wilt, C.C.; Herrmann, B.G.; Labelit, S.
J. Mol. Biol. 256, 556-563, 1996
A:Title: Genomic organization of M line titin and its tissue-specific expression in two
A:Reference number: S63665; MUID:96177761
A:Accession: S63665
A:Status: nucleic acid sequence not shown
A:Molecule type: DNA

A:Residues: 26729-26825 <KOL>
A:Cross-references: EMBL:X92412; NID:g1236761
R:Gautel, M.; Leonard, K.; Labelit, S.
EMBO J. 12, 3827-3834, 1993
A:Title: Phosphorylation of KSP motifs in the C-terminal region of titin in different
A:Reference number: S37393; MUID:94008990
A:Accession: S37393
A:Molecule type: mRNA
A:Residues: 26831-26926 <GAU>
R:Improta, S.; Politou, A.S.; Pastore, A.
submitted to the Brookhaven Protein Data Bank, February 1996
A:Reference number: A66736; PDB:1TIT
A:Contents: annotation; conformation by (1)H-NMR, residues 5253-5341
R:Pinhl, M.; Pastore, A.
submitted to the Brookhaven Protein Data Bank, August 1996
A:Reference number: A66201; PDB:1NCT
A:Contents: annotation; conformation by (1)H-NMR, residues 'S', 26059-26155
A:Genetics:
A:Gene: GDB:TTN
A:Cross-references: GDB:127867; OMIM:188840
A:Map position: 2q31-2q32
C:Function:
A:Description: structural protein forming filaments in striated muscle
C:Superfamily: titin; fibronectin type III repeat homology; immunoglobulin homology;
C:Keywords: alternative splicing; calmodulin binding; cardiac muscle; duplication; g1
structural protein
F:24752-25008/Domain: protein kinase homology <KIN>
F:84,177,905,2276,2378,2459,2481,2563,2669,2763,2896,3088,3179,3384,3432,3628,3772,40
98,11066,11488,11515,11635,11949,12170,12478,12526,12645,12875,13001,13036,13295,1354
tatus predicted
F:16780,16976,17579,17602,17681,17681,17845,17899,18121,18188,18209,18336,18670,18680
21960,21935,22295,22495,22627,22897,23049,2318,23883,24012,24177,24290,24447,24642,
F:26171,26178,26184,26190/Binding site: phosphate (ser) (covalent) #status experiment

Query Match 47.4%; Score 45; DB 1; Length 26926;
Best Local Similarity 52.9%; Pred. No. 2e+03;
Matches 9; Conservative 3; Mismatches 3; Indels 2; Gaps 1;

OY 1 PYKVKPNPPNMLSVIN 17
| | | | | | | | | |
DB 16337 PLY--KPGPPNPKVID 16351

RESULT 9
T28630
Y4CC protein - Rhizobium sp. plasmid pNGR234a
C:Species: Rhizobium sp.
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Mar-2000
C:Accession: T28630
R:Freiberg, C.; Fellay, R.; Bairoch, A.; Broughton, W.D.; Rosenthal, A.; Perret, X.
Nature 387, 394-401, 1997
A:Title: Molecular basis of symbiosis between Rhizobium and legumes.
A:Reference number: 214734; MUID:97305956
A:Accession: T28630
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-517 <FRE>
A:Cross-references: EMBL:AE00067; NID:g2182324; PID:g2182327; PIDN:AAB91633.1
A:Experimental source: strain NGR234
C:Genetics:
A:Gene: y4CC
A:Genome: plasmid pNGR234a
C:Superfamily: Rhizobium plasmid pNGR234a Y4CC protein

Query Match 46.3%; Score 44; DB 2; Length 517;
Best Local Similarity 57.1%; Pred. No. 35;
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

OY 3 YKVKPNPRLSVI 16
| | | | | | | | | |
DB 269 YKQPRPRLSVI 282

RESULT 10
S71930
neuron-derived receptor NOR-1 - human
C/Species: Homo sapiens (man)
C/Date: 04-Feb-1998 #sequence_revision 20-Feb-1998 #text_change 20-Feb-1998
C/Accession: S71930
R:Okura, N.; Ito, M.; Tsukada, T.; Sasaki, K.; Yamaguchi, K.; Miki, K.
Biochim. Biophys. Acta 1308, 205-214, 1996
A>Title: Structure, mapping and expression of a human NOR-1 gene, the third member of the
A/Reference number: S71930; MUID:96404972
A/Accession: S71930
A/Molecule type: mRNA
A/Residues: 1-625 <OHK>
A/Cross-references: EMBL:D78579
A/Note: DNA was also sequenced
C/Genetics:
A/Map position: 9q
C/Superfamily: probable hormone receptor N10, nuclear; erba transforming protein homolog
C/Keywords: DNA binding; receptor; zinc finger
F:290-544/Domain: erba transforming protein homology <ERBA>
F:290-377/Domain: DNA binding #status predicted <DNA>
F:292-312/Region: zinc finger CCCC motif
F:310-314/Region: P box
F:328-352/Region: zinc finger CCCC motif
F:329-333/Region: D box
F:370-376/Region: A box

Query Match 46.3%; Score 44; DB 2; Length 625;
Best Local Similarity 54.5%; Pred. No. 43;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
OY 1 PVYKVKPNPPH 11
||:|:|||||
Db 189 PVHFHFKSPPH 199

RESULT 11
T27136
hypothetical protein Y53C12B.3a - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C/Accession: T27136
R:Kershaw, J.; Lennard, N.
submitted to the EMBL Data Library, September 1997
A/Reference number: Z20316
A/Accession: T27136
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-867 <WIL>
A/Cross-references: EMBL:Z99278; PTDN:CAB16493.1; GSPDB:GN00020; CESP:Y53C12B.3a
A/Experimental source: clone Y53C12B
C/Genetics:
A/Gene: CESP:Y53C12B.3a
A/Map position: 2
A/Introns: 100/3; 177/3; 218/1; 423/3; 714/2; 864/3

Query Match 46.3%; Score 44; DB 2; Length 867;
Best Local Similarity 58.3%; Pred. No. 62;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
OY 1 PVYKVKPNPPH 12
||:|:|||||
Db 268 PVIOQRPPPH 279

RESULT 12
T27135
hypothetical protein Y53C12B.3b - Caenorhabditis elegans
C/Species: Caenorhabditis elegans

C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C/Accession: T27135
R:Kershaw, J.; Lennard, N.
submitted to the EMBL Data Library, September 1997
A/Reference number: Z20316
A/Accession: T27135
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-871 <WIL>
A/Cross-references: EMBL:Z99278; PTDN:CAB16492.1; GSPDB:GN00020; CESP:Y53C12B.3b
A/Experimental source: clone Y53C12B
C/Genetics:
A/Gene: CESP:Y53C12B.3b
A/Map position: 2
A/Introns: 100/3; 177/3; 218/1; 423/3; 717/2; 867/3

Query Match 46.3%; Score 44; DB 2; Length 871;
Best Local Similarity 58.3%; Pred. No. 62;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
OY 1 PVYKVKPNPPH 12
||:|:|||||
Db 268 PVIOQRPPPH 279

RESULT 13
T07622
extensin homolog - soybean (fragment)
N/Alternate names: hydroxyproline-rich glycoprotein
C/Species: Glycine max (soybean)
C/Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 11-May-2000
C/Accession: T07622
R:Hong, J.C.; Cheong, Y.H.; Nagao, R.T.; Bahk, J.D.; Cho, M.J.; Key, J.L.
Plant Physiol 104, 793-796, 1994
A>Title: Isolation and characterization of three soybean extensin cDNAs.
A/Reference number: Z16058; MUID:94211912
A/Accession: T07622
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-199 <HON>
A/Cross-references: EMBL:L22029; NID:g347452; PTDN:AAA33970.1; PID:g347453
A/Experimental source: strain Wayne; seedling
C/Genetics:
A/Gene: HRGP3
C/Superfamily: hydroxyproline-rich glycoprotein
C/Keywords: glycoprotein; hydroxyproline

Query Match 45.8%; Score 43.5; DB 2; Length 199;
Best Local Similarity 75.0%; Pred. No. 14;
Matches 9; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
OY 1 PVYKVK-PNPPH 11
|||||:|||||
Db 131 PVYKXKSPPH 142

RESULT 14
S06675
apidaecin Ib precursor - honeybee
C/Species: Apis mellifera (honeybee)
C/Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 16-Dec-1998
C/Accession: S06675
R:Castels, P.; Ampe, C.; Jacobs, F.; Vaeck, M.; Tempst, P.
EMBO J 8, 2387-2391, 1989
A>Title: Apidaecins: antibacterial peptides from honeybees.
A/Reference number: S05383; MUID:90005446
A/Accession: S06675
A/Molecule type: protein
A/Residues: 1-26 <CAS>
F:1-8/Domain: propeptide #status experimental <PRO>
F:9-26/Product: apidaecin Ib #status experimental <MAT>

Query Match 45.3%; Score 43; DB 2; Length 26;
 Best Local Similarity 63.6%; Pred. No. 1.8;
 Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 PVYKKVKNPPH 11
 ||| : | |||
 Db 13 PVYIPQPRPPH 23

RESULT 15

S35331
 apidaecin 22 precursor - honeybee
 C:Species: Apis mellifera (honeybee)
 C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jul-2000
 C:Accession: S35331
 R:Casteels-Josson, K.; Capaci, T.; Casteels, P.; Tempst, P.
 EMBO J. 12, 1569-1578, 1993
 A:Title: Apidaecin multipetide precursor structure: a putative mechanism for amplificat
 A:Reference number: S35330; MUID:93223697
 A:Accession: S35331
 A>Status: Preliminary
 A:Molecule type: DNA
 A:Residues: 1-144 <CAS>
 A:Cross-references: EMBL:X72576; NID:9297064; PIDN:CAAS1168.1; PID:9297065
 C:Superfamily: procyclic acidic repetitive protein

Query Match 45.3%; Score 43; DB 2; Length 144;
 Best Local Similarity 63.6%; Pred. No. 12;
 Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 PVYKKVKNPPH 11
 ||| : | |||
 Db 47 PVYIPQPRPPH 57

Search completed: December 19, 2001, 16:22:42
 Job time: 462 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: December 19, 2001, 16:26:19 ; Search time 48.45 Seconds
(without alignments)
12.865 Million cell updates/sec

Title: US-09-202-104A-10
Perfect score: 95
Sequence: 1 PYKVKRPNPHNLVIN 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 3664827 residues
Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	95	100.0	918	1	IL6B_HUMAN
2	75	78.9	918	1	IL6B_RAT
3	68	71.6	917	1	IL6B_MOUSE
4	47	49.5	400	1	BC1B_HUMAN
5	47	49.5	400	1	BC1B_MOUSE
6	46	48.4	427	1	IL31_HUMAN
7	44	46.3	517	1	Y4QC_RHISN
8	44	46.3	626	1	NR43_HUMAN
9	43	45.3	144	1	AP22_APIME
10	43	45.3	168	1	AP14_APIME
11	43	45.3	283	1	AP73_APIME
12	43	45.3	363	1	ALF1_LAMIA
13	43	45.3	630	1	PRUR_OREN
14	43	45.3	2212	1	RRLR_EBOZM
15	43	45.3	2248	1	CVAL_HUMAN
16	42	44.2	540	1	PYRG_METYA
17	42	44.2	608	1	PRLR_MOUSE
18	42	44.2	610	1	PRLR_RAT
19	42	44.2	1187	1	YH2M_CAEL
20	41	43.2	17	1	AP1D_BOMPA
21	41	43.2	88	1	ORRC_HERAV
22	41	43.2	199	1	CRAD_HUMAN
23	41	43.2	199	1	CRAD_MOUSE
24	41	43.2	248	1	GRL1_RAT
25	41	43.2	285	1	HMD4_XENLA
26	41	43.2	490	1	YMC2_YEAST
27	41	43.2	805	1	UBP5_YEAST
28	41	43.2	1630	1	PRP1_DROME
29	40	42.1	192	1	YAG6_ECOLI
30	40	42.1	214	1	CYC2_PSEAE
31	40	42.1	248	1	NKP1_RAT
32	40	42.1	258	1	VGIL_GPCMY
33	40	42.1	273	1	MT1B_MORBO

34	40	42.1	286	1	CH36_DROME
35	40	42.1	293	1	CH36_DROVI
36	40	42.1	306	1	EXFN_DAUCA
37	40	42.1	320	1	CH36_CERCA
38	40	42.1	324	1	IL2B_PIG
39	40	42.1	327	1	IL2B_BOVIN
40	40	42.1	327	1	IL2B_CEREL
41	40	42.1	327	1	IL2B_MARMO
42	40	42.1	327	1	IL2B_SHEEP
43	40	42.1	328	1	IL2B_CERTO
44	40	42.1	328	1	IL2B_HUMAN
45	40	42.1	328	1	IL2B_MACMU

ALIGNMENTS

RESULT 1
ID IL6B_HUMAN STANDARD; PRT; 918 AA.
AC P40189; O9UQ41; 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE INTERLEUKIN-6 RECEPTOR BETA CHAIN PRECURSOR (IL-6R-BETA) (INTERLEUKIN
DE 6 SIGNAL TRANSDUCER) (MEMBRANE GLYCOPROTEIN 130) (GP130) (ONCOSTATIN M
DE RECEPTOR) (CDW130) (CD130 ANTIGEN).
GN IL6ST.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Myeloma, and Placenta;
RX MEDLINE=91084844; PubMed=2261637;
RA Hibi M., Murakami M., Saito M., Hirano T., Taga T., Kishimoto T.:
RT "Molecular cloning and expression of an IL-6 signal transducer,
RT gp130.";
RL Cell 63:1149-1157(1990).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Synovium;
RX PubMed=10880057;
RA Tanaka M., Kishimura M., Ozaki S., Osakada F., Hashimoto H., Okubo M.,
RA Murakami M., Nakao K.:
RT "Cloning of novel soluble gp130 and detection of its neutralizing
RT autoantibodies in rheumatoid arthritis.";
RL J. Clin. Invest. 106:137-144(2000).
RN [3]
RP PARTIAL SEQUENCE, DISULFIDE BONDS, AND CARBOHYDRATE-LINKAGE SITES.
RX PubMed=11098061;
RA Moritz R.L., Hall N.E., Connolly L.M., Simpson R.J.:
RT "Determination of the disulfide structure and N-glycosylation sites of
RT the extracellular domain of the human signal transducer gp130.";
RL J. Biol. Chem. 276:8244-8253(2001).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 122-325.
RX MEDLINE=98169383; PubMed=9501088;
RA Bravo J., Staunton D., Heath J.K., Jones E.Y.:
RT "Crystal structure of a cytokine-binding region of gp130.";
RL EMBO J. 17:1665-1674(1998).
CC -I- FUNCTION: SIGNAL-TRANSDUCING MOLECULE. THE RECEPTOR SYSTEMS FOR
CC IL-6, LIF, OSM, CNTF, IL-11 AND CT-1 CAN UTILIZE GP130 FOR
CC INITIATING SIGNAL TRANSMISSION. BINDS TO IL-6/IL-6-R (ALPHA CHAIN)
CC COMPLEX, RESULTING IN THE FORMATION OF HIGH-AFFINITY IL-6 BINDING
CC SITES, AND TRANSDUCES THE SIGNAL. DOES NOT BIND IL-6. MAY HAVE A
CC ROLE IN EMBRYONIC DEVELOPMENT (BY SIMILARITY).
CC -I- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
CC -I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (ISOFORM 1) AND
CC SECRETED (ISOFORM 2).
CC -I- ALTERNATIVE PRODUCTS: 2 ISOFORMS: 1 (SHOWN HERE) AND 2/GP130-
CC RAPS; ARE PRODUCED BY ALTERNATIVE SPLICING.

```
CC -1- TISSUE SPECIFICITY: FOUND IN ALL THE TISSUES AND CELL LINES.
CC EXAMINED EXPRESSION NOT RESTRICTED TO IL-6 RESPONSIVE CELLS.
CC -1- DISEASE: GP130-RAPS IS AN AUTOANTIGEN FOUND IN RHEUMATOID
CC ARTHRITIS (RA) BUT IT IS NOT SPECIFIC TO PATIENTS WITH RA.
CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC -1- SIMILARITY: CONTAINS 5 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -1- DATABASE: NAME=PROV; NOTE=CD guide CD130 entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd130.htm".
CC -----
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CC -----
DR EMBL; M57230; AAA59155.1; -.
DR EMBL; AB015706; BAA78112.1; -.
DR PIR; A36337; A36337.
DR PDB; 1BQJ; 26-AUG-98.
DR MIM; 600694; -.
DR InterPro; IPR002996; CR1A.
DR InterPro; IPR001777; FN_III.
DR InterPro; IPR003529; Hematopo_receptor_L_F2.
DR Pfam; PF00041; fn3_3.
DR PRINTS; PR00014; ENTPERTII.
DR SMART; SMO0060; FN3_3.
DR PROSITE; PS01353; HEMATOPO_REC_L_F2; 1.
KW Receptor; Transmembrane; Glycoprotein; Immunoglobulin domain; Signal;
KW Repeat; 3D-structure; Alternative splicing.
FT SIGNAL 1 22
FT CHAIN 23 918 INTERLEUKIN-6 RECEPTOR BETA CHAIN.
FT DOMAIN 23 619 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 620 641 POTENTIAL.
FT DOMAIN 642 918 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 26 120 IG-LIKE C2-TYPE DOMAIN.
FT DOMAIN 124 222 FIBRONECTIN TYPE-III 1.
FT DOMAIN 223 324 FIBRONECTIN TYPE-III 2.
FT DOMAIN 325 423 FIBRONECTIN TYPE-III 3.
FT DOMAIN 424 517 FIBRONECTIN TYPE-III 4.
FT DOMAIN 518 613 FIBRONECTIN TYPE-III 5.
FT DOMAIN 725 755 SER-RICH.
FT DISULFID 28 54
FT DISULFID 48 103
FT DISULFID 134 144
FT DISULFID 172 182
FT DISULFID 458 466
FT CARBOHYD 43 43 N-LINKED (GLCNAC. . .)
FT CARBOHYD 83 83 N-LINKED (GLCNAC. . .)
FT CARBOHYD 131 131 N-LINKED (GLCNAC. . .)
FT CARBOHYD 157 157 N-LINKED (GLCNAC. . .)
FT CARBOHYD 227 227 N-LINKED (GLCNAC. . .)
FT CARBOHYD 379 379 N-LINKED (GLCNAC. . .)
FT CARBOHYD 383 383 N-LINKED (GLCNAC. . .)
FT CARBOHYD 553 553 N-LINKED (GLCNAC. . .)
FT CARBOHYD 564 564 N-LINKED (GLCNAC. . .)
FT VASAPLIC 325 329 RPSVA -> NIASF (IN GP130-RAPS).
FT VASAPLIC 330 918 MISSING (IN GP130-RAPS).
SQ SEQUENCE 918 AA; 103522 MW; D813F3672DD10D53 CRC64;
```

ID	IL6B_RAT	STANDARD;	PRT;	918 AA.
AC	IL6B_RAT			
AD	P40130;			
DT	01-FEB-1995 (Rel. 31, Created)			
DT	01-FEB-1995 (Rel. 31, Last sequence update)			
DT	20-AUG-2001 (Rel. 40, Last annotation update)			
DE	INTERLEUKIN-6 RECEPTOR BETA CHAIN PRECURSOR (IL-6R-BETA) (INTERLEUKIN-6 SIGNAL TRANSDUCER) (MEMBRANE GLYCOPROTEIN 130) (GP130).			
CN	IL6B7.			
OS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
OX	NCBI_TaxId=10116;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Liver;			
RX	MEDLINE=93052397; PubMed=1427893;			
RA	Wang Y., Nesbitt J.E., Fuentes N.L., Fuller G.M.;			
RT	"Molecular cloning and characterization of the rat liver IL-6 signal transducing molecule, gp130.";			
RL	Genomics 14:666-672(1992).			
CC	-1- FUNCTION: SIGNAL-TRANSDUCING MOLECULE. THE RECEPTOR SYSTEMS FOR IL-6, LIF, OSM, CNTF, AND IL-11 CAN UTILIZE GP130 FOR INITIATING SIGNAL TRANSMISSION. BINDS TO IL-6/IL-6-R (ALPHA CHAIN) COMPLEX, RESULTING IN THE FORMATION OF HIGH-AFFINITY IL-6 BINDING SITES, AND TRANSDUCES THE SIGNAL. DOES NOT BIND IL-6. MAY HAVE A ROLE IN EMBRYONIC DEVELOPMENT (BT SIMILARITY).			
CC	-1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.			
CC	-1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.			
CC	-1- TISSUE SPECIFICITY: FOUND IN HEPATOCYTES, ASTROCYTES, FIBROBLASTS, AND ENDOTHELIAL CELLS.			
CC	-1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.			
CC	-1- SIMILARITY: CONTAINS 5 FIBRONECTIN TYPE III-LIKE DOMAINS.			
CC	-1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.			
CC	-----			
CC	This SWISS-PROT entry is copyrighted. It is produced through a collabor between the Swiss Institute of Bioinformatics and the EMBL outstitch the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commen entities requires a license agreement (See http://www.isb-sdb.ch/anno or send an email to license@isb-sdb.ch).			
CC	-----			
DR	EMBL; M92340; -, NOT_ANNOTATED_CDS.			
DR	PIR; A44257; A44257.			
DR	HSSP; P40189; IBOU.			
DR	InterPro; IPR002996; CRIA.			
DR	InterPro; IPR001777; FN.III.			
DR	InterPro; IPR003529; Hematopo_receptor_L_F2.			
DR	Pfam; PF00041; FN3_3.			
DR	SMART; SM00060; FN3_3.			
DR	PROSITE; PS01353; HEMATOPO_REC_L_F2; 1.			
KW	Receptor; Transmembrane; Glycoprotein; Immunoglobulin domain; Signal;			
KW	Repeat.			
FT	SIGNAL	1	22	POTENTIAL.
FT	CHAIN	23	918	INTERLEUKIN-6 RECEPTOR BETA CHAIN.
FT	DOMAIN	23	618	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	619	640	POTENTIAL.
FT	DOMAIN	641	918	CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	26	120	IG-LIKE C2-TYPE DOMAIN.
FT	DOMAIN	124	221	FIBRONECTIN TYPE-III 1.
FT	DOMAIN	222	323	FIBRONECTIN TYPE-III 2.
FT	DOMAIN	324	422	FIBRONECTIN TYPE-III 3.
FT	DOMAIN	423	516	FIBRONECTIN TYPE-III 4.
FT	DOMAIN	517	612	FIBRONECTIN TYPE-III 5.
FT	DOMAIN	724	754	SER-RICH
FT	DISULEID	28	54	BY SIMILARITY.
FT	DISULEID	48	103	BY SIMILARITY.
FT	DISULEID	134	144	BY SIMILARITY.
FT	DISULEID	172	181	BY SIMILARITY.
FT	DISULEID	457	465	BY SIMILARITY.
FT	CARBOHYD	43	43	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	61	61	N-LINKED (GLCNAC. . .) (POTENTIAL).

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FT CARBOHYD 83 83 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 131 131 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 157 157 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 205 205 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 226 226 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 382 382 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 389 389 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 477 477 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 552 552 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 918 AA; 102450 MW; 9E18B6FECF087F7 CRC64;

Query Match 78.9%; Score 75; DB 1; Length 918;
Best Local Similarity 82.4%; Pred. No. 0.00034;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 PYKVKPNPPHNLSTVN 17
Db 215 PYDKVFPSPHNLSTVN 231

RESULT 3
ID IL6B_MOUSE STANDARD; PRT; 917 AA.
AC 000560;
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE 6 SIGNAL TRANSDUCER (MEMBRANE GLYCOPROTEIN 130) (GP130).
GN IL6ST.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ICR; TISSUE=Macrophage;
RX MEDLINE=92291532; PubMed=1602143;
RA Saito M., Yoshida K., Hibi M., Taga T., Kishimoto T.;
RT "Molecular cloning of a murine IL-6 receptor-associated signal
transducer, gp130, and its regulated expression in vivo.";
RL J. Immunol. 148:4066-4071(1992).
CC -1- FUNCTION: SIGNAL-TRANSDUCING MOLECULE. THE RECEPTOR SYSTEMS FOR
IL-6, LIF, OSF, CNTF, AND IL-11 CAN UTILIZE GP130 FOR INITIATING
SIGNAL TRANSMISSION. BINDS TO IL-6/IL-6-R (ALPHA CHAIN) COMPLEX,
RESULTING IN THE FORMATION OF HIGH-AFFINITY IL-6 BINDING SITES,
AND TRANSDUCES THE SIGNAL. DOES NOT BIND IL-6. MAY HAVE A ROLE IN
EMBRYONIC DEVELOPMENT.
CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
CC -1- TISSUE SPECIFICITY: FOUND IN TISSUES SUCH AS BRAIN, HEART, THYMUS,
SPLEEN, KIDNEY, LUNG AND LIVER. FOUND IN ALL THE CELL LINES TESTED
EXCEPT BAF-B03. EXPRESSION NOT RESTRICTED TO IL-6-RESPONSIVE
CELLS.
CC -1- DEVELOPMENTAL STAGE: IN EMBRYONIC STEM CELLS IT IS FOUND FROM DAY
6 OF GESTATION. IT REACHES A PEAK ON DAY 8 AND GRADUALLY DECLINES
DURING THE REST OF EMBRYOGENESIS.
CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC -1- SIMILARITY: CONTAINS 5 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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or send an email to license@sib-sib.ch).
CC -----
CC EMBL: X62646; CAA44515.1; -
CC EMBL: M83336; AAA37723.1; -
CC HSSP: P40189; 1BDU.

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DR MGD; MG1:96560; 116st.
DR InterPro: IPR002996; CRA1.
DR InterPro: IPR001777; FN_III.
DR InterPro: IPR003529; Hematopo_receptor_L_F2.
DR Pfam: PF00041; fn3; 4.
DR PRINTS: PR00014; FNTYPEIII.
DR SMART: SM00060; FN3; 2.
DR PROSITE: PS01353; HEMATOPO_REC_L_F2; 1.
DR Receptor; Transmembrane; Glycoprotein; Immunoglobulin domain; signal;
KW Repeat.
FT SIGNAL 1 22
FT CHAIN 23 917
FT DOMAIN 23 617
FT TRANSMEM 618 639
FT DOMAIN 640 917
FT DOMAIN 26 120
FT DOMAIN 124 220
FT DOMAIN 323 322
FT DOMAIN 422 515
FT DOMAIN 516 611
FT DOMAIN 723 741
FT DISULFID 28 54
FT DISULFID 48 103
FT DISULFID 134 144
FT DISULFID 172 180
FT DISULFID 456 464
FT CARBOHYD 43 43
FT CARBOHYD 61 61
FT CARBOHYD 83 83
FT CARBOHYD 131 131
FT CARBOHYD 157 157
FT CARBOHYD 225 225
FT CARBOHYD 388 388
FT CARBOHYD 476 476
FT CARBOHYD 551 551
SQ SEQUENCE 917 AA; 102452 MW; FCEFD220BC2466F4 CRC64;

Query Match 71.6%; Score 68; DB 1; Length 917;
Best Local Similarity 76.5%; Pred. No. 0.0043;
Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 PYKVKPNPPHNLSTVN 17
Db 214 PYDKVFPSPHNLSTVN 230

RESULT 4
ID BG1B_HUMAN STANDARD; PRT; 400 AA.
AC 006430;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE N-ACETYLGLUCOSAMINIDE BETA-1,6-N-ACETYLGLUCOSAMINYLTRANSFERASE
DE (EC 2.4.1.150) (N-ACETYLGLUCOSAMINYLTRANSFERASE) (I-BRANCHING ENZYME)
DE (IGNT).
GN GCNT2 OR II.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93194065; PubMed=8449405;
RA Bieriuten M.F.A., Mattel M.-G., Fukuda M.;
RT "Expression of the developmental I antigen by a cloned human cDNA
encoding a member of a beta-1,6-N-acetylglucosaminyltransferase gene
family.";
RL Genes Dev. 7:468-478(1993).
RN [2]
RP SEQUENCE FROM N.A.

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RC		TISSUE-Placenta; PubMed=759796;
RA	MEDLINE=96078409;	
RA	Bierhuizen M.F.A., Maemura K., Kudo S., Fukuda M. ;	
RT	"Genomic organization of core 2 and I branching beta-1,6-N-	
RT	acetylglucosaminyltransferases. Implication for evolution of the	
RT	beta-1,6-N-acetylglucosaminyltransferase gene family."	
RL	Glycobiology 5:417-425(1995).	
RN	[3]	
RP	TISSUE SPECIFICITY.	
RX	MEDLINE=96070745; Pubmed=9405606;	
RA	Sasaki K., Kurata-Mura K., Ujita M., Angata K., Nakagawa S.,	
RA	Sekine S., Nishi T., Fukuda M. ;	
RT	"Expression cloning of cDNA encoding a human beta-1,3-N-	
RT	acetylglucosaminyltransferase that is essential for poly-N-	
RT	acetylglucosamine synthesis."	
RL	Proc. Natl. Acad. Sci. U.S.A. 94:14294-14299(1997).	
CC	-I- FUNCTION: BRANCHING ENZYME THAT CONVERTS LINEAR INTO BRANCHED	
CC	POLY-N-ACETYLGLUCOSAMINOGLYCANS. INTRODUCES THE BLOOD GROUP I	
CC	ANTIGEN DURING EMBRYONIC DEVELOPMENT. IT IS CLOSELY ASSOCIATED	
CC	WITH THE DEVELOPMENT AND MATURATION OF ERYTHROID CELLS.	
CC	-I- CATALYTIC ACTIVITY: UDP-N-ACETYL-D-GLUCOSAMINE + BETA-D-GALACTOSYL	
CC	-1,4-N-ACETYL-D-GLUCOSAMINYL-R -> UDP + N-ACETYL-BETA-D-	
CC	GLUCOSAMINYL-1,6-BETA-D-GALACTOSYL-1,4-N-ACETYL-D-GLUCOSAMINYL-R.	
CC	-I- PATHWAY: GLYCOSTYLATION.	
CC	-I- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. GOLGI.	
CC	-I- TISSUE SPECIFICITY: IN THE ADULT, HIGHLY EXPRESSED IN PROSTATE AND	
CC	TO A LESSER EXTENT IN SMALL INTESTINE AND COLON. BARLEY DETECTED	
CC	IN HEART, BRAIN, KIDNEY AND PANCREAS. NO EXPRESSION IN PLACENTA,	
CC	LUNG, LIVER, SKELETAL MUSCLE, SPLEEN, THYMUS, TESTIS, OVARY AND	
CC	PERIPHERAL BLOOD LEUKOCYTES. IN FETUS, HIGHLY EXPRESSED IN BRAIN	
CC	AND TO A LESSER EXTENT IN LUNG AND KIDNEY. BARELY DETECTED IN	
CC	LIVER.	
CC	-I- DEVELOPMENTAL STAGE: ITS EXPRESSION INCREASES DRAMATICALLY DURING	
CC	DEVELOPMENT AND ONCOGENESIS.	
CC	-I- SIMILARITY: TO CORE 2 BRANCHING ENZYME (C2GNT).	
CC	-----	
CC	THIS SWISS-PROT entry is copyright. It is produced through a collaboration	
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/	
CC	or send an email to license@isb-sib.ch).	
CC	-----	
DR	EMBL: L19659; AAA81777.1; .	
DR	EMBL: Z19550; CAAT9610.1; .	
DR	EMBL: L41607; AAA99832.1; .	
DR	EMBL: L41605; AAA99832.1; JOINED.	
DR	EMBL: L41606; AAA99832.1; JOINED.	
DR	PIR: A46297; A46297.	
DR	MIM: 600429; .	
DR	MIM: 110800; .	
DR	InterPro: IPRO03406; Branch.	
DR	Pfam: PF02485; Branch; 1.	
KW	Transferase; Glycosyltransferase; Transmembrane; Signal-anchor;	
FT	GOlg stack; Glycoprotein.	
FT	DOMAIN 1	
FT	TRANSEM 7 25	
FT	TRANSMEM 6	
FT	CYTOPLASMIC (POTENTIAL).	
FT	SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)	
FT	(POTENTIAL).	
FT	DOMAIN 26 400	
FT	CARBHYD 37 37	
FT	CARBHYD 255 255	
FT	CARBHYD 314 314	
FT	CARBHYD 388 388	
FO	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FO	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FO	SEQUENCE 400 AA: 45654 MW: 1469628650A1F43B CCK64;	

Dn	248	LKPPPHNLUT1	258
RESULT	5		
BGIB-MOUSE			
ID	BGIB-MOUSE	STANDARD:	FRT: 400 AA.
AC	P97402;		
DT	15-JUL-1999 (Rel. 38, Created)		
DT	15-JUL-1999 (Rel. 38, Last sequence update)		
DT	15-JUL-1999 (Rel. 38, Last annotation update)		
DE	N-ACEYLGLUCOSAMINIDE BETA-1,6-N-ACEYLGLUCOSAMINYLTRANSFERASE		
DE	(EC 2.4.1.150) (N-ACEYLGLUCOSAMINYLTRANSFERASE) (I-BRANCHING ENZYME)		
DE	(ICNT) (LARGE I ANTIGEN-FORMING BETA-1,6-N-		
DE	ACEYLGLUCOSAMINYLTRANSFERASE).		
GN	GCONT2..		
OS	Mus musculus (Mouse).		
OC	Eumetazoa; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TaxID:10090;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE-97280061; Pubmed-9134435;		
RA	Magnet A.D., Fukuda M.;		
RT	"Expression of the large I antigen forming beta-1,6-N-		
RT	acetylglucosaminyltransferase in various tissues of adult mice.";		
RL	Glycobiology 7:285-295(1997).		
CC	-1- FUNCTION: BRANCHING ENZYME THAT CONVERTS LINEAR INTO BRANCHED		
CC	POLY-N-ACEYLGLUCOSAMINOGLYCANS. INTRODUCES THE BLOOD GROUP I		
CC	ANTIGEN DURING EMBRYONIC DEVELOPMENT. IT IS CLOSELY ASSOCIATED		
CC	WITH THE DEVELOPMENT AND MATURATION OF ERYTHROID CELLS.		
CC	-1- CATALYTIC ACTIVITY: UDP-N-ACETYL-D-GLUCOSAMINE + BETA-D-GALACTOSYL		
CC	-1,4-N-ACETYL-D-GLUCOSAMINYLR -> UDP + N-ACETYL-BETA-D-		
CC	GLUCOSAMINYLR-1,6-BETA-D-GALACTOSYL-1,4-N-ACETYL-D-GLUCOSAMINYLR.		
CC	-1- PATHWAY: GLYCOSYLATION		
CC	-1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. GOLGI.		
CC	-1- SIMILARITY: TO CORE 2 BRANCHING ENZYME (C2GNT).		
CC			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration		
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CC	use by non-profit institutions as long as its content is in no way		
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/		
CC	or send an email to license@isb-sib.ch).		
CC	-----		
DR	EMBL; D08182; AAB39621.1; -		
DR	MGD; MG1:1100870; Gcont2.		
DR	InterPro; IPRO03406; Branch.		
KM	Pfam; PF02485; Branch; 1.		
KW	Transferase; Glycosyltransferase; Transmembrane; Signal-anchor;		
KW	Golgi stack; Glycoprotein.		
FT	DOMAIN	1	6
FT	TRANSMEM	7	25
FT			CYTOPLASMIC (POTENTIAL)
FT			SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT	DOMAIN	26	400
FT	CARBOHYD	37	
FT	CARBOHYD	255	
FT	CARBOHYD	314	
FT	CARBOHYD	388	
SO	SEQUENCE	400 AA;	45507 MW;
			193FE3882E3B5691 CRC64;
Query Match	Best Local Similarity	49.5%;	Score 47; DB 1; Length 400;
Matches	7; Conservative	3; Mismatches	1; Indels 0; Gaps 0;

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5 VKPNPPhNLsv 15
:| | | | | :
QY

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RESULT 6
I131_HUMAN

ID 1131 HUMAN STANDARD: PRT: 427 AA.
AC P78552: 099656; 095646;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE INTERLEUKIN-13 RECEPTOR ALPHA-1 CHAIN PRECURSOR (IL-13R-ALPHA-1) (IL-13RA-1).
GN IL13RA1 OR IL13RA OR IL13R.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Carcinoma;
RX MEDLINE=97165986; PubMed=9013879;
RA Miloux B., Laurent P., Bonnin O., Lampker J., Caput D., Vita N., Ferrara P.;
RT "Cloning of the human IL-13R alpha chain and reconstruction with the ILR alpha of a functional IL-4/IL-13 receptor complex.";
RL FEBS Lett. 401:163-166(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=B-cell;
RA Gauchat J.F.M., Schlagenhaut E., Peng N.P., Moser R., Yamage M., Jeannin P., Alouani S., Elson G., Nolarangelo L.D., Wells T., Eugster H.P., Bonnefoy J.Y.;
RL Submitted (Jan-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=T-cell;
RX MEDLINE=97067184; PubMed=8910586;
RA Amen N.J., Tayebi N., Odiri N.I., Puri R.K., Modi W.S., Leonard W.J.;
RT "CDNA cloning and characterization of the human interleukin 13 receptor alpha chain.";
RL J. Biol. Chem. 271:29265-29270(1996).
RN [4]
RP SEQUENCE FROM N.A.
RX Wada M., Hisano T., Kuwano M.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: BINDS IL-13 WITH A LOW AFFINITY. TOGETHER WITH IL-4R-ALPHA CAN FORM A FUNCTIONAL RECEPTOR FOR IL-13. ALSO SERVES AS AN ALTERNATE ACCESSORY PROTEIN TO THE COMMON CYTOKINE RECEPTOR GAMMA CHAIN FOR IL-4 SIGNALING, BUT CANNOT REPLACE THE FUNCTION OF GAMMA-C IN ALLOWING ENHANCED IL-2 BINDING ACTIVITY.
CC -1- SUBUNIT: INTERLEUKIN-13 RECEPTOR IS A COMPLEX OF IL4R-ALPHA, IL13R-ALPHA, AND POSSIBLY OTHER COMPONENTS.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: UBIQUITOUS. HIGHEST LEVELS IN HEART, LIVER, SKELETAL MUSCLE AND OVARY; LOWEST LEVELS IN BRAIN, LUNG AND KIDNEY. ALSO FOUND IN B-CELLS, T-CELLS AND ENDOTHELIAL CELLS.
CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -----
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CC -----
CC EMBL: Y10659; CAA71669.1; -;
DR EMBL: Y09328; CAA70508.1; -;
DR EMBL: U62858; AAB37127.1; -;
DR EMBL: U81379; AAD00510.3; -;
DR HSP: P31785; IILN.
DR MIM: 300119; -;
DR InterPro: IPR002996; CR1A.
DR InterPro: IPR001777; FN_III.
DR InterPro: IPR003532; Hematopo_rptor_S_F2.

DR Pfam: PF00041; fn3; 1.
DR PROSITE: PS01356; HEMATOPO_REC_S_F2; 1.
KW Receptor; Transmembrane; Glycoprotein; Immunoglobulin domain; Signal.
FT SIGNAL 1 21
FT CHAIN 22 427
FT DOMAIN 22 343
FT TRANSMEM 344 367
FT DOMAIN 368 427
FT DOMAIN 39 102
FT DISULFID 46 95
FT DISULFID 134 144
FT DISULFID 173 185
FT CARBOHYD 37 37
FT CARBOHYD 61 61
FT CARBOHYD 105 105
FT CARBOHYD 138 138
FT CARBOHYD 157 157
FT CARBOHYD 235 235
FT CARBOHYD 265 265
FT CARBOHYD 293 293
FT CARBOHYD 329 329
FT CARBOHYD 341 341
FT CONFLICT 130 130
FT CONFLICT 358 358
SQ SEQUENCE 427 AA; 48759 MW; 5983B3BE8F554107B CRC64;

Query Match 48.4%; Score 46; DB 1; Length 427;
Best Local Similarity 62.5%; Pred. No. 5.7;
Matches 10; Conservative 2; Mismatches 2; Indels 2; Gaps 1;

OY 4 KYKPNPPH--NLSVIN 17
:||||| | | | |
DB 225 RVPDPPIHKISFHN 240

RESULT 7
YACC_RHISN STANDARD: PRT: 517 AA.
AC P53585;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE HYPOTHETICAL 57.8 KDA PROTEIN YACC.
GN YACC.
OS Rhizobium sp. (strain NGR234).
OC Plasmid sym pNGR234a.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Rhizobiaceae; Rhizobium.
OX NCBI_TaxID=394;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97305956; PubMed=9163424;
RA Freilberg C.A., Fellay R., Bairoch A., Broughton W.J., Rosenthal A., Perret X.;
RT "Molecular basis of symbiosis between Rhizobium and legumes.";
RL Nature 387:394-401(1997).
CC -1- SIMILARITY: NONE OBVIOUS.
CC -----
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CC -----
CC EMBL: AE000067; AAB91633.1; -;
KW Hypothetical protein; Plasmid.
SQ SEQUENCE 517 AA; 57803 MW; F6F375F9F8621124 CRC64;

Query Match 46.3%; Score 44; DB 1; Length 517;

or send an email to license@isb-sib.ch.

CC EMBL: X72576; CAAS1168.1; -
DR PIR: S05383; S05383.
DR PIR: S06675; S06675.
DR PIR: S35331; S35331.
DR InterPro: IPR001979; Apidaecin.
DR Pfam: PF00807; Apidaecin.
KM Insect immunity; Antibiotic; Hemolymph; Signal; Multigene family;
KW Cleavage on pair of basic residues; Repeat.
FT SIGNAL 1 19 POTENTIAL.
FT PROPEP 35 42 APIDAEIN IB.
FT PEPTIDE 43 60
FT PROPEP 63 70
FT PEPTIDE 71 88 APIDAEIN IB.
FT PROPEP 91 98
FT PEPTIDE 99 116 APIDAEIN IB.
FT PROPEP 119 126
FT PEPTIDE 127 144
SQ SEQUENCE 144 AA; 16539 MW; 6FA1AD74CB77108D CRC64;

Query Match 45.3%; Score 43; DB 1; Length 144;
Best Local Similarity 63.6%; Pred. No. 5.3;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 PYKYKPNPPH 11
DB 47 PYIPOPMPPH 57
111 :111

RESULT 10
AP14.APIME STANDARD; PRT; 168 AA.
ID AP14.APIME P11525; P11526; P11527;
AC Q06601; P11525; P11526; P11527;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE APIDAEIN PRECURSOR, TYPE 14.
GN APID14.
OS Apis mellifera (Honeybee).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Apocrita; Aculeata;
OC Apoidea; Apidae; Apis.
OX NCBI_TaxID=7460;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93223697; PubMed=8467807;
RA Casteels-Josson K., Capaci T., Casteels P., Tempst P.;
RT "Apidaecin multipetide precursor structure: a putative mechanism for
amplification of the insect antibacterial response.";
RL EMBL J. 12:1569-1578(1993).
RN [2]
RP SEQUENCE OF APIDAEIN IA/IB/II.
RC TISSUE=Hemolymph;
RX MEDLINE=90005446; PubMed=2676519;
RA Casteels P., Ampe C., Jacobs F., Vaeck M., Tempst P.;
RT "Apidaecins: antibacterial peptides from honeybees.";
RL EMBL J. 8:2387-2391(1989).
CC -1- FUNCTION: APIDAEIN HAVE BACTERICIDAL ACTIVITY; PREDOMINANTLY
AGAINST GRAM-NEGATIVE BACTERIA. THEY SEEM TO INTERFERE WITH CELL
PROLIFERATION.
CC
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CC or send an email to license@isb-sib.ch).
CC
DR EMBL: X72575; CAAS1167.1; -
DR PIR: S05383; S05383.

PIR: S06675; S06675.
DR PIR: S06676; S06676.
DR PIR: S35330; S35330.
DR InterPro: IPR001979; Apidaecin.
DR Pfam: PF00807; Apidaecin; 5.
DR ProDom: PD153432; Apidaecin; 1.
KM Insect immunity; Antibiotic; Hemolymph; Signal; Multigene family;
KW Cleavage on pair of basic residues; Repeat.
FT SIGNAL 1 19 POTENTIAL.
FT PROPEP 35 42 APIDAEIN II.
FT PEPTIDE 43 60
FT PROPEP 63 70 APIDAEIN II.
FT PEPTIDE 71 88
FT PROPEP 91 98
FT PEPTIDE 99 116 APIDAEIN IB.
FT PROPEP 119 124
FT PEPTIDE 125 142 APIDAEIN IB.
FT PROPEP 145 150
FT PEPTIDE 151 168
SQ SEQUENCE 168 AA; 19380 MW; 594B931254C0A37 CRC64;

Query Match 45.3%; Score 43; DB 1; Length 168;
Best Local Similarity 63.6%; Pred. No. 6.2;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 PYKYKPNPPH 11
DB 103 PYIPOPMPPH 113
111 :111

RESULT 11
AP13.APIME STANDARD; PRT; 283 AA.
ID AP13.APIME P11525; P11526;
AC Q06602; P11525; P11526;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE APIDAEIN PRECURSOR, TYPE 73 (FRAGMENT).
GN APID73.
OS Apis mellifera (Honeybee).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Apocrita; Aculeata;
OC Apoidea; Apidae; Apis.
OX NCBI_TaxID=7460;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93223697; PubMed=8467807;
RA Casteels-Josson K., Capaci T., Casteels P., Tempst P.;
RT "Apidaecin multipetide precursor structure: a putative mechanism for
amplification of the insect antibacterial response.";
RL EMBL J. 12:1569-1578(1993).
RN [2]
RP SEQUENCE OF APIDAEIN IA/IB.
RC TISSUE=Hemolymph;
RX MEDLINE=90005446; PubMed=2676519;
RA Casteels P., Ampe C., Jacobs F., Vaeck M., Tempst P.;
RT "Apidaecins: antibacterial peptides from honeybees.";
RL EMBL J. 8:2387-2391(1989).
CC -1- FUNCTION: APIDAEIN HAVE BACTERICIDAL ACTIVITY; PREDOMINANTLY
AGAINST GRAM-NEGATIVE BACTERIA. THEY SEEM TO INTERFERE WITH CELL
PROLIFERATION.
CC
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CC
DR EMBL: X72577; CAAS1169.1; -
DR PIR: S05383; S05383.

DR PIR; S06675; S06675.
 DR PIR; S35332; S35332.
 DR InterPro: IPR001979; Apidaecin.
 DR Pfam: PF00807; Apidaecin; 9.
 DR Prodom: PD153432; Apidaecin; 2.
 DR Insect Immunity; Antibiotic; Hemolymph; Signal; Multigene family;
 DR Cleavage on pair of basic residues; Repeat.
 KW NON_TER 1
 FT SIGNAL <1 18 POTENTIAL.
 FT PROPEP 34 41
 FT PEPTIDE 42 59 APIDAEICIN IB.
 FT PROPEP 62 69
 FT PEPTIDE 70 87 APIDAEICIN IB.
 FT PROPEP 90 97
 FT PEPTIDE 98 115 APIDAEICIN.
 FT PROPEP 118 125
 FT PEPTIDE 126 143 APIDAEICIN IB.
 FT PROPEP 146 153
 FT PEPTIDE 154 171 APIDAEICIN.
 FT PROPEP 174 182
 FT PEPTIDE 183 199 APIDAEICIN IB.
 FT PROPEP 202 209
 FT PEPTIDE 210 227 APIDAEICIN IB.
 FT PROPEP 230 237
 FT PEPTIDE 238 255 APIDAEICIN IB.
 FT PROPEP 258 265
 FT PEPTIDE 266 283 APIDAEICIN IA.
 SQ SEQUENCE 283 AA; 32695 MW; 4EA5FEDCDE5E142B CRC64;

Query Match 45.3%; Score 43; DB 1; Length 283;
 Best Local Similarity 63.6%; Pred. No. 11;
 Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 PVYKVPKPPH 11
 |||:|||||
 DB 46 PVYIPQPPRH 56

RESULT 12
 ALFL1AMJA STANDARD; PRT: 363 AA.
 AC P53445; 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-MAY-2000 (Rel. 39, Last annotation update)
 DE FRUCTOSE-BISPHOSPHATE ALDOLASE, MUSCLE TYPE (EC 4.1.2.13).
 OS Lampetra japonica (Japanese lamprey) (Phlebotomus japonicus).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
 OC Petromyzontiformes; Petromyzontidae; Lampetra.
 NCBI_Taxid=7749;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95355304; PubMed=7629020;
 RA Zhang R., Yatsuki H., Kusakabe T., Iwabe N., Miyata T., Imai T.,
 RA Yoshida M., Hori K.;
 RT "Structures of cDNAs encoding the muscle-type and non-muscle-type
 RT isozymes of lamprey fructose biphosphate aldolases and the evolution
 RT of aldolase genes.";
 RL J. Biochem. 117:545-553(1995).
 CC -1- CATALYTIC ACTIVITY: D-FRUCTOSE 1,6-BISPHOSPHATE - GLYCERONE-
 CC PHOSPHATE + D-GLYCERALDEHYDE 3-PHOSPHATE.
 CC -1- PATHWAY: SIXTH STEP IN GLYCOLYSIS.
 CC -1- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
 CC -1- TISSUE SPECIFICITY: EXPRESSED MAINLY IN THE SKELETAL MUSCLE, HEART
 CC MUSCLE, BRAIN, AND SOME OTHER TISSUES, BUT PROBABLY NOT IN LIVER.
 CC -1- SIMILARITY: BELONGS TO CLASS I FRUCTOSE-BISPHOSPHATE ALDOLASE
 CC FAMILY.
 CC -----
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 CC -----
 DR EMBL; D38620; BAA07608.1; -
 DR HSSP; P04075; 1ALD.
 DR InterPro: IPR000741; Aldolase-I.
 DR Pfam: PF00274; glycolytic-enz; 1.
 DR Prodom: PD001128; Aldolase-I; 1.
 DR PROSITE: PS00158; Aldolase-CLASS I; 1.
 KW lysase; Schiff base; Glycolysis; Multigene family.
 FT BINDING 56 56 C-1-PHOSPHATE GROUP OF THE SUBSTRATE
 FT BINDING 147 147 (BY SIMILARITY).
 FT BINDING 230 230 C-1-PHOSPHATE GROUP OF THE SUBSTRATE
 FT BINDING 230 230 (BY SIMILARITY).
 FT ACT_SITE 363 363 SCHIFF-BASE WITH DIHYDROXYACETONE-P
 FT ACT_SITE 363 363 (BY SIMILARITY).
 FT ACT_SITE 363 363 ESSENTIAL FOR ENHANCED ACTIVITY OF THE
 FT ACT_SITE 363 363 ENZYME TOWARD FRUCTOSE 1,6-BISPHOSPHATE
 FT ACT_SITE 363 363 AS COMPARED WITH FRUCTOSE 1-PHOSPHATE.
 SQ SEQUENCE 363 AA; 39239 MW; 15BC9A0A7FB9EFC CRC64;

Query Match 45.3%; Score 43; DB 1; Length 363;
 Best Local Similarity 46.7%; Pred. No. 14;
 Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

OY 2 VYKVPKPPHLSVI 16
 |||:|||||
 DB 151 VLKISPNTPSRLSIV 165

RESULT 13
 PRLR_ORENI STANDARD; PRT: 630 AA.
 AC Q91513; 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE PROLACTIN RECEPTOR PRECURSOR (PRL-R).
 GN PRLR.
 OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorphia; Acanthopterygii; Perciformes; Labroidae;
 CC Clariidae; Oreochromis.
 NCBI_Taxid=8128;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Kidney;
 RX MEDLINE=95320210; PubMed=7597076;
 RA Sandra O., Scham F., de lauze A., Prunet P., Edery M., Kelly P.A.;
 RT "Expression cloning of a cDNA encoding a fish prolactin receptor.";
 RL Proc. Natl. Acad. Sci. U.S.A. 92:6037-6041(1995).
 CC -1- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
 CC PROLACTIN.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 CC -1- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC -----
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 CC -----
 CC EMBL; L34783; AAA98997.1; -
 DR HSSP; P16471; 1BP3.
 DR InterPro: IPR002996; CRLA.
 DR InterPro: IPR001777; FN_III.
 DR InterPro: IPR003528; Hematopo_rcp_for_L_FL1.

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DR Pfam: PF00041; fn3; 2.
DR SMART: SMO0060; FN3; 2.
DR PROSITE: PS01352; HEMATOPO. REC. L.F1; 1.
KM Receptor: Transmembrane; Glycoprotein; signal; Repeat.
FT SIGNAL 1 23
FT CHAIN 24 630
FT DOMAIN 24 234 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 235 258 POTENTIAL.
FT DOMAIN 259 630 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 124 123 FIBRONECTIN TYPE-III 1.
FT DOMAIN 124 228 FIBRONECTIN TYPE-III 2.
FT DISULFID 37 47 BY SIMILARITY.
FT DISULFID 76 87 BY SIMILARITY.
FT CARBOHYD 92 92 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 101 101 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 630 AA: 70810 MM; A451563F3D12979D CRC64;

Query Match
Best Local Similarity 45.3%; Score 43; DB 1; Length 630;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 VYKVKPNPHNLV 15
DB 123 VYVOPHPPEKLEV 136

RESULT 14
RRPL_EBOZM STANDARD; PRT; 2212 AA.
AC 005318; 039794;
DT 01-FEB-1994 (rel. 28, Created)
DT 30-MAY-2000 (rel. 39, Last sequence update)
DT 30-MAY-2000 (rel. 39, Last annotation update)
DE RNA-DIRECTED RNA POLYMERASE (EC 2.7.7.48) (LARGE STRUCTURAL PROTEIN)
DE (L PROTEIN).
GN L.
OS Ebola virus (strain Zaire Mayinga) (Ebo).
OC Viruses; ssRNA negative-strand viruses; Mononegavirales; Filoviridae;
OC Filovirus.
OX NCB1_TaxID-128952;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-99171703; PubMed-10073695;
RA Volchikov V.E., Volchkova V.A., Chepurinov A.A., Blinov V.M.,
RA Netesov S.V., Feldmann H.;
RT "Characterization of the L gene and 5' trailer region of Ebola
RT virus.";
RL J. Gen. Virol. 80:355-362(1999).
RN [2]
RP SEQUENCE OF 1-54 FROM N.A.
RX MEDLINE-94055391; PubMed-8237108;
RA Sanchez A., Kiley M.P., Holloway B.P., Auperin D.D.;
RT "Sequence analysis of the Ebola virus genome: organization, genetic
RT elements, and comparison with the genome of Marburg virus.";
RL Virus Res. 29:215-240(1993).
CC -1- FUNCTION: THIS PROTEIN IS A COMPONENT OF THE ACTIVE POLYMERASE. IT
CC MAY FUNCTION IN RNA SYNTHESIS, CAPPING, AS WELL AS METHYLATION OF
CC CAPS, AND POLY(A) SYNTHESIS. ALSO INVOLVED IN TRANSCRIPTIONAL RNA
CC EDITING.
CC -1- SIMILARITY: PRIMARILY WITH THE N-TERMINAL HALF OF THE L PROTEINS
CC OF RHADOVIRUSES AND PARAMYXOVIRUSES.
CC -----
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CC -----
CC EMBL: X67110; CAA47483.1; -
CC DR EMBL: AF086833; AAD14589.1; -

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DR EMBL: L11365; AAB81007.1; -
DR InterPro: IPR001016; Paramyx_RNA_POL.
DR Pfam: PF00946; Paramyx_RNA_POL; 1.
KM Transferase; RNA-directed RNA polymerase.
SQ SEQUENCE 2212 AA: 252722 MM; 5B07EDDC370E2934 CRC64;

Query Match
Best Local Similarity 45.3%; Score 43; DB 1; Length 2212;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 8 NPHNLVSVIN 17
DB 681 NPHNLVSVIN 690

RESULT 15
CYAL_DROME STANDARD; PRT; 2248 AA.
AC P32870;
DT 01-OCT-1993 (rel. 27, Created)
DT 01-OCT-1993 (rel. 27, Last sequence update)
DT 30-MAY-2000 (rel. 39, Last annotation update)
DE CA2+/CALMODULIN-RESPONSIVE ADENYLATE CYCLASE (EC 4.6.1.1) (ATP
DE PYROPHOSPHATE-LYASE) (RUTABAGA PROTEIN).
DE RUT.
GN Drosophila melanogaster (Fruit fly).
OS Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCB1_TaxID-7227;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-CANTON-S; TISSUE-Head;
RX MEDLINE-92154654; PubMed-173965;
RA Levin L.R., Han P.-L., Hwang P.M., Feinstein P.G., Davis R.L.,
RA Reed R.R.;
RT "The Drosophila learning and memory gene rutabaga encodes a
RT Ca2+/calmodulin-responsive adenylyl cyclase.";
RL Cell 68:479-489(1992).
CC -1- FUNCTION: THIS A MEMBRANE-BOUND, CALMODULIN-SENSITIVE ADENYLATE
CC CYCLASE. INACTIVATION OF THIS CYCLASE LEADS TO A LEARNING AND
CC MEMORY DEFECT.
CC -1- CATALYTIC ACTIVITY: ATP -> 3',5'-CYCLIC AMP + PYROPHOSPHATE.
CC -1- ENZYME REGULATION: ACTIVATED BY CA(2+)/CALMODULIN AND G PROTEIN.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: MUSHROOM BODIES OF THE FLY BRAIN.
CC -1- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: BELONGS TO ADENYLATE CYCLASE CLASS-4/GUANYLYL CYCLASE
CC FAMILY.
CC -----
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CC -----
CC EMBL: M81887; AAA28844.1; -
CC DR PIR: D42088; D42088.
CC DR HSP: P19754; 1ANK.
CC DR FlyBase: FBgn0003501; rut.
CC DR InterPro: IPR001054; Guanylyl_cyclase.
CC DR Pfam: PF00211; guanylate_cyc; 2.
CC DR SMART: SMO0044; CYC2; 2.
CC DR PROSITE: PS00452; GUANYLATE_CYCLASES_1; 2.
CC DR PROSITE: PS0125; GUANYLATE_CYCLASES_2; 2.
CC DR Lyase; CAMP synthetase; Transmembrane; Glycoprotein; Duplication.
KW DOMAIN 1 41 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 42 60 POTENTIAL.
FT TRANSMEM 65 84 POTENTIAL.
FT TRANSMEM 101 115 POTENTIAL.

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OM protein - protein search, using sw model

Run on: December 19, 2001, 16:25:26 ; Search time 157.32 Seconds
(without alignments)
15.806 Million cell updates/sec

Title: US-09-202-104A-10
Perfect score: 95
Sequence: 1 PYYKVKPNPNNLSVIN 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :
1: SP-archaea:*
2: SP-bacteria:*
3: SP-fungi:*
4: SP-human:*
5: SP-invertebrate:*
6: SP-mammal:*
7: SP-mhc:*
8: SP-organelle:*
9: SP-phage:*
10: SP-plant:*
11: SP-protent:*
12: SP-virus:*
13: SP-vertebrate:*
14: SP-unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	95	100.0	329	4	Q9U041
2	51	53.7	918	13	Q9W699
3	47	49.5	325	10	Q39599
4	47	49.5	346	13	Q93404
5	47	49.5	491	10	Q82066
6	46.5	48.9	1166	11	Q9QVNA
7	46.5	48.9	1215	11	P97686
8	46	48.4	279	4	Q9UDY5
9	46	47.4	572	6	Q29117
10	45	47.4	693	3	Q08001
11	45	47.4	26926	4	Q10466
12	44	46.3	164	5	Q9TZY5
13	44	46.3	443	4	Q14979
14	44	46.3	446	6	Q97727
15	44	46.3	484	9	Q980C3
16	44	46.3	610	5	Q9N505
17	44	46.3	643	6	Q97726
18	44	46.3	670	5	Q25271
19	44	46.3	867	5	Q18218

20	44	46.3	871	5	Q62486	Q62486 caenorhabdi
21	44	46.3	924	2	Q92IG3	Q92IG3 rhodothermu
22	44	46.3	924	2	Q9X582	Q9X582 rhodothermu
23	43.5	45.8	199	10	Q39864	Q39864 glycine max
24	43	45.3	217	6	Q46386	Q46386 mustela vis
25	43	45.3	259	5	Q45911	Q45911 caenorhabdi
26	43	45.3	260	5	Q9VD91	Q9VD91 dirosophila
27	43	45.3	268	11	Q62712	Q62712 rattus norv
28	43	45.3	281	2	Q91220	Q91220 pseudomonas
29	43	45.3	314	4	Q9HCVR	Q9HCVR homo sapien
30	43	45.3	335	11	Q9R278	Q9R278 rattus norv
31	43	45.3	710	13	Q57520	Q57520 xenopus lae
32	43	45.3	881	13	Q57519	Q57519 xenopus lae
33	43	45.3	2212	12	Q9DDP1	Q9DDP1 ebola virus
34	43	45.3	2248	5	Q9YX17	Q9YX17 dirosophila
35	42.5	44.7	714	5	Q94795	Q94795 trypanosoma
36	42.5	44.7	1180	4	Q15051	Q15051 homo sapien
37	42.5	44.7	1236	4	Q90H13	Q90H13 homo sapien
38	42.5	44.7	1299	4	Q92823	Q92823 homo sapien
39	42.5	44.7	1308	4	Q9UH14	Q9UH14 homo sapien
40	42	44.2	121	1	Q9YC27	Q9YC27 aeropyrum p
41	42	44.2	313	10	Q9M7N9	Q9M7N9 arabidopsis
42	42	44.2	313	10	Q9LZJ7	Q9LZJ7 arabidopsis
43	42	44.2	358	2	Q44538	Q44538 azotobacter
44	42	44.2	364	13	Q9W673	Q9W673 xenopus lae
45	42	44.2	497	4	Q9BSJ3	Q9BSJ3 homo sapien

ALIGNMENTS

RESULT 1
ID Q9U041 PRELIMINARY; PRT; 329 AA.
AC Q9U041;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, last annotation update)
DE Q9U041 OF THE RHEUMATOID ARTHRITIS ANTIGENIC PEPTIDE-BEARING SOLUBLE
DE FORM (GPI30-RAPS).
GN GPI30.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RS SEQUENCE FROM N.A.
RC TISSUE=SYNOVIAL;
RA Tanaka M., Kishimura M., Ozaki S., Hashimoto H., Osakada F., Okubo M.,
RA Murakami M., Nakao K.;
RT "Cloning of novel soluble GPI30 and detection of its neutralizing
RT autoantibodies in rheumatoid arthritis.",
RT Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
RL EMBL; AB015706; BAA78112.1; -.
DR HSSP; P40189; 1BOU.
DR InterPro: IPR002996; CR1A.
DR InterPro: IPR003962; FN1L_repeat.
DR InterPro: IPR003961; FN_LIT.
DR Pfam; PF00041; fn3; 1.
DR PRINTS; PR00014; FNTYPEP11.
DR SMART; SM00060; FN3; 1.
KW Repeat.
SQ
SEQUENCE 329 AA; 37484 MW; D9776576E34FC596 CRC64;

Query Match 100.0%; Score 95; DB 4; Length 329;
Best Local Similarity 100.0%; Pred. No. 5.3e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PYYKVKPNPNNLSVIN 17
DB 216 PYYKVKPNPNNLSVIN 232

RESULT 2

Q9W6U9 PRELIMINARY; PRT: 918 AA.

AC Q9W6U9; 01-NOV-1999 (TREMBLrel. 12, Created)
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE GLYCOPROTEIN 130 PRECURSOR.
 GN GP130.

OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OC NCBI_TaxID=9031;
 RN [1]

RP SEQUENCE FROM N.A.
 RC TISSUE-EMBRYONIC HEART PRIMARY CULTURE (E7, E8);
 RX MEDLINE=99026068; PubMed=9806927;

RA Geissen M., Heller S., Pennica D., Ernberger U., Rohrer H.;
 RT "The specification of sympathetic neurotransmitter phenotype depends
 on gp130 cytokine receptor signaling.";
 RL Development 125:4791-4801(1998).

DR HSSP; P40189; 180U.
 DR Interpro: IPR002996; CRLA.
 DR Interpro: IPR003961; FN_III.
 DR Interpro: IPR003529; Hematopo_receptor_L_F2.
 DR Pfam: PF00041; fn3; 4.
 DR SMART: SM00060; FN3; 3.
 DR PROSITE: PS01353; HEMATOPO_REC_L_F2; UNKNOWN_1.
 KW SIGNAL.
 FT SIGNAL.
 SQ SEQUENCE 918 AA: 102495 MW; FE7625FF3E3613EF CRC64;

Query Match 53.7%; Score 51; DB 13; Length 918;
 Best Local Similarity 66.7%; Pred. No. 10;
 Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 PVYKVPNPPHNSV 15

DB 221 PVYKVPNPPHNSV 235

RESULT 3
 ID Q39599 PRELIMINARY; PRT: 225 AA.

DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
 DE EXTENSIN.

GN CYC15.
 OS Catharanthus roseus (Rosy periwinkle) (Madagascar periwinkle).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; easterids I; Gentianales; Apocynaceae; Catharanthus.
 OC NCBI_TaxID=4058;
 RN [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE=98145469; PubMed=9484475;

RA Ito M., Kodama H., Komamine A., Matanabe A.;
 RT "Expression of extensin genes is dependent on the stage of the cell
 cycle and cell proliferation in suspension-cultured Catharanthus
 roseus cells.";
 RL Plant Mol. Biol. 36:343-351(1998).

DR EMBL: D86853; BAA13175.1;
 DR Mendei: 24261; Cattrio:2930.24261.
 SQ SEQUENCE 225 AA: 25299 MW; 0253CDDAA7368D9 CRC64;

Query Match 49.5%; Score 47; DB 10; Length 225;

Best Local Similarity 72.7%; Pred. No. 10;
 Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 PVYKVPNPPH 11

DB 91 PVYKVPNPPH 101

RESULT 4
 ID Q93404 PRELIMINARY; PRT: 346 AA.

AC Q93404; 01-NOV-1998 (TREMBLrel. 08, Created)
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE PROLACTIN RECEPTOR (FRAGMENT).

OS Oreochromis mossambicus (Mozambique tilapia) (Tilapia mossambica).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthopterygia; Acanthopterygii; Perciformes; Perciformes; Labroidae;
 OC Cichlidae; Oreochromis.
 OC NCBI_TaxID=8127;
 RN [1]

RP SEQUENCE FROM N.A.
 RC TISSUE-GILL;
 RA Shiraiishi K., Matsuda M., Mori T., Tetsuya H.;
 RT "Expression of prolactin and cortisol receptor gene in early-life
 stages of tilapia (Oreochromis mossambicus).";
 RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.

DR HSSP: AF080247; AAC31825.1;
 DR HSSP: P14787; IAN3.
 DR Interpro: IPR002996; CRLA.
 DR Interpro: IPR003961; FN_III.
 DR Interpro: IPR003528; Hematopo_receptor_L_F1.
 DR Pfam: PF00041; fn3; 2.
 DR SMART: SM00060; FN3; 2.
 DR PROSITE: PS01352; HEMATOPO_REC_L_F1; UNKNOWN_1.
 FT NON_TER
 SQ SEQUENCE 346 AA: 39203 MW; E05AE4079326C530 CRC64;

Query Match 49.5%; Score 47; DB 13; Length 346;
 Best Local Similarity 64.3%; Pred. No. 16;
 Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 VYKVPNPPHNSV 15

DB 123 VYKVPNPPHNSV 136

RESULT 5
 ID Q82066 PRELIMINARY; PRT: 491 AA.

DT 01-NOV-1998 (TREMBLrel. 08, Created)
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
 DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
 DE PROLINE-RICH PROTEIN.

GN GP1.
 OS Solanum tuberosum (Potato).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; easterids I; Solanales; Solanaceae; Solanum.
 OC NCBI_TaxID=4113;
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN=CV; DESIREE;
 RA Menke U., Renault N., Mueller-Reber B.;

RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AJ000997; CAA04449.1;
 SQ SEQUENCE 491 AA: 54112 MW; AAE6486860845F0C CRC64;

Best Local Similarity 52.9%; Pred. No. 67;
Matches 9; Conservative 3; Mismatches 4; Indels 1; Gaps 1;
Db 643 PIVDY-PNPPDLELIN 658

RESULT 8
Q9UDY5 PRELIMINARY; PRT: 279 AA.

AC Q9UDY5; 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE INTERLEUKIN-13 RECEPTOR SOLUBLE FORM.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Mada M., Hisano T., Kuwano M.;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; U81380; AAD00511.2; -.
DR HSSP; P40189; 1BOU.
DR InterPro; IPR002996; CRIA.
DR InterPro; IPR003532; Hematopoietic_S_F2.
DR PROSITE; PS01356; HEMATOPOIETIC_S_F2; UNKNOWN_1.
KW Receptor.
SQ SEQUENCE 279 AA; 31658 MW; E74141FE9F89EBB CRC64;

Query Match 48.4%; Score 46; DB 4; Length 279;
Best Local Similarity 62.5%; Pred. No. 19;
Matches 10; Conservative 2; Mismatches 2; Indels 2; Gaps 1;

QY 4 KVKKPNP--NLGVIN 17
Db 225 RVKDPPIKLNLSFN 240

RESULT 9
Q29117 PRELIMINARY; PRT: 572 AA.
AC Q29117; 029033: 029034;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE TITIN (CONNECTIN) (FRAGMENT).
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.
OX NCBI_Taxid=9823;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-93365278; Pubmed-8359022;
RA Fritz J.D., Wolf J.A., Greaser M.L.;
RT "Characterization of a partial cDNA clone encoding porcine skeletal
muscle titin: comparison with rabbit and mouse skeletal muscle titin
sequences."
RT Comp. Biochem. Physiol. 105B:357-360(1993).
RN [2]
RP SEQUENCE OF 62-121 AND 181-231 FROM N.A.
RC TISSUE=MUSCLE;
RA Tanabe R., Muroya S., Nakajima I., Chikuni K., Nakai H.;
RT "Skeletal muscle connectin primary structures as related to animal
species and muscle type."
RL J. Food Sci. 62:451-461(1997).
DE TITIN, HEART ISOFORM N2-B (EC 2.7.1.-) (CONNECTIN).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC DOMAIN
DR EMBL; M97767; AAA02948.1; -.
DR EMBL; D85840; BAA12876.1; -.
DR

DR EMBL; D85841; BAA12877.1; -.
DR InterPro; IPR003962; FNIII_repeat.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR003600; Ig_Like.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00041; fn3; 3.
DR Pfam; PF00047; Ig_2.
DR PRINTS; PR00014; FNTPETII.
DR SMART; SM00060; FN3; 2.
DR SMART; SM00408; IgC2; 1.
DR SMART; SM00410; Ig_Like; 1.
KW Repeat.
FT NON_TER
FT NON_TER
SQ SEQUENCE 572 AA; 62977 MW; 7423328093F59C9D CRC64;

Query Match 47.4%; Score 45; DB 6; Length 572;
Best Local Similarity 52.9%; Pred. No. 54;
Matches 9; Conservative 3; Mismatches 3; Indels 2; Gaps 1;

QY 1 PVYKVPNPNHLSVIN 17
Db 49 PIY--KGPNNPKVID 63

RESULT 10
Q08001 PRELIMINARY; PRT: 693 AA.
AC Q08001; 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE CHROMOSOME XII READING FRAME ORF YLR072W.
GN YLR072W.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_Taxid=4932;
RN [1]
RP SEQUENCE FROM N.A.
RA Pohl T.M.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA MIPS;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z73244; CAA97629.1; -.
DR SGD; S0004062; YLR072W.
SQ SEQUENCE 693 AA; 78212 MW; FACE2F16326B36F6 CRC64;

Query Match 47.4%; Score 45; DB 3; Length 693;
Best Local Similarity 70.0%; Pred. No. 65;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 PVYKVPNPNP 10
Db 371 PVYKVPNPNP 380

RESULT 11
Q10466 PRELIMINARY; PRT: 26926 AA.
ID Q10466
AC Q10466;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE TITIN, HEART ISOFORM N2-B (EC 2.7.1.-) (CONNECTIN).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
CC

NCBI_TaxID=9606;
 [1]
 SEQUENCE FROM N.A.
 TISSUE=HEART;
 MEDLINE=96026330; PubMed=7569978;
 RA Labelt S., Kolmer B.;
 RT "Titins: giant proteins in charge of muscle ultrastructure and
 elasticity.";
 RL Science 270:293-296(1995).
 [2]
 SEQUENCE OF 22277-25376 FROM N.A.
 MEDLINE=92258380; PubMed=1582406;
 RA Labelt S., Gautel M., Lakey A., Trinick J.;
 RT "Towards a molecular understanding of titin.";
 RL EMBO J. 11:1711-1716(1992).
 [3]
 SEQUENCE OF 1976-2014 FROM N.A.
 RA Labelt S.;
 RL Submitted (DEC-1994) to the EMBL/Genbank/DBJ databases.
 [4]
 CHARACTERIZATION.
 MEDLINE=95533114; PubMed=7607248;
 RA Gautel M., Castiglione-Morelli M.A., Pfuhl M., Motta A., Pastore A.;
 RT "A calmodulin-binding sequence in the C-terminus of human cardiac
 titin kinase.";
 RL Eur. J. Biochem. 230:752-759(1995).
 -1- FUNCTION: THIS GIANT MUSCLE PROTEIN MAY BE INVOLVED IN MUSCLE
 ASSEMBLY AND IN MAINTAINING THE STRUCTURAL INTEGRITY OF
 SARCOMERES. MAY HAVE PROTEIN KINASE ACTIVITY.
 -1- ALTERNATIVE PRODUCTS: A NUMBER OF FORMS OF THIS PROTEIN ARE
 PRODUCED BY ALTERNATIVE SPLICING WHICH DIFFER IN TISSUE
 DISTRIBUTION. DIFFERENT SIZE TRANSCRIPTS MAY ALSO EXIST WITHIN ANY
 ONE TISSUE. THE SEQUENCE SHOWN HERE IS THAT OF THE HEART ISOFORM
 N2-B.
 -1- TISSUE SPECIFICITY: MUSCLE-SPECIFIC.
 -1- SIMILARITY: TO THE CATALYTIC DOMAINS OF OTHER SERINE/THREONINE
 KINASES.
 -1- SIMILARITY: BELONGS TO IMMUNOGLOBULIN SUPERFAMILY. CONTAINS 112
 IMMUNOGLOBULIN C2-LIKE DOMAINS AND 132 FIBRONECTIN TYPE III-LIKE
 DOMAINS.
 EMBL: X64698; CAA45939.1; -;
 EMBL: X83270; CAA58243.1; -;
 EMBL: X64697; CAA45938.1; -;
 EMBL: X90568; CAA62188.1; -;
 EMBL: X64699; CAA45940.1; -;
 HSP: P56276; 1TLK.
 DR InterPro: IPR000282; Cytok_receptor_2.
 DR InterPro: IPR000719; Euk_kinase.
 DR InterPro: IPR000577; FGCV_kin.
 DR InterPro: IPR003962; FnIII_repeat.
 DR InterPro: IPR003961; FN_III.
 DR InterPro: IPR003015; HLM_Myc.
 DR InterPro: IPR003598; Iq_C2.
 DR InterPro: IPR003600; Iq_Like.
 DR InterPro: IPR003006; Iq_MHC.
 DR InterPro: IPR000129; Peptidase_S24.
 DR InterPro: IPR002016; Peroxidase.
 DR InterPro: IPR002290; Ser_thr_kin_actsite.
 DR InterPro: IPR001245; Tyr_kin.
 DR Pfam: PF00041; fn3; 132.
 DR Pfam: PF00047; Iq; 95.
 DR Pfam: PF00069; pkinase; 1.
 DR PRINTS: PRO0014; FNTPELTI.
 DR SMART: SM00060; FN3; 127.
 DR SMART: SM00408; Igc2; 23.
 DR SMART: SM00410; Iq_Like; 79.
 DR SMART: SM00220; S_TKc; 1.
 DR PROSITE: PS00933; FGCV_KINASES_1; UNKNOWN_1.
 DR PROSITE: PS00038; HELIX_LOOP_HELIX; UNKNOWN_1.
 DR PROSITE: PS00290; IG_MHC; UNKNOWN_1.
 DR PROSITE: PS00435; PEROXIDASE_1; UNKNOWN_1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.

DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
 KW Muscle protein: Cytoskeleton: Structural protein: Calmodulin-binding;
 KW Serine/threonine-protein kinase: Alternative splicing: Repeat;
 KW Immunoglobulin domain: Phosphorylation.
 FT DOMAIN 1370 1389
 FT DOMAIN 4429 4614
 FT DOMAIN 24731 25070
 FT DOMAIN 25030 25056
 FT MOD_RES 1372 1372
 FT MOD_RES 1377 1377
 FT MOD_RES 1382 1382
 FT MOD_RES 1387 1387
 FT MOD_RES 26171 26171
 FT MOD_RES 26178 26178
 FT MOD_RES 26184 26184
 FT MOD_RES 26190 26190
 FT MOD_RES 22277 22277
 FT CONFLICT 22449 22449
 FT CONFLICT 22454 22454
 FT CONFLICT 23324 23324
 SO SEQUENCE 26926 AA; 2993428 MW; D5FECB3254DF5523 CRC64;

Query Match 47.4%; Score 45; DB 4; Length 26926;
 Best local Similarity 52.9%; Pred. No. 2.4e+03;
 Matches 9; Conservative 3; Mismatches 3; Indels 2; Gaps 1;

QY 1 PYKVKPNNPPHNSVIN 17
 DB 16337 PLY--KPGPPNNPKVID 16351

RESULT 12
 ID Q9TZY5 PRELIMINARY; PRT; 164 AA.
 AC Q9TZY5;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DE 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
 DE VITELLINE ENVELOPE RECEPTOR FOR SPERM LYSIN (FRAGMENT).
 OS Haliotis sorenseni (White abalone).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Archaeogastropoda;
 OC Haliotidae; Haliotis.
 OX NCBI_TaxID=6458;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98350210; PubMed=9685267;
 RA Swanson W.J., Vacquier V.D.;
 RT "Concerted evolution in an egg receptor for a rapidly evolving abalone
 RT sperm protein.";
 RL Science 281:710-712(1998).
 DR EMBL: AF053656; AAC31399.1; -;
 DR Receptor.
 KW NON_TER 1
 FT NON_TER 164
 FT NON_TER 164
 SO SEQUENCE 164 AA; 18058 MW; BFF50CD96F263D12 CRC64;

Query Match 46.3%; Score 44; DB 5; Length 164;
 Best local Similarity 61.5%; Pred. No. 22;
 Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 VYKVKPNNPPHNS 14
 DB 110 VYSDPAPPNNOS 122
 RESULT 13
 ID Q14979 PRELIMINARY; PRT; 443 AA.
 AC Q14979;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)

DT 01-JUN-2001 (Tremblrel. 17, last annotation update)
 DE NUCLEAR RECEPTOR.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=HEART;
 RX MEDLINE=96177652; PubMed=8634690;
 RA Labelle Y., Zucman J., Stenman G., Kindblom L.G., Knight J.,
 RA Turc-Carel C., Dockhorn-Dworitczak B., Mandahl N., Desmaziere C.,
 RA Peter M., Aurias A., Delattre O., Thomas G.;
 RT "Oncogenic conversion of a novel orphan nuclear receptor by chromosome
 RT translocation.";
 RL Hum. Mol. Genet. 4:2219-2226(1995).
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 CC -1- SIMILARITY: TO C4-TYPE STEROID RECEPTOR ZINC FINGER FAMILY.
 DR EMBL; X89894; CAA61984.1; -.
 DR HSSP; P19793; 2NUL.
 DR InterPro; IPR001628; zf-C4.
 DR Pfam; PF00105; zf-C4; 1.
 DR PRINTS; PRO0047; STROIDFINGER.
 DR SMART; SM00399; znf_C4; 1.
 DR PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
 DR DNA-binding; Nuclear protein; Receptor; Transcription regulation;
 KW Zinc-finger.
 SQ SEQUENCE 443 AA; 47822 MW; 42E97CAE053BA5EF CRC64;

Query Match 46.3%; Score 44; DB 4; Length 443;
 Best Local Similarity 54.5%; Pred. No. 60;
 Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 QY 1 PVYKVKPPNPH 11
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 DB 189 PLHFHFKSPPH 199

RESULT 14
 097727 PRELIMINARY; PRT; 446 AA.
 AC 097727;
 DT 01-MAY-1999 (Tremblrel. 10, Created)
 DT 01-MAY-1999 (Tremblrel. 10, last sequence update)
 DT 01-JUN-2001 (Tremblrel. 17, last annotation update)
 DE NEURON-DERIVED ORPHAN RECEPTOR-1 BETA.
 GN NOR-1.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC Cases-Langhoff C., Castello A., Martinez-Gonzalez J., Badimon L.;
 RT "De-differentiated smooth muscle cells in atherosclerotic plaques
 RT express NOR-1.";
 RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 CC -1- SIMILARITY: TO C4-TYPE STEROID RECEPTOR ZINC FINGER FAMILY.
 DR EMBL; AJ011768; CAA09764.1; -.
 DR HSSP; P19793; 2NUL.
 DR InterPro; IPR001628; zf-C4.
 DR Pfam; PF00105; zf-C4; 1.
 DR PRINTS; PRO0047; STROIDFINGER.
 DR SMART; SM00399; znf_C4; 1.
 DR PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
 DR DNA-binding; Nuclear protein; Receptor; Transcription regulation;
 KW Zinc-finger.
 SQ SEQUENCE 446 AA; 47716 MW; E21960657606FB92 CRC64;

Best Local Similarity 54.5%; Pred. No. 60;
 Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 QY 1 PVYKVKPPNPH 11
 |::||:||||
 DB 201 PLHFHFKSPPH 211

Query Match 46.3%; Score 44; DB 9; Length 484;
 Best Local Similarity 52.9%; Pred. No. 65;
 Matches 9; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
 QY 1 PVYKVKPPNPHLSVIN 17
 |:|::|:|||||
 DB 143 PMFIRLNPNNLSVGN 159

Search completed: December 19, 2001, 16:25:28
 Job time: 553 sec

Query Match 46.3%; Score 44; DB 6; Length 446;

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: December 19, 2001, 16:21:02 ; Search time 78.52 Seconds
(without alignments)
4.872 Million cell updates/sec

Title: US-09-202-104A-10

Perfect score: 95
Sequence: 1 PVYKVKPNPNNLSVIN 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: Issued_Patents_AA:*
2: /cgn2_6/ptodata/2/1aa/5A.COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/5B.COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/6A.COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/6B.COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/PCYUS.COMB.pep:*
7: /cgn2_6/ptodata/2/1aa/PCYUS.COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	95	100.0	488	2	US-08-599-455B-5
2	95	100.0	488	4	US-09-069-781B-5
3	95	100.0	658	2	US-08-825-558-4
4	95	100.0	708	1	US-07-797-556-2
5	95	100.0	708	1	US-08-308-881-2
6	95	100.0	708	2	US-09-058-263-2
7	95	100.0	708	2	US-09-059-099-2
8	95	100.0	708	2	US-09-058-264-2
9	95	100.0	708	5	PCT-US95-06530-2
10	95	100.0	918	2	US-08-825-558-6
11	47	49.5	400	1	US-08-118-906-14
12	47	49.5	400	1	US-08-486-196-14
13	47	49.5	400	1	US-08-486-196-14
14	47	49.5	400	2	US-08-474-065-14
15	47	49.5	400	2	US-09-233-506-4
16	46	48.4	427	4	US-08-969-125-9
17	43	45.3	18	1	US-08-205-938A-23
18	43	45.3	18	1	US-08-205-938A-24
19	43	45.3	18	4	US-08-205-938A-26
20	43	45.3	18	4	US-09-230-180-20
21	43	45.3	18	5	PCT-US95-02626-23
22	43	45.3	18	5	PCT-US95-02626-24
23	43	45.3	18	5	PCT-US95-02626-26
24	42	44.2	18	1	US-08-205-938A-25
25	42	44.2	18	5	PCT-US95-02626-25
26	42	44.2	185	1	US-07-676-647-9
27	42	44.2	185	1	US-08-449-329-9

28	42	44.2	185	2	US-08-445-073-9	Sequence 9, Appl1
29	42	44.2	185	2	US-08-585-258-9	Sequence 9, Appl1
30	42	44.2	185	5	PCT-US91-03896-9	Sequence 9, Appl1
31	42	44.2	592	4	US-09-000-145-6	Sequence 6, Appl1
32	41	43.2	16	1	US-08-205-938A-28	Sequence 28, Appl1
33	41	43.2	16	5	PCT-US95-02626-28	Sequence 28, Appl1
34	41	43.2	17	1	US-08-205-938A-27	Sequence 27, Appl1
35	41	43.2	17	5	PCT-US95-02626-27	Sequence 27, Appl1
36	41	43.2	199	4	US-08-995-159-2	Sequence 2, Appl1
37	40	42.1	248	2	US-08-851-974-3	Sequence 3, Appl1
38	40	42.1	248	2	US-09-213-390-3	Sequence 3, Appl1
39	40	42.1	273	2	US-08-424-641B-9	Sequence 9, Appl1
40	40	42.1	273	2	US-08-820-980-9	Sequence 9, Appl1
41	40	42.1	273	2	US-08-826-439-9	Sequence 9, Appl1
42	40	42.1	306	1	US-08-217-327-6	Sequence 6, Appl1
43	40	42.1	306	1	US-08-424-682A-1	Sequence 1, Appl1
44	40	42.1	328	1	US-08-265-087-2	Sequence 2, Appl1
45	40	42.1	328	2	US-08-965-688-2	Sequence 2, Appl1

ALIGNMENTS

RESULT 1
US-08-599-455B-5
Sequence 5, Application US/0859455B
Patent No. 5972621
GENERAL INFORMATION:
APPLICANT: Tartaglia, Louis A.
APPLICANT: Tepper, Robert I.
TITLE OF INVENTION: METHODS OF IDENTIFYING COMPOUNDS THAT
MODULATE BODY WEIGHT USING THE OB RECEPTOR
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08599, 455B
FILING DATE: 22-JAN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/583, 153
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: 08/570, 142
FILING DATE: 11-DEC-1995
APPLICATION NUMBER: 08/569, 485
FILING DATE: 08-DEC-1995
APPLICATION NUMBER: 08/566, 622
FILING DATE: 04-DEC-1995
APPLICATION NUMBER: 08/562, 663
FILING DATE: 27-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: Meikiejohn, Ph.D., Anita L.
REGISTRATION NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 07334/017001
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 488 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: protein
US-08-599-455B-5

Query Match 100.0%; Score 95; DB 2; Length 488;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PYVKVKNPPHNLNVIN 17
|
Db 187 PYVKVKNPPHNLNVIN 203

RESULT 2
US-09-069-781B-5
; Sequence 5, Application US/09069781B
; Patent No. 6287782

GENERAL INFORMATION:
APPLICANT: Tartaglia, Louis A.
APPLICANT: Tepper, Robert I.
APPLICANT: Culpepper, Janice A.
APPLICANT: White, David W.
TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR
TITLE OF INVENTION: THE DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS,
TITLE OF INVENTION: INCLUDING OBESITY AND CACHEXIA
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804

COMPUTER READABLE FORM:
MEDIUM TYPE: diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/069,781B
FILING DATE: 29-APRIL-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/864,564
FILING DATE: 28-MAY-1997
APPLICATION NUMBER: US 08/708,123
FILING DATE: 03-SEP-1996
APPLICATION NUMBER: US 08/638,524
FILING DATE: 26-APR-1996
APPLICATION NUMBER: US 08/599,455
FILING DATE: 22-JAN-1996
APPLICATION NUMBER: US 08/583,153
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: US 08/570,142
FILING DATE: 11-DEC-1995
APPLICATION NUMBER: US 08/569,485
FILING DATE: 08-DEC-1995
APPLICATION NUMBER: US 08/566,622
FILING DATE: 04-DEC-1995
APPLICATION NUMBER: US 08/562,663
FILING DATE: 27-NOV-1995

ATTORNEY/AGENT INFORMATION:
NAME: Melkietohn, Ph.D., Anita L.

REGISTRATION NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 07334/082001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906

TELEX: 200154

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:
LENGTH: 488 amino acids
TYPE: amino acid
TOPOLOGY: unknown

MOLECULE TYPE: protein
US-09-069-781B-5

Query Match 100.0%; Score 95; DB 4; Length 488;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PYVKVKNPPHNLNVIN 17
|
Db 187 PYVKVKNPPHNLNVIN 203

RESULT 3
US-08-825-558-4
; Sequence 4, Application US/08825558
; Patent No. 5965724

GENERAL INFORMATION:
APPLICANT: SHARKEY, ANDREW
APPLICANT: SMITH, STEPHEN K.
APPLICANT: DELLOW, KIMBERLEY A.
TITLE OF INVENTION: GP 130 Lacking the Transmembrane Domain
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX
STREET: 1100 NEW YORK AVENUE
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/825,558
FILING DATE: 19-MAR-1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: ESMOND, ROBERT W.

REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 0623.0530001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)371-2600
TELEFAX: (202)371-2540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 658 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-825-558-4

Query Match 100.0%; Score 95; DB 2; Length 658;
Best Local Similarity 100.0%; Pred. No. 2.9e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PYVKVKNPPHNLNVIN 17
|
Db 216 PYVKVKNPPHNLNVIN 232

RESULT 4
US-07-797-556-2
; Sequence 2, Application US/07797556
; Patent No. 5262522

GENERAL INFORMATION:
APPLICANT: Gearing, David P.
TITLE OF INVENTION: Receptor for Oncostatin M and Leukemia
TITLE OF INVENTION: Inhibitory Factor
NUMBER OF SEQUENCES: 17

ATTORNEY/AGENT INFORMATION:
 NAME: Anderson, Kathryn A.
 REGISTRATION NUMBER: 32,172
 REFERENCE/DOCKET NUMBER: 2614-WO
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 587-0430
 TELEFAX: (206) 233-0644
 TELEX: 756822
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 708 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 PCT-US95-06530-2

Query Match 100.0%; Score 95; DB 5; Length 708;
 Best Local Similarity 100.0%; Pred. No. 3.2e-07;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PYKVKPNPNNLSVIN 17
 DB 216 PYKVKPNPNNLSVIN 232

RESULT 10
 US-08-825-558-6
 Sequence 6, Application US/08825558
 Patent No. 5965724
 GENERAL INFORMATION:
 APPLICANT: SHARKEY, ANDREW
 APPLICANT: SMITH, STEPHEN K.
 APPLICANT: DELLOW, KIMBERLEY A.
 TITLE OF INVENTION: GP 130 Lacking the Transmembrane Domain
 NUMBER OF SEQUENCES: 14
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX
 STREET: 1100 NEW YORK AVENUE
 CITY: WASHINGTON
 STATE: DC
 COUNTRY: USA
 ZIP: 20005
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/825,558
 FILING DATE: 19-MAR-1997
 CLASSIFICATION: 536
 ATTORNEY/AGENT INFORMATION:
 NAME: ESMOND, ROBERT W.
 REGISTRATION NUMBER: 32, 893
 REFERENCE/DOCKET NUMBER: 0623.0530001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202)371-2600
 TELEFAX: (202)371-2540
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 918 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-825-558-6

Query Match 100.0%; Score 95; DB 2; Length 918;
 Best Local Similarity 100.0%; Pred. No. 4.3e-07;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 PYKVKPNPNNLSVIN 17

DB 216 PYKVKPNPNNLSVIN 232

RESULT 11
 US-08-118-906-14
 Sequence 14, Application US/08118906
 Patent No. 5484590
 GENERAL INFORMATION:
 APPLICANT: Fukuda, Minoru
 APPLICANT: Bierhuizen, Marti F.A.
 TITLE OF INVENTION: Expression of the Developmental I
 TITLE OF INVENTION: Antigen By a Cloned Human cDNA Encoding a Member of a
 TITLE OF INVENTION: Beta-1,6-N-Acetylglucosaminyltransferase Gene Family
 NUMBER OF SEQUENCES: 14
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Campbell and Flores
 STREET: 4370 La Jolla Village Drive, Suite 700
 CITY: San Diego
 STATE: California
 COUNTRY: USA
 ZIP: 92122
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/118,906
 FILING DATE: 09-SEP-1993
 CLASSIFICATION: 536
 ATTORNEY/AGENT INFORMATION:
 NAME: Campbell, Cathryn A.
 REGISTRATION NUMBER: 31,815
 REFERENCE/DOCKET NUMBER: P-LJ 9526
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (619) 535-9001
 TELEFAX: (619) 535-8949
 INFORMATION FOR SEQ ID NO: 14:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 400 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-118-906-14

Query Match 49.5%; Score 47; DB 1; Length 400;
 Best Local Similarity 63.6%; Pred. No. 6.5;
 Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 5 VKPNNPNNLSV 15
 DB 248 LKPPNNLTI 258

RESULT 12
 US-08-486-196-14
 Sequence 14, Application US/08486196
 Patent No. 5731420
 GENERAL INFORMATION:
 APPLICANT: Fukuda, Minoru
 APPLICANT: Bierhuizen, Marti F.A.
 TITLE OF INVENTION: Expression of the Developmental I
 TITLE OF INVENTION: Antigen By a Cloned Human cDNA Encoding a Member of a
 TITLE OF INVENTION: Beta-1,6-N-Acetylglucosaminyltransferase Gene Family
 NUMBER OF SEQUENCES: 14
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Campbell and Flores
 STREET: 4370 La Jolla Village Drive, Suite 700
 CITY: San Diego
 STATE: California
 COUNTRY: USA

ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,196
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/118,906
FILING DATE: 09-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 9526
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 400 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-486-196-14

Query Match 49.5%; Score 47; DB 1; Length 400;
Best Local Similarity 63.6%; Pred. No. 6.5;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
5 VKPNPHNLV 15
: || |||||:
Db 248 LKPPPHNLTI 258

RESULT 13
US-08-488-135-14
Sequence 14, Application US/08488135
Patent No. 5766910
GENERAL INFORMATION:
APPLICANT: Fukuda, Minoru
TITLE OF INVENTION: Expression of the Developmental I
TITLE OF INVENTION: Antigen By a Cloned Human cDNA Encoding a Member of a
TITLE OF INVENTION: Beta-1,6-N-Acetylglucosaminyltransferase Gene Family
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,135
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/118,906
FILING DATE: 09-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 9526
TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 400 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-488-135-14

Query Match 49.5%; Score 47; DB 1; Length 400;
Best Local Similarity 63.6%; Pred. No. 6.5;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
5 VKPNPHNLV 15
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Db 248 LKPPPHNLTI 258

RESULT 14
US-08-474-065-14
Sequence 14, Application US/08474065
Patent No. 5830465
GENERAL INFORMATION:
APPLICANT: Fukuda, Minoru
TITLE OF INVENTION: Expression of the Developmental I
TITLE OF INVENTION: Antigen By a Cloned Human cDNA Encoding a Member of a
TITLE OF INVENTION: Beta-1,6-N-Acetylglucosaminyltransferase Gene Family
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,065
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/118,906
FILING DATE: 09-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 9526
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 400 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-474-065-14

Query Match 49.5%; Score 47; DB 2; Length 400;
Best Local Similarity 63.6%; Pred. No. 6.5;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
5 VKPNPHNLV 15
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Db 248 LKPPPHNLTI 258

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RESULT 15
US-09-233-506-4
; Sequence 4, Application US/09233506
; Patent No. 6136580
; GENERAL INFORMATION:
; APPLICANT: Fukuda, Minoru
; APPLICANT: Yeh, Jinn-Chern
; TITLE OF INVENTION: A Beta-1-6-N-Acetylglucosaminyltransferase That Forms
; TITLE OF INVENTION: Core 2, Core 4 and I Branches
; FILE REFERENCE: P-LJ 3415
; CURRENT APPLICATION NUMBER: US/09/233,506
; CURRENT FILING DATE: 1999-01-19
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 400
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-233-506-4
    
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Query Match          49.5%; Score 47; DB 4; Length 400;
Best Local Similarity 63.6%; Pred. No. 6.5;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 5 VKPNPPHNLTV 15
   :||| |||||:
Db 248 LKPPPHNLTI 258
    
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Search completed: December 19, 2001, 16:21:03
 Job time: 408 sec

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us-09-202-104a-11.rag

Page 1

GenCore version 4.5
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OM protein: protein search, using sw model

Run on: December 19, 2001, 16:19:37 ; Search time 170.68 Seconds
(without alignments)
12.152 Million cell updates/sec

Title: US-09-202-104A-11

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Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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2: /SIDSB/gcgdata/geneseq/geneseq/AA1980.DAT: *
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22: /SIDSB/gcgdata/geneseq/geneseq/AA2000.DAT: *
23: /SIDSB/gcgdata/geneseq/geneseq/AA2001.DAT: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	146	100.0	28	19	AAW52211	Interleukin-6 anta
2	146	100.0	182	17	AAW00403	Interleukin-6 anta
3	146	100.0	315	20	AAW70805	Amino acid sequenc
4	146	100.0	315	21	AAW92200	Soluble human IL-6
5	146	100.0	323	10	AAW90527	B cell stimulating
6	146	100.0	325	21	AAW15385	Human interleukin
7	146	100.0	325	21	AAW15390	Bovine interleukin
8	146	100.0	344	10	AAW90528	B cell stimulating
9	146	100.0	345	21	AAW55071	SR345 protein sequ
10	146	100.0	360	20	AAW70804	Amino acid sequenc
11	146	100.0	360	21	AAW92199	Soluble human IL-6

12	146	100.0	419	20	AAW30938	Human IL-6 recepto
13	146	100.0	468	10	AAW90525	B cell stimulating
14	146	100.0	468	10	AAW90284	Sequence of a rece
15	146	100.0	468	14	AAW37215	IL-6 receptor. Sy
16	146	100.0	468	17	AAW98364	Interleukin-6 rece
17	146	100.0	468	21	AAW92196	Human IL-6R-alpha
18	146	100.0	468	22	AAW36655	Human IL-6 recepto
19	146	100.0	477	21	AAW92197	Human IL-6R-alpha
20	146	100.0	500	18	AAW36847	Human fusion polyp
21	146	100.0	515	18	AAW15404	IL-6R/IL-6 fusion
22	146	100.0	525	18	AAW36846	Human fusion polyp
23	146	100.0	543	20	AAW03184	Chimeric sIL-6R/IL
24	146	100.0	592	20	AAW70797	Human interleukin-
25	146	100.0	592	21	AAW92185	Human IL-6R-alpha
26	146	100.0	590	21	AAW92195	Human IL-6R-alpha
27	146	100.0	1042	16	AAW70122	IL-6 type 1-Gbp 1
28	146	100.0	1158	21	AAW92205	Fusion polypeptide
29	146	100.0	1168	21	AAW92204	Fusion polypeptide
30	134	91.8	468	19	AAW1371	Human interleukin-
31	119	81.5	386	10	AAW90526	B cell stimulating
32	112	76.7	25	11	AAW06591	Interleukin-6 -com
33	102	69.9	21	19	AAW52205	Interleukin-6 anta
34	102	69.9	21	22	AAW88666	Human Interleukin-
35	102	69.9	21	22	AAW88682	Human Interleukin-
36	102	69.9	21	22	AAW88698	Human Interleukin-
37	99	67.8	21	22	AAW88699	Human Interleukin-
38	98	67.1	21	22	AAW88667	Human Interleukin-
39	98	67.1	21	22	AAW88705	Human Interleukin-
40	98	67.1	21	22	AAW88708	Human Interleukin-
41	97	66.4	21	22	AAW88706	Human Interleukin-
42	97	66.4	21	22	AAW88707	Human Interleukin-
43	97	66.4	21	22	AAW88710	Human Interleukin-
44	97	66.4	21	22	AAW88711	Human Interleukin-
45	97	66.4	21	22	AAW88712	Human Interleukin-

ALIGNMENTS

RESULT 1	AAW52211	standard; peptide: 28 AA.
ID	AAW52211	standard; peptide: 28 AA.
XX	AAW52211;	
XX	09-JUN-1998	(first entry)
XX	Interleukin-6	antagonist peptide.
XX	Interleukin-6; IL-6;	antagonist; IL-6 related disease; multiple myeloma;
XX	acquired immune deficiency syndrome-related lymphoma;	immune response;
XX	rheumatoid arthritis; psoriasis; sepsis; osteoporosis;	therapy;
XX	Alzheimer's disease.	
XX	Synthetic.	
XX	Homo sapiens.	
XX	MO9748728-A1.	
XX	24-DEC-1997.	
XX	19-JUN-1997;	97W0-NL00345.
XX	20-JUN-1996;	96EP-0201720.
XX	(KOSTV) KOSTER H W.	
XX	Hoebe KHN, Van Leengoed LAMG;	
XX	WPI, 1998-063080/06.	
XX	New peptide(s) with interleukin-6 agonist or antagonist activity	
XX	useful for treatment, prevention and diagnosis of IL-6 associated	
PT		

PT diseases

PS Claim 7; Page 17; 28pp; English.

CC This sequence represents a interleukin-6 (IL-6) antagonist peptide. This
 CC sequence is a peptide of the invention, which are of 5-30 amino acids
 CC and have antagonistic activity against: (a) IL-6; (b) the alpha chain
 CC and/or beta chain of the IL-6 receptor (IL-6R); or (c) IL-6 activity. The
 CC antagonists are used to treat or prevent IL-6 related diseases (typical
 CC of many exemplified are multiple myeloma, acquired immune deficiency
 CC syndrome-related lymphoma, rheumatoid arthritis, psoriasis, sepsis,
 CC osteoporosis, Alzheimer's disease etc.), also to remove IL-6 or IL-6R
 CC from extracorporeal blood. They may also be used diagnostically for such
 CC specific for the antagonists are additives for cell cultures. Antibodies
 CC treated with the antagonists may be administered to subjects previously
 CC extracorporeal dialysis and diagnosis. The antagonists are too small to
 CC induce an immune response and have minimal side effects (they are not
 CC lytic for erythrocytes nor toxic for polymorphonuclear cells or
 CC hepatocytes); contrast no-human anti-IL-6 antibodies. The mixtures, or
 CC and the peptides can be engineered to increase half-life or to target
 CC organs by incorporating unnatural aa or altering the
 CC hydrophilic/lipophilic balance.

CC Sequence 28 AA;

Query Match 100.0%; Score 146; DB 19; Length 28;

Best Local Similarity 100.0%; Pred. No. 5, 7e-16;

Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EWGPRSTSLTKAVLVKRFNSPAED 28

DB 1 ewgprstsltkavlvkrfnspsaed 28

RESULT 2

AAW00403

ID AAW00403 standard; peptide; 182 AA.

AC AAW00403;

DT 29-AUG-1996 (first entry)

DE Interleukin-6 antagonist peptide.

KM IL-6; antagonist; autoimmune disease.

OS Synthetic.

PN JP07324097-A.

PD 12-DEC-1995.

PF 30-MAY-1994; 94JP-0117259.

PR 30-MAY-1994; 94JP-0117259.

PA (DAIL) DAICEL CHEM IND LTD.

PA (FUJI) FUJISAWA PHARM CO LTD.

WPI; 1996-065476/07.

Interleukin 6 antagonist - useful for treating autoimmune diseases

Claim 1; Page 2; 19pp; Japanese.

CC New IL-6 antagonists are provided which are of formula X-W-Y, in
 CC which X is H or an amino-protecting group, Y is OH or a carboxy-
 CC protecting group, and W is a peptide containing all or part of the
 CC sequence as given in AAW00401, AAW00402, AAW00403 (the present sequence)
 CC AAW00404, where any free mercapto groups in the sequence are

CC optionally protected. Specifically preferred partial peptides from the
 CC present sequence (AAW00428 - AAW00435) are claimed as new chemical
 CC compounds. The IL-6 antagonists are useful for treating autoimmune
 CC diseases.

SO Sequence 182 AA;

Query Match 100.0%; Score 146; DB 17; Length 182;

Best Local Similarity 100.0%; Pred. No. 5, 1e-15;

Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EWGPRSTSLTKAVLVKRFNSPAED 28

DB 14 ewgprstsltkavlvkrfnspsaed 41

RESULT 3

AAW70805

ID AAW70805 standard; protein; 315 AA.

AC AAW70805;

DT 03-FEB-1999 (first entry)

DE Amino acid sequence of the interleukin (IL)-6R-alpha-313 domain.

KM gp130; cytokine antagonist; interleukin; gamma-interferon;

KW granulocyte macrophage colony-stimulating factor; J peptide;

OS Synthetic.

FN Key Location/Qualifiers

FT Protein 1..313 /note="truncated interleukin (IL)-6R-alpha domain"

PN US5844099-A.

PD 01-DEC-1998.

PF 27-NOV-1995; 95US-0563105.

PR 27-NOV-1995; 95US-0563105.

PR 20-OCT-1993; 93US-0140222.

PA (REG-) REGENERON PHARM INC.

PI Economides A, Stahl N, Yancopoulos GD;

WPI; 1999-044669/04.

Cytokine antagonists - comprising extracellular domains of

specificity-determining and signal-transducing components of

cytokine receptor

Example 4; Fig 16; 46pp; English.

CC The present sequence represents the amino acid sequence of interleukin
 CC (IL)-6R-alpha-313 domain. The protein is used in the course of the
 CC invention. The specificity-determining domain of the cytokine receptor
 CC only the extracellular domain of the specificity-determining component of
 CC the cytokine receptor and the extracellular domain of a
 CC signal-transducing component of the cytokine receptor. The cytokine
 CC is an interleukin (IL-1, IL-2, IL-3, IL-4, IL-5 or IL-15),
 CC granulocyte macrophage colony-stimulating factor (GM-CSF),
 CC gamma-interferon or transforming growth factor-beta (TGF-beta). The
 CC antagonist is capable of binding the cytokine to form a nonfunctional
 CC complex. The compounds have therapeutic activity as cytokine antagonists
 CC and can also be used in assays for identifying novel agonists and
 CC antagonists of cytokines.

Sequence 315 AA;

Query Match 100.0%; Score 146; DB 20; Length 315;
 Best Local Similarity 100.0%; Pred. No. 9.6e-15;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EWGPRSTPSLTTRKAVLLVRKFQNSPAED 28
 ||||||||||||||||||||||||||||||||
 DB 133 ewgprstpslttkavllvrkfqnspeed 160

RESULT 4
 AAY92200
 ID AAY92200 standard; protein; 315 AA.
 XX AAY92200;
 AC AAY92200;
 DT 01-AUG-2000 (first entry)
 DE Soluble human IL-6-R-alpha-313.
 XX
 KW Soluble IL-6-R-alpha-313; cytokine; antagonist; CNTF, receptor;
 XX fusion protein; cytosolic; immunomodulator; osteopathic.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Protein 1..313
 FT /label= truncated_IL-6-R-alpha
 FT Peptide 314..315
 FT /note= "Thr-Gly bridge"
 XX
 PN WO200018932-A2.
 XX
 PD 06-APR-2000.
 XX
 PF 22-SEP-1999; 99WO-US22045.
 XX
 PR 25-SEP-1998; 98US-0101858.
 PR 19-MAY-1999; 99US-0313942.
 XX
 PA (REGG-) REGENERON PHARM INC.
 XX
 PI Stahl N, Yancopoulos GD;
 DR WPI: 2000-293165/25.
 XX
 PT Isolated nucleic acid molecule for treating cytokine-related diseases
 PT or disorders encodes a fusion polypeptide capable of binding a cytokine
 PT to form a nonfunctional complex
 XX
 PS Example 4; Fig 16; 152pp; English.
 XX
 CC The invention concerns production of antagonists to any cytokine that
 CC utilizes an alpha specificity determining component, which when combined
 CC with the cytokine, binds to a first beta signal transducing component to
 CC form a non-functional intermediate which then binds to a second beta
 CC signal transducing component causing beta-receptor dimerization, the
 CC soluble alpha specificity determining component of the receptor
 CC (SR-alpha) and the extracellular domain of the first beta signal
 CC transducing component of the cytokine receptor (beta-1) are combined to
 CC form heterodimers (SR-alpha:beta-1) that act as antagonist to the
 CC cytokine by binding the cytokine to form a non-functional complex. The
 CC receptor components are shared by cytokines such as the CNTF (ciliary
 CC neurotrophic factor) family of cytokines. The invention provides the
 CC basis for the development of IL-6 antagonists, as they show that if, in
 CC the presence of a ligand, a non-functional intermediate complex,
 CC consisting of the ligand, its alpha receptor and its beta-1 receptor
 CC component can be formed, it will effectively block the action of the
 CC ligand. Effective antagonists of IL-6 or CNTF consist of heterodimers
 CC of the extracellular domains of the alpha specificity determining
 CC components of their receptors and the extracellular domain of gp130.
 CC The resultant heterodimers, function as high-affinity traps, rendering

CC the cytokine inaccessible to form a signal transducing complex with the
 CC native membrane-bound forms of their receptor. The nucleic acids and
 CC polypeptides are useful for treating cytokine-related diseases or
 CC disorders such as osteoporosis and primary and secondary effects of
 CC cancer including multiple myeloma or cachexia.
 XX
 SQ Sequence 315 AA:

Query Match 100.0%; Score 146; DB 21; Length 315;
 Best Local Similarity 100.0%; Pred. No. 9.6e-15;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EWGPRSTPSLTTRKAVLLVRKFQNSPAED 28
 ||||||||||||||||||||||||||||||||
 DB 133 ewgprstpslttkavllvrkfqnspeed 160

RESULT 5
 AAP90527
 ID AAP90527 standard; protein; 323 AA.
 XX AAP90527;
 AC AAP90527;
 DT 25-JAN-1990 (first entry)
 DE B cell stimulating factor-2 receptor.
 XX
 KW B cell stimulating factor-2 receptor; monocytic U937 cell line.
 XX
 OS Homo sapiens.
 XX
 PN A08928720-A.
 XX
 PD 27-JUL-1989.
 XX
 PF 23-JAN-1989; 89AU-0028720.
 XX
 PR 22-JAN-1988; 88JP-0012387.
 PR 25-JAN-1988; 88JP-0012599.
 PR 04-AUG-1988; 88JP-0194885.
 PR 14-JAN-1989; 89JP-0007461.
 XX
 PA (KISH) TADAMITSU KISHIMOTO.
 XX
 PI Kishimoto T;
 DR WPI: 1989-264012/37.
 DR N-PSDB; AAP90525.
 XX
 PT Receptor protein for human B cell stimulating factor-2 - used for
 PT developing prophylactic, therapeutic and diagnostic agents for
 PT associated disorders.
 XX
 PS Claim 6, page 39; 76pp; english.
 XX
 CC The BSF2 receptor has amino acids at the C-terminal deleted. The receptor
 CC is derived from a monocytic U937 cell line. It can be used to develop
 CC prophylactic and therapeutic pharmaceuticals, as agents to relate
 CC diseases and disorders to abnormal BSF-2 prodn. It can also be used to
 CC study an immune mechanism with which BSF-2 or the receptor is concerned.
 XX
 SQ Sequence 323 AA:

Query Match 100.0%; Score 146; DB 10; Length 323;
 Best Local Similarity 100.0%; Pred. No. 9.9e-15;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EWGPRSTPSLTTRKAVLLVRKFQNSPAED 28
 ||||||||||||||||||||||||||||||||
 DB 133 ewgprstpslttkavllvrkfqnspeed 160

```
RESULT 6
AAB15389
ID AAB15389 standard; Protein; 325 AA.
XX
AC AAB15389;
XX
DT 11-DEC-2000 (first entry)
XX
DE Human Interleukin 6 receptor protein.
XX
KM Human; Interleukin-6 receptor; fungus; Pichia pastoris; PCR primer;
XX expression vector; immunoglobulin-like region; cytokine receptor region.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 57 /note= "encoded by GGC"
FT Misc-difference 281 /note= "encoded by CAA"
FT Misc-difference 281 /note= "encoded by CAA"
XX
PN JP2000157280-A.
XX
PD 13-JUN-2000.
XX
PF 26-NOV-1998; 98JP-0335464.
XX
PR 26-NOV-1998; 98JP-0335464.
XX
PS (TOYU ) TOSOH CORP.
XX
PA WPI; 2000-468203/41.
XX
DR N-PSDB; AAA70701.
XX
PT Yeasts transformed with IL-6 receptor gene -
XX
PS Example 1; Page 6-8; 10pp; Japanese.
XX
CC The invention relates to the production of human interleukin-6 receptor
CC (IL-6R) protein in the fungus Pichia pastoris. The fungus was
CC transformed with an expression vector (pOTC9-A201L) containing a gene
CC encoding an IL-6R protein having an immunoglobulin-like region and
CC cytokine receptor region and spanning amino acids from Leu20-Ala323. The
CC human IL-6R region was PCR amplified using the primers AAA70702-A70703.
CC This sequence represents the recombinant IL-6R protein of the invention.
XX
SQ Sequence 325 AA;

Query Match 100.0%; Score 146; DB 21; Length 325;
Best Local Similarity 100.0%; Pred. No. 1e-14;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EWGPRSTPSLTTRKAVLLVRKQNSPAD 28
DB 114 ewgprstpslttkavllvrkfgnspad 141

RESULT 7
AAB15390
ID AAB15390 standard; Protein; 325 AA.
XX
AC AAB15390;
XX
DT 15-DEC-2000 (first entry)
XX
DE Bovine Interleukin-12 p35 subunit protein.
XX
KM Antifective; bovine; Interleukin 12; IL12; heterodimer; infection.
XX
OS Bos taurus.
XX
```

```
PN JP2000157274-A.
XX
PD 13-JUN-2000.
XX
PF 20-NOV-1998; 98JP-0331052.
XX
PR 20-NOV-1998; 98JP-0331052.
XX
PS (DAUC ) DAIICHI PHARM CO LTD.
XX
PA WPI; 2000-468201/41.
XX
DR N-PSDB; AAA70708.
XX
PT Preparation of bovine Interleukin 12 comprising using a vector
PT containing the gene encoding it; useful for the prevention and
PT treatment of chronic and opportunistic infections -
XX
PS Example 1; Page 8; 11pp; Japanese.
XX
CC The invention relates to a method for the preparation of bovine
CC Interleukin 12 (Boil12). Boil12 consists of a heterodimer of p35
CC and p40 subunits. Boil12 is produced by introducing into a host cell,
CC recombinant vectors containing genes encoding the p35 and p40 subunits.
CC This sequence represents the bovine IL12 p35 subunit. Interleukin 12
CC is used for the prevention and treatment of chronic infections and
CC opportunistic infections.
XX
SQ Sequence 325 AA;

Query Match 100.0%; Score 146; DB 21; Length 325;
Best Local Similarity 100.0%; Pred. No. 1e-14;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EWGPRSTPSLTTRKAVLLVRKQNSPAD 28
DB 114 ewgprstpslttkavllvrkfgnspad 141

RESULT 8
AAP90528
ID AAP90528 standard; protein; 344 AA.
XX
AC AAP90528;
XX
DT 25-JAN-1990 (first entry)
XX
DE B cell stimulating factor-2 receptor.
XX
KM B cell stimulating factor-2 receptor; monocyte U937 cell line.
XX
OS Homo sapiens.
XX
PN A08928720-A.
XX
PD 27-JUL-1989.
XX
PF 23-JAN-1989; 89AU-0028720.
XX
PR 22-JAN-1988; 88JP-0012387.
PR 25-JAN-1988; 88JP-0012559.
PR 04-AUG-1988; 88JP-0194885.
PR 14-JAN-1989; 89JP-0007461.
XX
PA (KISH ) TADAMITSU KISHIMOTO.
XX
PI Kishimoto T;
XX
DR WPI; 1989-264012/37.
DR N-PSDB; AAP90525.
XX
PT Receptor protein for human B cell stimulating factor-2 - used for
PT developing prophylactic, therapeutic and diagnostic agents for
```



```

XX 23-JAN-1990 (first entry)
XX
XX B cell stimulating factor-2 receptor.
XX
XX B cell stimulating factor-2 receptor; monocytic U937 cell line.
XX
XX Homo sapiens.
XX
XX AUB928720-A.
XX
XX 27-JUL-1989.
XX
XX 23-JAN-1989; 89AU-0028720.
XX
XX 22-JAN-1988; 88JP-0012387.
XX
XX 25-JAN-1988; 88JP-0012599.
XX
XX 04-AUG-1988; 88JP-0194885.
XX
XX 14-JAN-1989; 89JP-0007461.
XX
XX (KISH ) TADAMITSU KISHIMOTO.
XX
XX Kishimoto T;
XX
XX WPI; 1989-264012/37.
XX
XX N-PSDB; AAP90525.
XX
XX Receptor protein for human B cell stimulating factor-2 - used for
XX developing prophylactic, therapeutic and diagnostic agents for
XX associated disorders.
XX
XX Claim 2; page 36; 76pp; english.
XX
XX The BSF2 receptor is derived from a monocytic U937 cell line. It can be
XX used to develop prophylactic and therapeutic pharmaceuticals, as agents to
XX relate diseases and disorders to abnormal BSF-2 prodn. It can also be
XX used to study an immune mechanism with which BSF-2 or the receptor is
XX concerned.
XX
XX Sequence 468 AA;
XX
Query Match 100.0%; Score 146; DB 10; Length 468;
Best Local Similarity 100.0%; Pred. No. 1.5e-14;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 EWGPRSTPLTTKAVLVKRFQNSPAED 28
DB 133 ewgprstpslttkavllvrkfgnspaed 160

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XX 26-JUL-1989.
XX
XX 20-JAN-1989; 89EP-0300536.
XX
XX 14-JAN-1989; 89JP-0017461.
XX
XX 22-JAN-1988; 88JP-0012387.
XX
XX 25-JAN-1988; 88JP-0012599.
XX
XX 04-AUG-1988; 88JP-0194885.
XX
XX 20-JAN-1989; 89JP-0009774.
XX
XX (KISH/) KISHIMOTO T.
XX
XX Kishimoto T;
XX
XX WPI; 1989-214667/30.
XX
XX N-PSDB; AAN90340.
XX
XX Receptor protein for human B cell stimulating factor-2 - obtd. by
XX recombinant DNA techniques and used as diagnostic, prophylactic or
XX therapeutic agent
XX
XX Claim 2; page 19-21; 63pp; English.
XX
XX The cDNA in AAN90340 was derived from monocytic cell line U937.
XX Isolated BSF2 receptor and DNA encoding it are claimed, as are
XX (b) expression vectors; (c) host organisms; (d) antibodies; and
XX (e) hybridomas.
XX
XX Sequence 468 AA;
XX
Query Match 100.0%; Score 146; DB 10; Length 468;
Best Local Similarity 100.0%; Pred. No. 1.5e-14;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 EWGPRSTPLTTKAVLVKRFQNSPAED 28
DB 133 ewgprstpslttkavllvrkfgnspaed 160

```

```

RESULT 14
AAP90284
ID AAP90284 standard; Protein: 468 AA.
XX
XX AAP90284;
XX
XX 31-MAR-1992 (first entry)
XX
XX Sequence of a receptor protein for human B cell stimulating
XX factor-2 (BSF2 receptor).
XX
XX B cell; immune disorder; therapy; diagnosis; prophylaxis.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Region 2..22
XX Region /label= hydrophobic region
XX Region 362..386
XX Region /label= hydrophobic region
XX
XX EP325474-A.
XX

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```

RESULT 15
AAR37215
ID AAR37215 standard; Protein: 468 AA.
XX
XX AAR37215;
XX
XX 13-SEP-1993 (first entry)
XX
XX IL-6 receptor.
XX
XX Interleukin-6; IL-6; receptor; immunoglobulin-like; domain; truncated;
XX transmembrane; multiple myeloma; binding; ability; signal transfer;
XX disease; intracellular.
XX
XX Synthetic.
XX
XX JP05091892-A.
XX
XX 16-APR-1993.
XX
XX 02-OCT-1991; 91JP-0255521.
XX
XX 02-OCT-1991; 91JP-0255521.
XX
XX (CHUS ) CHUGAI PHARM CO LTD.
XX (KISH/) KISHIMOTO C.
XX (TOYT ) TOSOH CORP.
XX
XX WPI; 1993-161739/20.
XX N-PSDB; AAO41746.
XX
XX New interleukin-6 receptor deriv. - for treating diseases caused
XX

```

PT by IL-6, e.g. multiple myeloma
 XX
 PS Disclosure; Page 10-12; 23pp; Japanese.
 XX
 CC This sequence represents an interleukin-6 (IL-6) receptor. Variants
 CC of the receptor lacking either the immunoglobulin-like domain or the
 CC transmembrane and intracellular domain have IL-6 binding ability and
 CC signal transfer ability. Either the full length or truncated IL-6
 CC receptors may be used for diseases caused by IL-6 such as multiple
 CC myeloma.
 XX
 SQ Sequence 468 AA;

Query Match 100.0%; Score 146; DB 14; Length 468;
 Best Local Similarity 100.0%; Pred. No. 1.5e-14;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EWGPRSTPSLTTKAVLVKRFQNSPAED 28
 |||||
 Db 133 ewgprstpslttkavlvkrkfqnspaed 160

Search completed: December 19, 2001, 16:19:37
 Job time: 362 sec

	Matches	21: Conservative	0: Mismatches	0: Indels	0: Gaps
QY	1	PRSTPSLTTKAVLVKRFQNS	21		
Db	1	prstpslttkavllvrkfqs	21		

RESULT	4
AAB88698	
ID	AAB88698 standard; Peptide; 21 AA

DE Human interleukin-6 domain II fragment #33.

KW Interleukin-6; ligand; IL-6 receptor; antagonist; cancer; allergy
 KW rheumatoid arthritis; diabetes; multiple sclerosis; infection;
 KW autoimmune disease; inflammatory disease.

OS	Homo sapiens.
XX	
PN	WO200116166-A2

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

PT Polypeptides which inhibit the binding of interleukin (IL)-6 ligand
PT with the IL-6 receptor, and the nucleic acids that encode them, useful
PT for treating e.g. inflammation and autoimmune diseases -

CC The present invention describes a number of peptides which are able to
CC bind to the human interleukin-6 (IL-6) receptor and inhibitor-6 binding-
CC site. These peptides are useful in the treatment of diseases associated with abnormal
CC IL-6 expression, including multiple myeloma, plasmacytoma, haematological
CC diseases such as plasma cell dyscrasias, leukaemia and lymphoma,
CC meningial proliferative glomerulonephritis, polyclonal B cell activation
CC conditions, allergies, rheumatoid arthritis, diabetes, multiple
CC sclerosis, septic shock, infections, post-menopausal osteoporosis,
CC chronic immune deficiency, autoimmune diseases and inflammatory diseases.

Query Match	100.0%	Score 102;	DB 22;	Length 21;
Best Local Similarity	100.0%;	Pred. No. 9.3e-11;		
Matches 21; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0

RESULT	5
AAW52211	
ID	AAW52211 standard; peptide; 28 AA

DE	Interleukin-6 antagonist peptide.
XX	
KW	Interleukin-6; IL-6; antagonist; IL-6-related disease; multiple myeloma;
KW	acquired immune deficiency syndrome-related lymphoma; immune response;
KW	rheumatoid arthritis; psoriasis; sepsis; osteoporosis; therapy;
KW	Alzheimer's disease.

OS	Synthetic.
OS	Homo sapiens
XX	
PN	W09748728-A1

PF	19-JUN-1997;	97WO-NL00345.
XX		
PR	20-JUN-1996;	96EP-0201720

PI Hoebe KHN, van Leengoed LAMG;
XX
DR WPI; 1998-063080/06.

PT New peptide(s) with interleukin-6 agonist or antagonist activity
 PI useful for treatment, prevention and diagnosis of IL-6 associated
 PT diseases
 PS Claim 7; Page 17; 28pp; English.

This sentence represents a interleukin-6 (IL-6 antagonist peptide. This sequence is a peptide of the invention, which are of 5-30 amino acids and have antagonistic activity against: (a) IL-6; (b) the alpha chain and/or beta chain of the IL-6 receptor (IL-6R); or (c) IL-6 activity. The antagonists are used to treat or prevent IL-6 related diseases (typical or many exemplified are multiple myeloma, acquired immune deficiency syndrome-related lymphoma, rheumatoid arthritis, psoriasis, sepsis, osteoporosis, Alzheimer's disease etc.), also to remove IL-6 or IL-6R from extracorporeal blood. They may also be used diagnostically for such diseases and IL-6 antagonists are additives for cell cultures. Antibodies specific for the antagonists may be administered to subjects previously treated with the antagonists to counter their effects, also in extracorporeal dialysis and diagnosis. The antagonists are too small to induce an immune response and have minimal side effects (they are not lytic for erythrocytes nor toxic for polymorphonuclear cells or hepatocytes), contrast non-human anti-IL-6 antibodies. The mixtures, or multimers, have greater activity (acting on both IL-6 and its receptor) and the peptides can be engineered to increase half-life or to target organs by incorporating unnatural aa or altering the hydrophilic/lipophilic balance.

Query Match	100.0%	Score 102;	DB 19;	Length 28;
Best Local Similarity	100.0%;	Pred. No. 1.3e-10;		
Matches 21; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;

ID	AAW00403	standard; peptide; 182 AA.
XX		
AC	AAW00403;	

KW IL-6; antagonist; autoimmune disease.
 XX
 OS Synthetic.
 PN JP07324097-A.
 XX
 PD 12-DEC-1995.
 PF 30-MAY-1994; 94JP-0117259.
 XX
 PR 30-MAY-1994; 94JP-0117259.
 XX
 PA (DAIIC) DAICEL CHEM IND LTD.
 XX (FUJII) FUJISAWA PHARM CO LTD.
 DR WPI; 1996-065476/07.
 XX
 PT Interleukin 6 antagonist - useful for treating autoimmune diseases
 PS Claim 1; Page 2; 19pp; Japanese.
 CC New IL-6 antagonists are provided which are of formula X-W-Y, in
 CC which X is H or an amino-protecting group, Y is OH or a carboxy-
 CC protecting group, and W is a peptide containing all or part of the
 CC sequence as given in AAW00401, AAW00402, AAW00403 (the present sequence)
 CC or AAW00404, where any free mercapto groups in the sequence are
 CC optionally protected. Specifically preferred partial peptides from the
 CC present sequence (AAW00428 - AAW00435) are claimed as new chemical
 CC compounds. The IL-6 antagonists are useful for treating autoimmune
 CC diseases.
 XX
 SQ Sequence 182 AA;
 QY
 Query Match 100.0%; Score 102; DB 17; Length 182;
 Best Local Similarity 100.0%; Pred. No. 1.2e-09;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 1 PRSTPSLTTRKAVLVRRKFRNS 21
 17 prstpslttkavllvrkfrqns 37
 RESULT 7
 AAW70805
 ID AAW70805 standard; protein; 315 AA.
 XX
 AC AAW70805;
 XX
 DT 03-FEB-1999 (first entry)
 XX
 DE Amino acid sequence of the interleukin (IL)-6R-alpha-313 domain.
 XX
 KW gp130: cytokine antagonist; interleukin; gamma-interferon;
 KW granulocyte macrophage colony-stimulating factor; J peptide;
 KW transforming growth factor-beta.
 XX
 OS Synthetic.
 XX
 FT Key Location/Qualifiers
 FT Protein 1..313
 /note= "truncated interleukin (IL)-6R-alpha domain"
 XX
 PN US5844099-A.
 XX
 PD 01-DEC-1998.
 PF 27-NOV-1995; 95US-0563105.
 XX
 PR 27-NOV-1995; 95US-0563105.
 XX
 PR 20-OCT-1993; 93US-0140222.
 XX
 PA (REGG-) REGENERON PHARM INC.

XX
 PI Economidis A, Stahl N, Yancopoulos GD;
 XX
 DR WPI; 1999-044669/04.
 XX
 PT Cytokine antagonists - comprising extracellular domains of
 PT specificity-determining and signal-transducing components of
 PT cytokine receptor
 PS Example 4; Fig 16; 46pp; English.
 XX
 CC The present sequence represents the amino acid sequence of interleukin
 CC (IL)-6R-alpha-313 domain. The protein is used in the course of the
 CC invention. The specification describes cytokine antagonists comprising
 CC only the extracellular domain of the specificity-determining component of
 CC the cytokine receptor and the extracellular domain of a
 CC signal-transducing component of the cytokine receptor. The cytokine
 CC is an interleukin (IL-1, IL-2, IL-3, IL-4, IL-5 or IL-15),
 CC granulocyte macrophage colony-stimulating factor (GM-CSF),
 CC gamma-interferon or transforming growth factor-beta (TGF-beta). The
 CC antagonist is capable of binding the cytokine to form a nonfunctional
 CC complex. The compounds have therapeutic activity as cytokine antagonists
 CC and can also be used in assays for identifying novel agonists and
 CC antagonists of cytokines.
 XX
 SQ Sequence 315 AA;
 QY
 Query Match 100.0%; Score 102; DB 20; Length 315;
 Best Local Similarity 100.0%; Pred. No. 2.2e-09;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 1 PRSTPSLTTRKAVLVRRKFRNS 21
 136 prstpslttkavllvrkfrqns 156
 RESULT 8
 AAY92200
 ID AAY92200 standard; protein; 315 AA.
 XX
 AC AAY92200;
 XX
 DT 01-AUG-2000 (first entry)
 XX
 DE Soluble human IL-6-R-alpha-313.
 XX
 KW Soluble IL-6-R-alpha-313; cytokine; antagonist; CNTF; receptor;
 KW fusion protein; cytoskeletal; immunomodulator; osteopathic.
 XX
 OS Homo sapiens.
 XX
 FT Key Location/Qualifiers
 FT Protein 1..313
 /label= "truncated_IL-6-R-alpha
 FT Peptide 314..315
 /note= "Tmr-Gly bridge"
 XX
 PN W0200018932-A2.
 XX
 PD 06-APR-2000.
 PF 22-SEP-1999; 99WO-US22045.
 XX
 PR 25-SEP-1998; 98US-0101858.
 XX
 PR 19-MAY-1999; 99US-0313942.
 XX
 PA (REGG-) REGENERON PHARM INC.
 XX
 PI Stahl N, Yancopoulos GD;
 XX
 DR WPI; 2000-293165/25.

PT Isolated nucleic acid molecule for treating cytokine-related diseases
 PT or disorders encodes a fusion polypeptide capable of binding a cytokine
 PT to form a nonfunctional complex

XX Example 4; Fig 16; 152pp; English.

CC The invention concerns production of antagonists to any cytokine that
 CC utilizes an alpha specificity determining component, which when combined
 CC with the cytokine, binds to a first beta signal transducing component to
 CC form a non-functional intermediate which then binds to a second beta
 CC signal transducing component causing beta-receptor dimerization, the
 CC soluble alpha specificity determining component of the receptor
 CC (SR-alpha) and the extracellular domain of the first beta signal
 CC transducing component of the cytokine receptor (beta-1) are combined to
 CC form heterodimers (SR-alpha:beta-1) that act as antagonist to the
 CC cytokine by binding the cytokine to form a non-functional complex. The
 CC receptor components are shared by cytokines such as the CNTF (ciliary
 CC neurotrophic factor) family of cytokines. The invention provides the
 CC basis for the development of IL-6 antagonists, as they show that if, in
 CC the presence of a ligand, a non-functional intermediate complex,
 CC consisting of the ligand, its alpha receptor and its beta-1 receptor
 CC component, can be formed, it will effectively block the action of the
 CC ligand. Effective antagonists of IL-6 or CNTF consist of heterodimers
 CC of the extracellular domains of the alpha specificity determining
 CC components of their receptors and the extracellular domain of gp130.
 CC The resultant heterodimers, function as high-affinity traps, rendering
 CC the cytokine inaccessible to form a signal transducing complex with the
 CC native membrane-bound forms of their receptor. The nucleic acids and
 CC polypeptides are useful for treating cytokine-related diseases or
 CC disorders such as osteoporosis and primary and secondary effects of
 CC cancer including multiple myeloma or cachexia.

SO Sequence 315 AA:

Query Match 100.0%; Score 102; DB 21; Length 315;
 Best Local Similarity 100.0%; Pred. No. 2,2e-09;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PRSTPSLTTRKAVLLVRKFQNS 21

DB 136 prstpslttkavllvrkfkqns 156

RESULT 9

ID AAP90527 standard; protein; 323 AA.

AC AAP90527;

XX 25-JAN-1990 (first entry)

DE B cell stimulating factor-2 receptor.

KW B cell stimulating factor-2 receptor; monocytic U937 cell line.

OS Homo sapiens.

PN A08928720-A.

PD 27-JUL-1989.

PF 23-JAN-1989; 89AU-0028720.

PR 22-JAN-1988; 88JP-0012387.

PR 25-JAN-1988; 88JP-0012599.

PR 04-AUG-1988; 88JP-0194885.

PR 14-JAN-1989; 89JP-0007461.

XX (KISH) TADAMITSU KISHIMOTO.

PA Kishimoto T;

DR WPI; 1989-264012/37.

DR N-PSDB; AAP90525.

PT Receptor protein for human B cell stimulating factor-2 - used for

PT developing prophylactic, therapeutic and diagnostic agents for

PT associated disorders.

PS Claim 6; page 39; 76pp; english.

XX The BSF2 receptor has amino acids at the C-terminal deleted. The receptor

CC is derived from a monocytic U937 cell line. It can be used to develop

CC prophylactic and therapeutic pharmaceuticals, as agents to relate

CC diseases and disorders to abnormal BSF-2 prodn. It can also be used to

CC study an immune mechanism with which BSF-2 or the receptor is concerned.

QY 1 PRSTPSLTTRKAVLLVRKFQNS 21

DB 136 prstpslttkavllvrkfkqns 156

RESULT 10

ID AAB15389 standard; protein; 325 AA.

AC AAB15389;

DT 11-DEC-2000 (first entry)

DE Human interleukin 6 receptor protein.

KW Human: interleukin-6 receptor; fungus; Pichia pastoris; PCR primer;

KW expression vector; immunoglobulin-like region; cytokine receptor region.

OS Homo sapiens.

FT Key Location/Qualifiers

FT Misc-difference 57 /note= "encoded by GGC"

FT Misc-difference 281 /note= "encoded by CAA"

PN JP2000157280-A.

PD 13-JUN-2000.

PF 26-NOV-1998; 98JP-0335464.

PR 26-NOV-1998; 98JP-0335464.

PA (TOYI) TOSOH CORP.

DR WPI; 2000-468203/41.

DR N-PSDB; AAA70701.

PT Yeasts transformed with IL-6 receptor gene -

PS Example 1; Page 6-8; 10pp; Japanese.

CC The invention relates to the production of human interleukin-6 receptor

CC (IL-6R) protein in the fungus Pichia pastoris. The fungus was

CC transformed with an expression vector (pPIC9-A20UL) containing a gene

CC encoding an IL-6R protein having an immunoglobulin-like region and

CC cytokine receptor region and spanning amino acids from Leu20-Ala323. The

CC human IL-6R region was PCR amplified using the primers AAA70702-A70703.

CC This sequence represents the recombinant IL-6R protein of the invention.

SQ Sequence 325 AA;

Query Match 100.0%; Score 102; DB 21; Length 325;
 Best Local Similarity 100.0%; Pred. No. 2.3e-09;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PRSTPSLTTRKAVLLVRKFGNS 21
 |||||
 Db 117 prstpslttkavllvrkfngs 137

RESULT 11

AAB15390 standard; Protein; 325 AA.

AAB15390;

AC AAB15390;

XX 15-DEC-2000 (first entry)

XX Bovine Interleukin-12 p35 subunit protein.

XX Antifluorescent; bovine; Interleukin 12; IL12; heterodimer; infection.

XX Bos taurus.

XX JP2000157274-A.

XX 13-JUN-2000.

XX 20-NOV-1998; 98JP-0331052.

XX 20-NOV-1998; 98JP-0331052.

XX (DAUC) DAICHI PHARM CO LTD.

XX WPI; 2000-468201/41.

XX N-PSDB; AAA/0708.

XX Preparation of bovine interleukin 12 comprising using a vector

XX containing the gene encoding it, useful for the prevention and

XX treatment of chronic and opportunistic infections -

XX Example 1; Page 8; 11pp; Japanese.

XX The invention relates to a method for the preparation of bovine

XX interleukin 12 (Boil12). Boil12 consists of a heterodimer of p35

XX and p40 subunits. Boil12 is produced by introducing into a host cell,

XX recombinant vectors containing genes encoding the p35 and p40 subunits.

XX This sequence represents the bovine IL12 p35 subunit. Interleukin 12

XX is used for the prevention and treatment of chronic infections and

XX opportunistic infections.

SQ Sequence 325 AA;

Query Match 100.0%; Score 102; DB 21; Length 325;
 Best Local Similarity 100.0%; Pred. No. 2.3e-09;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PRSTPSLTTRKAVLLVRKFGNS 21
 |||||
 Db 117 prstpslttkavllvrkfngs 137

RESULT 12

AAP90528 standard; Protein; 344 AA.

AAP90528;

XX 25-JAN-1990 (first entry)

XX

DE B cell stimulating factor-2 receptor.

XX B cell stimulating factor-2 receptor; monocytic U937 cell line.

XX Homo sapiens.

XX AU8928720-A.

XX 27-JUL-1989.

XX 23-JAN-1989; 89AU-0028720.

XX 22-JAN-1988; 88JP-0012387.

XX 25-JAN-1988; 88JP-0012599.

XX 04-AUG-1988; 88JP-0194885.

XX 14-JAN-1989; 89JP-0007461.

XX (KISH)-TADAMITSU KISHIMOTO.

XX Kishimoto T;

XX WPI; 1989-264012/37.

XX N-PSDB; AAP90525.

XX Receptor protein for human B cell stimulating factor-2 - used for

XX developing prophylactic, therapeutic and diagnostic agents for

XX associated disorders.

XX Claim 7; page 40; 76pp; English.

XX The BSF2 receptor has amino acids at the C-terminal deleted. The receptor

XX is derived from a monocytic U937 cell line. It can be used to develop

XX prophylactic and therapeutic pharmaceuticals, as agents to relate

XX diseases and disorders to abnormal BSF-2 prodn. It can also be used to

XX study an immune mechanism with which BSF-2 or the receptor is concerned.

XX SQ Sequence 344 AA;

Query Match 100.0%; Score 102; DB 10; Length 344;
 Best Local Similarity 100.0%; Pred. No. 2.4e-09;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PRSTPSLTTRKAVLLVRKFGNS 21
 |||||
 Db 136 prstpslttkavllvrkfngs 156

RESULT 13

AA155071 standard; Protein; 345 AA.

AA155071;

XX 25-FEB-2000 (first entry)

XX SR345 protein sequence.

XX Gene isolation; membrane-bound protein; fusion protein; drug production;

XX antigen-binding cell; secreted functional protein; antigenic protein;

XX protein isolation; diagnosis; SR345 protein.

XX Homo sapiens.

XX WO9960113-A1.

XX 25-NOV-1999.

XX 30-APR-1999; 99WO-JP02341.

XX 20-MAY-1998; 98JP-0138652.

XX 01-OCT-1998; 98JP-0279876.

PA (CHUS) CHUGAI SEIYAKU KK.
 XX
 PI Tsuchiya M, Saito M, Ohtomo T;
 XX WPI: 2000-039382/03.
 DR N-PSDB: AA240288.
 XX
 XX Efficient and selective isolation of a gene encoding membrane protein
 PT with low or no antigenic binding activity, for diagnosis, study of, and
 PI production of drugs treating abnormal functions of the protein
 XX
 XX Example 1; Page 49-52; 120pp; Japanese.
 PS
 CC This sequence represents the SR345 protein.
 CC The invention relates to a method for isolating a gene encoding a
 CC membrane-bound protein, comprising introducing a vector into a cell,
 CC contacting an antigen with the cell expressing the fused protein encoded
 CC by the vector on its surface to select an antigen-binding cell, and
 CC isolating the cDNA. The vector contains DNA encoding a secretable
 CC functional protein with antigenicity and binding affinity, and a cDNA
 CC ligated to DNA downstream of the 3' end of the coding sequence. The
 CC method can be used to isolate a membrane-bound protein for diagnosis and
 CC study. It can also be used for producing drugs treating abnormal
 CC functions of the protein. Such a technique is efficient and selective,
 CC which is different from the prior-art transmembrane trap (TMT) method
 CC wherein an epitope recognised by an antibody is carried in a fused
 CC protein.
 CC
 CC Sequence 345 AA:
 SQ

Query Match 100.0%; Score 102; DB 21; Length 345;
 Best Local Similarity 100.0%; Pred. No. 2.4e-09;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PRSTPSLTTRKAVLLVRRKFNQNS 21
 ||||||||||||||||||
 DB 136 prstpslttkavllvrkfkns 156

RESULT 14
 AAW70804
 ID AAW70804 standard; protein; 360 AA.
 XX
 AC AAW70804;
 XX
 DT 03-FEB-1999 (first entry)
 XX
 DE Amino acid sequence of the interleukin (IL)-6R-alpha domain.
 XX
 KM gp130; cytokine antagonist; interleukin; gamma-interferon;
 KM granulocyte macrophage colony-stimulating factor; J peptide;
 KW transforming growth factor-beta.
 XX
 OS Synthetic.
 OS
 FH Key Location/Qualifiers
 FT 1..358
 FT Protein /note="soluble interleukin (IL)-6R-alpha domain"
 PN US584409-A
 XX
 PD 01-DEC-1998.
 XX
 PF 27-NOV-1995; 95US-0563105.
 XX
 PR 27-NOV-1995; 95US-0563105.
 PR 20-OCT-1993; 93US-0140222.
 XX
 PA (REGC-) REGENERON PHARM INC.
 XX
 PI Economides A, Stahl N, Yancopoulos GD;
 XX

DR WPI: 1999-044669/04.
 XX
 PT Cytokine antagonists - comprising extracellular domains of
 PT specifically-determining and signal-transducing components of
 PT cytokine receptor
 XX
 PS Example 4; Fig 15; 46pp; English.
 XX
 CC The present sequence represents the amino acid sequence of interleukin
 CC (IL)-6R-alpha domain. The protein is used in the course of the invention.
 CC The specification describes cytokine antagonists comprising only the
 CC extracellular domain of the specifically-determining component of
 CC the cytokine receptor and the extracellular domain of a
 CC signal-transducing component of the cytokine receptor. The cytokine
 CC is an interleukin (IL-1, IL-2, IL-3, IL-4, IL-5 or IL-15),
 CC granulocyte macrophage colony-stimulating factor (GM-CSF),
 CC gamma-interferon or transforming growth factor-beta (TGF-beta). The
 CC antagonist is capable of binding the cytokine to form a nonfunctional
 CC complex. The compounds have therapeutic activity as cytokine antagonists
 CC and can also be used in assays for identifying novel agonists and
 CC antagonists of cytokines.
 CC
 CC Sequence 360 AA:
 SQ

Query Match 100.0%; Score 102; DB 20; Length 360;
 Best Local Similarity 100.0%; Pred. No. 2.6e-09;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PRSTPSLTTRKAVLLVRRKFNQNS 21
 ||||||||||||||||||
 DB 136 prstpslttkavllvrkfkns 156

RESULT 15
 AAY92199
 ID AAY92199 standard; protein; 360 AA.
 XX
 AC AAY92199;
 XX
 DT 01-AUG-2000 (first entry)
 XX
 DE Soluble human IL-6-R-alpha.
 XX
 KM Soluble IL-6-R-alpha; cytokine; antagonist; CNTF; receptor;
 KW fusion protein; cytosstatic; immunomodulator; osteopathic.
 XX
 OS Homo sapiens.
 OS
 PN WO200018932-A2.
 XX
 PD 06-APR-2000.
 XX
 PF 22-SEP-1999; 99WO-US22045.
 XX
 PR 25-SEP-1998; 98US-0101858.
 PR 19-MAY-1999; 99US-0313942.
 XX
 PA (REGC-) REGENERON PHARM INC.
 XX
 PI Stahl N, Yancopoulos GD;
 XX
 DR WPI: 2000-293165/25.
 XX
 PT Isolated nucleic acid molecule for treating cytokine-related diseases
 PT or disorders encodes a fusion polypeptide capable of binding a cytokine
 PT to form a nonfunctional complex
 XX
 PS Example 4; Fig 15; 152pp; English.
 XX
 CC The invention concerns production of antagonists to any cytokine that
 CC utilizes an alpha specificity determining component, which when combined
 CC with the cytokine, binds to a first beta signal transducing component to

CC form a non-functional intermediate which then binds to a second beta
 CC signal transducing component causing beta-receptor dimerization, the
 CC soluble alpha specificity determining component of the receptor
 CC (SR-alpha) and the extracellular domain of the first beta signal
 CC transducing component of the cytokine receptor (beta-1) are combined to
 CC form heterodimers (SR-alpha:beta-1) that act as antagonist to the
 CC cytokine by binding the cytokine to form a non-functional complex. The
 CC receptor components are shared by cytokines such as the CNTF (ciliary
 CC neurotrophic factor) family of cytokines. The invention provides the
 CC basis for the development of IL-6 antagonists, as they show that if, in
 CC the presence of a ligand, a non-functional intermediate complex,
 CC consisting of the ligand, its alpha receptor and its beta-1 receptor
 CC component, can be formed, it will effectively block the action of the
 CC ligand. Effective antagonists of IL-6 or CNTF consist of heterodimers
 CC of the extracellular domains of the alpha specificity determining
 CC components of their receptors and the extracellular domain of gp130.
 CC The resultant heterodimers, function as high-affinity traps, rendering
 CC the cytokine inaccessible to form a signal transducing complex with the
 CC native membrane-bound forms of their receptor. The nucleic acids and
 CC polypeptides are useful for treating cytokine-related diseases or
 CC disorders such as osteoporosis and primary and secondary effects of
 CC cancer including multiple myeloma or cachexia.

XX
 SQ Sequence 360 AA;

Query Match 100.0%; Score 102; DB 21; Length 360;
 Best Local Similarity 100.0%; Pred. No. 2.6e-09;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PRSTPSLTTRKAVLVKRFQNS 21
 |||
 DB 136 prstpslttkavllvrkfqs 156

Search completed: December 19, 2001, 16:19:34
 Job time: 359 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: December 19, 2001, 16:22:37 ; Search time 88.82 Seconds
(without alignments)
18.010 Million cell updates/sec

Title: US-09-202-104a-5
Perfect score: 102
Sequence: 1 PRSTPSLTKAVLLVRKFNONS 21

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :
1: PIR:68:*
2: PIR1:*
3: PIR2:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	102	100.0	468	1 A41242	interleukin-6 rece
2	58	36.9	440	2 J10144	interleukin-6 rece
3	58	56.9	460	2 J10145	interleukin-6 rece
4	56	54.9	462	1 A37986	interleukin-6 rece
5	50	49.0	242	2 D82609	hypothetical prote
6	43	42.2	321	2 J05460	intracellular alka
7	43	42.2	322	2 G83922	intracellular alka
8	43	42.2	322	2 J05460	intracellular alka
9	43	42.2	322	2 J05460	intracellular alka
10	43	42.2	322	2 J05460	intracellular alka
11	43	42.2	322	2 J05460	intracellular alka
12	43	42.2	322	2 J05460	intracellular alka
13	43	42.2	322	2 J05460	intracellular alka
14	43	42.2	322	2 J05460	intracellular alka
15	43	42.2	322	2 J05460	intracellular alka
16	43	42.2	322	2 J05460	intracellular alka
17	43	42.2	322	2 J05460	intracellular alka
18	43	42.2	322	2 J05460	intracellular alka
19	43	42.2	322	2 J05460	intracellular alka
20	43	42.2	322	2 J05460	intracellular alka
21	43	42.2	322	2 J05460	intracellular alka
22	43	42.2	322	2 J05460	intracellular alka
23	43	42.2	322	2 J05460	intracellular alka
24	43	42.2	322	2 J05460	intracellular alka
25	43	42.2	322	2 J05460	intracellular alka
26	43	42.2	322	2 J05460	intracellular alka
27	43	42.2	322	2 J05460	intracellular alka
28	43	42.2	322	2 J05460	intracellular alka
29	43	42.2	322	2 J05460	intracellular alka

30	40	39.2	710	2 T10654	hypothetical prote
31	40	39.2	1038	1 B42641	kinesin-related pr
32	40	39.2	1130	2 T21134	hypothetical prote
33	40	39.2	2870	2 A35548	319K protein nrbB
34	39.5	38.7	217	2 T33890	hypothetical prote
35	39.5	38.7	301	2 E72566	hypothetical prote
36	39.5	38.7	336	2 T20854	hypothetical prote
37	39.5	38.7	410	2 T06655	hypothetical prote
38	39	38.2	55	2 T11026	H+-transporting AT
39	39	38.2	90	2 S55417	hypothetical prote
40	39	38.2	107	2 H72480	hypothetical prote
41	39	38.2	115	2 G72493	hypothetical prote
42	39	38.2	192	1 UCFFPP	cuticle protein pr
43	39	38.2	194	1 LNRTC	pulmonary surfacta
44	39	38.2	269	2 T24637	hypothetical prote
45	39	38.2	316	2 T39656	probable golgi uri

ALIGNMENTS

RESULT 1
A41242
Interleukin-6 receptor precursor - human
N:Contains: interleukin-6 receptor, soluble form
C:Species: Homo sapiens (man)
C>Date: 27-Mar-1992 #sequence-revision 02-Dec-1994 #text-change 21-Jul-2000
C:Accession: A41242; J00080; S17468; A61459; S14621
R:Yamasaki, K.; Taga, T.; Hirata, Y.; Yawata, H.; Kawanshi, Y.; Seed, B.; Taniguchi, Science 241, 825-828, 1988
A:Title: Cloning and expression of the human interleukin-6 (BSF-2/IL6beta 2) receptor
A:Reference number: A41242; MUID:88305347
A:Accession: A41242
A:Molecule type: mRNA
A:Residues: 1-468 <YAM>
A:Cross-references: GB:M20566; NID:933845; PIDN:CAA31312.1; PID:933846
R:Yamasaki, K.; Taga, T.; Hirata, Y.; Yawata, H.; Kawanshi, Y.; Seed, B.; Taniguchi, Proc. Jpn. Acad. 64, 209-211, 1988
A:Title: Molecular structure of Interleukin 6 receptor.
A:Reference number: J00080
A:Accession: J00080
A:Molecule type: mRNA
A:Residues: 1-468 <YAM>
R:Schmidt, H.; Stoyan, T.; Lenz, D.; Schmitz, H.; Hirano, T.; Kishimoto, T.; Heinrich, J. 277, 659-664, 1991
A:Title: Structural and functional studies on the human hepatic interleukin-6 receptor
A:Reference number: S17468; MUID:91336983
A:Accession: S17468
A:Molecule type: mRNA
A:Residues: 1-468 <SCH>
A:Cross-references: EMBL:X58298; NID:932580; PIDN:CAA41231.1; PID:932581
A:Experimental source: hepatoma cell line Hep2
R:Novick, D.; Engelmann, H.; Wallach, D.; Rubinstein, M. J. Exp. Med. 170, 1409-1414, 1989
A:Title: Soluble cytokine receptors are present in normal human urine.
A:Reference number: A61459; MUID:90010793
A:Accession: A61459
A:Molecule type: protein
A:Residues: 20-49 <NOV>
C:Comment: Through this receptor, interleukin-6 induces proliferation, activation, an C:Comment: This growth factor receptor does not have a tyrosine kinase domain.
C:Genetics:
A:Gene: GDB: IL6R
A:Cross-references: GDB:127966; OMIM:147880
A:Map position: 1q21-1q21
C:Superfamily: ciliary neurotrophic factor receptor; cytokine receptor homology; immu C:Keywords: acute phase; cytokine receptor; glycoprotein; transmembrane protein F:1-19/Domain: signal sequence #status predicted <Sig> F:20-468/Product: interleukin-6 receptor #status predicted <MAT> F:20-363/Domain: extracellular #status predicted <EXT> F:40-98/Domain: immunoglobulin homology <IMM2> F:121-309/Domain: cytokine receptor homology <CRS> F:364-386/Domain: transmembrane #status predicted <TM>

F:387-468/Domain: intracellular #status predicted <INT>
 F:47-96/Disulfide bonds: #status predicted
 F:55,93,221,245,350/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 102; DB 1; Length 468;
 Best Local Similarity 100.0%; Pred. No. 1.5e-09;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PRSPSLTTKAVLLVRKFNQNS 21
 |||||
 Db 136 PRSPSLTTKAVLLVRKFNQNS 156

RESULT 2

JL0144 Interleukin-6 receptor precursor (clone lambda p1) - mouse

C:Species: Mus musculus (house mouse)

C>Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 21-Jan-2000

C:Accession: JL0144

R:Sugita, T.; Totsuka, T.; Salto, M.; Yamasaki, K.; Taga, T.; Hirano, T.; Kishimoto, T. J. Exp. Med. 171, 2001-2009, 1990

A:Title: Functional murine interleukin 6 receptor with the intracisternal a particle get

A:Reference number: JL0144; MUID:90278354

A:Accession: JL0144

A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-440 <SUG>

A:Cross-references: GB:X51976; NID:953548; PIDN:CAA36238.1; PID:953549

C:Superfamily: ciliary neurotrophic factor receptor; cytokine receptor homology; immunog

C:Keywords: cytokine receptor; transmembrane protein

F:1-19/Domain: signal sequence #status predicted <SIG>

F:20-440/Product: interleukin-6 receptor #status predicted <MAT>

F:40-94/Domain: immunoglobulin homology <IMM>

F:117-306/Domain: cytokine receptor homology <CRS>

F:358-385/Domain: transmembrane #status predicted <TRA>

Query Match 56.9%; Score 58; DB 2; Length 440;
 Best Local Similarity 57.1%; Pred. No. 0.051;

Matches 12; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

OY 1 PRSPSLTTKAVLLVRKFNQNS 21
 | |||||
 Db 132 PRSPSLTTKAVLLVRKFNQNS 152

RESULT 3

JL0145 Interleukin-6 receptor precursor (clone lambda 301) - mouse

C:Species: Mus musculus (house mouse)

C>Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 21-Jan-2000

C:Accession: JL0145; S14543

R:Sugita, T.; Totsuka, T.; Salto, M.; Yamasaki, K.; Taga, T.; Hirano, T.; Kishimoto, T. J. Exp. Med. 171, 2001-2009, 1990

A:Title: Functional murine interleukin 6 receptor with the intracisternal a particle get

A:Reference number: JL0144; MUID:90278354

A:Accession: JL0145

A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-460 <SUG>

A:Cross-references: GB:X51975; NID:949725; PIDN:CAA36237.1; PID:949726

A:Experimental source: clone lambda 301

A:Reference number: A82515; MUID:20365717

A:Note: for a complete list of authors see reference number A59328 below

A:Accession: D82609

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-242 <STM>

A:Cross-references: GB:AE004021; GB:A3003849; NID:99107139; PIDN:AAF84844.1; GSPDB:CN

A:Experimental source: strain 9a5c

A:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvares, R. Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Carraro, D.M.; Carer

C:Keywords: cytokine receptor; transmembrane protein
 F:1-19/Domain: signal sequence #status predicted <SIG>
 F:20-460/Product: interleukin-6 receptor #status predicted <MAT>
 F:40-94/Domain: immunoglobulin homology <IMM>
 F:117-306/Domain: cytokine receptor homology <CRS>
 F:358-385/Domain: transmembrane #status predicted <TRA>

Query Match 56.9%; Score 58; DB 2; Length 460;
 Best Local Similarity 57.1%; Pred. No. 0.054;

Matches 12; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

OY 1 PRSPSLTTKAVLLVRKFNQNS 21
 | |||||
 Db 132 PRSPSLTTKAVLLVRKFNQNS 152

RESULT 4

A37986 Interleukin-6 receptor precursor - rat

N:Alternate names: IL-6 receptor

C:Species: Rattus norvegicus (Norway rat)

C>Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 22-Jun-1999

C:Accession: A37986

R:Baumann, M.; Baumann, H.; Fey, G.H. J. Biol. Chem. 265, 19853-19862, 1990

A:Title: Molecular cloning, characterization and functional expression of the rat Ilv

A:Reference number: A37986; MUID:91060602

A:Accession: A37986

A:Molecule type: mRNA

A:Residues: 1-462 <BAU>

A:Cross-references: GB:M58587; GB:J05668; NID:9204921; PIDN:AAA41431.1; PID:9204922

C:Comment: After binding IL-6, this chain associates with a 130k glycoprotein that is

C:Superfamily: ciliary neurotrophic factor receptor; cytokine receptor homology; immu

C:Keywords: acute phase; cytokine receptor; transmembrane protein

F:1-19/Domain: signal sequence #status predicted <SIG>

F:20-462/Product: interleukin-6 receptor #status predicted <MAT>

F:40-94/Domain: immunoglobulin homology <IMM>

F:117-306/Domain: cytokine receptor homology <CRS>

F:363-385/Domain: transmembrane #status predicted <TRA>

F:386-462/Domain: intracellular #status predicted <INT>

F:47-92/Disulfide bonds: #status predicted

Query Match 54.9%; Score 56; DB 1; Length 462;
 Best Local Similarity 52.4%; Pred. No. 0.12;

Matches 11; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

OY 1 PRSPSLTTKAVLLVRKFNQNS 21
 | |||||
 Db 132 PRSPSLTTKAVLLVRKFNQNS 152

RESULT 5

D82609 hypothetical protein XF2042 [imported] - Xylella fastidiosa (strain 9a5c)

C:Species: Xylella fastidiosa

C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000

C:Accession: D82609

R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Seq

A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.

A:Reference number: A82515; MUID:20365717

A:Note: for a complete list of authors see reference number A59328 below

A:Accession: D82609

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-242 <STM>

A:Cross-references: GB:AE004021; GB:A3003849; NID:99107139; PIDN:AAF84844.1; GSPDB:CN

A:Experimental source: strain 9a5c

A:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvares, R. Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Carraro, D.M.; Carer

A:Experimental source: strain 972h-; cosmid c1271
C:Genetics:
A:Gene: SPDB:SPBC1271.15c
A:Map position: 2
A:Genome: nuclear
C:Superfamily: translation initiation factor IF-2; translation elongation factor Tu homolog
C:Keywords: mitochondrion
F:172-283/Domain: translation elongation factor Tu homolog

Query Match 42.2%; Score 43; DB 2; Length 686;
Best Local Similarity 50.0%; Pred. No. 31;
Matches 10; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 1 PRSTPSLTAKAVLVKRFON 20
DB 84 PKSTPLTLPAVLVSASFAN 103

RESULT 10
T16693
hypothetical protein R05F9.12 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 01-Dec-2000
C:Accession: T16693; T27894
R:Hallsworth, K.
Submitted to the EMBL Data Library, November 1995
A:Description: The sequence of C. elegans cosmid R05F9.
A:Reference number: Z18559
A:Accession: T16693
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-919 <HAL>
A:Cross-references: EMBL:U41533; NID:g1109807; PID:g1109820; PIDN:AAA83174.1; CESP:R05F9
R:Hallsworth, K.
Submitted to the EMBL Data Library, June 1995
A:Description: The sequence of C. elegans cosmid ZK546.
A:Reference number: Z20437
A:Accession: T27894
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-575 <HA2>
A:Cross-references: EMBL:U29380; PIDN:AAA68743.1; CESP:ZK546.10
A:Experimental source: strain Bristol N2
C:Genetics:
A:Gene: CESP:R05F9.12; CESP:ZK546.10
A:Introns: 31/3; 94/2; 174/3; 329/3; 524/3; 575/2; 607/2; 645/2; 739/1; 816/3
C:Superfamily: lysosomal alpha-glucosidase; sucrase/isomaltase homology; trefoil homology

Query Match 42.2%; Score 43; DB 2; Length 919;
Best Local Similarity 72.7%; Pred. No. 43;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 PRSTPSLTAKA 11
DB 744 PROPTSLTTTA 754

RESULT 11
T31419
cyclic beta 1-2 glucan synthetase - Brucella abortus
C:Species: Brucella abortus
C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 07-Dec-1999
C:Accession: T31419
R:Ion de Iannino, N.; Briones, G.; Tolmasky, M.; Ugalde, R.A.
J. Bacteriol. 180, 4392-4400, 1998
A:Title: Molecular cloning and characterization of cgs, the Brucella abortus cyclic beta chv mutants.
A:Reference number: Z21023; MUID:98389650
A:Accession: T31419
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA

A:Residues: 1-2831 <INO>
A:Cross-references: EMBL:AF047823; NID:g3551790; PID:g3551791; PIDN:AA634747.1
A:Experimental source: strain 519
C:Genetics:
A:Gene: cgs

Query Match 42.2%; Score 43; DB 2; Length 2831;
Best Local Similarity 60.0%; Pred. No. 1.5e+02;
Matches 12; Conservative 1; Mismatches 5; Indels 2; Gaps 1;

QY 1 PRSTPSLT--KAVLVKRF 18
DB 678 PRVTPSLTTGDEASFLQRF 697

RESULT 12
T46527
probable dTDP4-keto-6-deoxyhexose reductase [imported] - Streptomyces violaceoruber
C:Species: Streptomyces violaceoruber
C>Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 11-May-2000
C:Accession: T46527
R:Richiose, K.; Bedford, D.J.; Tornus, D.; Bechthold, A.; Bibb, M.J.; Revill, W.P.; F
Chem. Biol. 5, 647-659, 1998
A:Title: The granaticlin biosynthetic gene cluster of Streptomyces violaceoruber Tu22;
A:Reference number: Z23045; MUID:99051446
A:Accession: T46527
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-304 <ICH>
A:Cross-references: EMBL:A011500; PIDN:CAA09643.1
A:Experimental source: strain Tu22
C:Genetics:
A:Note: gra-orf22

Query Match 41.2%; Score 42; DB 2; Length 304;
Best Local Similarity 60.0%; Pred. No. 19;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 RSTPSLTAKAVLVKRF 16
DB 42 RGAGVTTTRAVDLVR 56

RESULT 13
T21480
hypothetical protein F28C6.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T21480
R:Burton, J.
Submitted to the EMBL Data Library, December 1995
A:Reference number: Z19429
A:Accession: T21480
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-535 <WIL>
A:Cross-references: EMBL:Z68315; PIDN:CAA92668.1; GSPDB:GN00020; CESP:F28C6.2
A:Experimental source: clone F28C6
C:Genetics:
A:Gene: CESP:F28C6.2
A:Map position: 2
A:Introns: 83/3; 278/2; 365/2

Query Match 41.2%; Score 42; DB 2; Length 535;
Best Local Similarity 52.6%; Pred. No. 35;
Matches 10; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 2 RSTPSLTAKAVLVKRFON 20
DB 418 RSYLSIVERAVLCEKTON 436

RESULT 14

A56731
 chromatin assembly factor I p150 chain - human
 C:Species: Homo sapiens (man)
 C:Date: 08-Feb-1996 #sequence_revision 08-Feb-1996 #text_change 21-Jul-2000
 C:Accession: A56731
 R:Kaufman, P.D.; Kobayashi, R.; Kessler, N.; Stillman, B.
 Cell 61, 1105-1114, 1995
 A:Title: The p150 and p60 subunits of chromatin assembly factor I: a molecular link betw
 A:Reference number: A56731; MUID:95323966
 A:Accession: A56731
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-938 <KAU>
 A:Cross-references: GB:U0979; NID:9882257; PIDN:AA76736.1; PID:9882258

Query Match 41.2%; Score 42; DB 2; Length 938;
 Best Local Similarity 47.6%; Pred.No. 65;
 Matches 10; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

OY 1 PRSTPSLTTKAVLVKRFQNS 21
 ||| | ||: : || | : |
 Db 186 PRSCPRLTSGPRNCPKREDS 206

RESULT 15

T31434
 densin-180 - rat
 N:Alternate names: postsynaptic density protein
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 07-Dec-1999
 C:Accession: T31434
 R:Apperson, M.L.; Moon, I.S.; Kennedy, M.B.
 J. Neurosci. 16, 6839-6852, 1996
 A:Title: Characterization of densin-180, a new brain-specific synaptic protein of the O-
 A:Reference number: 221033; MUID:96421675
 A:Accession: T31434
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-1495 <APP>
 A:Cross-references: EMBL:U66707; NID:g1657757; PID:g1657758; PIDN:AAC52881.1
 A:Experimental source: strain Sprague Dawley
 C:Function:
 A:Description: supposed to participate in specific adhesion between presynaptic and post

Query Match 41.2%; Score 42; DB 2; Length 1495;
 Best Local Similarity 66.7%; Pred.No. 11e+02;
 Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 10 KAVLVKRFQNS 21
 |||||: |||:
 Db 1473 KAVLVKRFQNS 1484

Search completed: December 19, 2001, 16:22:38
 Job time: 458 sec

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as-Neto, E.; Docena, C.; El-Dorri, H.; Facincani, A.P.; Ferreira, A.J.S.
 Submitted to GenBank, June 2000
 A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; From
 J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laig
 Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, H
 A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
 F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A
 Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
 A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir
 M.; Tsubako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
 A:Reference number: A59328
 A:Contents: annotation
 C:Genetics:
 A:Gene: XF2042

Query Match 38.4%; Score 56; DB 2; Length 242;
 Best Local Similarity 52.4%; Pred. No. 0.55;
 Matches 11; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

OY 3 GPRSPSLTKAVLVKRFON 23
 DB 44 GPLLDLTMTSTAVLLIRGFON 64

RESULT 6

LNRC1
 pulmonary surfactant protein C precursor - rabbit
 N:Alternate names: surfactant-associated protein SP-C
 C:Species: Oryctolagus cuniculus (domestic rabbit)
 C:Date: 01-Sep-1995 #sequence_revision 25-Apr-1997 #text_change 18-Feb-2000
 C:Accession: A56766; S14815; A56860; S19946; A56655
 R:Boggrang, V.; Margana, R.K.
 Am. J. Physiol. 263, L634-L644, 1992
 A:Title: Rabbit surfactant protein C: cDNA cloning and regulation of alternatively splic
 A:Reference number: A56766; MUID:9118799
 A:Accession: A56766
 A:Molecule type: mRNA
 A:Residues: 1-189 <BOG>
 A:Cross-references: GB:S51963; NID:g262767; PIDN:AMB24761.1; PID:g262766; GB:S51597; NID
 A:Experimental source: lung
 A:Note: sequence extracted from NCBI backbone (NCBIN:121728, NCBIPI:121729)
 R:Johnson, J.; Persson, P.; Loewenadler, B.; Robertson, B.; Joernvall, H.; Cursedt, T
 FEBS Lett. 281, 119-122, 1991
 A:Title: Canine hydrophobic surfactant polypeptide SP-C. A lipopeptide with one thioeste
 A:Reference number: S14813; MUID:91200266
 A:Accession: S14815
 A:Molecule type: protein
 A:Residues: 24-37 'XXXXXXXXXXXXXXXXXXXX' <JOH>
 R:Connelly, I.; Possnayer, F.
 Biochim. Biophys. Acta 1127, 199-207, 1992
 A:Title: cDNA sequence and alternative mRNA splicing of surfactant-associated protein C
 A:Reference number: A56860; MUID:92353123
 A:Accession: A56860
 A:Molecule type: mRNA
 A:Residues: 24-58 <CON>
 A:Cross-references: EMBL:X65078; NID:g1720; PIDN:CAA46204.1; PID:g1721
 A:Experimental source: fetal lung
 A:Note: sequence extracted from NCBI backbone (NCBIN:110198, NCBIPI:110234); the complete
 R:Connelly, I.; Possnayer, F.
 submitted to the EMBL data library, March 1992
 A:Description: cDNA sequence and alternative splicing of surfactant-associated protein C
 A:Reference number: S19946
 A:Accession: S19946
 A:Molecule type: mRNA
 A:Residues: 3-115, 117-161, 'R', 163-189 <CO2>
 A:Cross-references: EMBL:X65078; NID:g1720; PIDN:CAA46204.1; PID:g1721
 R:Durham, P.L.; Nanthakumar, E.J.; Snyder, J.M.
 Exp. Lung Res. 18, 775-793, 1992
 A:Title: Developmental regulation of surfactant-associated proteins in rabbit fetal lung
 A:Reference number: A56655; MUID:93105936
 A:Accession: A56655

A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 24-115, 117-186 'Y', 188-189 <DOR>
 A:Cross-references: GB:S51096; NID:g262066; PIDN:AMB24576.1; PID:g262067
 A:Experimental source: fetal lung
 A:Note: sequence extracted from NCBI backbone (NCBIN:121095, NCBIPI:121096); sequence
 C:Comment: Pulmonary surfactant is a complex of phospholipids and proteins that lower
 C:Comment: This protein is synthesized by alveolar type II cells.
 C:Comment: The precursor of the hydrophobic proteolipid protein C lacks a typical sig
 C:Superfamily: pulmonary surfactant protein C
 C:Keywords: gaseous exchange; lipoprotein; lung; pulmonary surfactant; thioester bon
 F:1-23/Domain: propeptide #status predicted <PRO>
 F:24-58/Product: pulmonary surfactant protein C #status experimental <MAT>
 F:28,29/Binding site: palmitate (Cys) (covalent) #status experimental

Query Match 34.2%; Score 50; DB 1; Length 189;
 Best Local Similarity 54.2%; Pred. No. 3.5;
 Matches 13; Conservative 1; Mismatches 6; Indels 4; Gaps 1;

OY 4 PRSPSLTKAVLVKRFONSPAE 27
 DB 129 PDSPSLTA---LARKFOANPAE 148

RESULT 7

C40899
 hypothetical protein 2 - Chinese hamster intracisternal A-particle CHIAp34
 C:Species: Chinese hamster intracisternal A-particle CHIAp34
 C:Date: 06-Mar-1992 #sequence_revision 06-Mar-1992 #text_change 16-Feb-1997
 C:Accession: C40899
 R:Donner, A.J.; Bonneville, F.; Kriz, R.; Kelleher, K.; Bean, K.; Kaufman, R.J.
 J. Virol. 65, 4713-4719, 1991
 A:Title: Molecular cloning and characterization of a complete Chinese hamster proviru
 A:Reference number: A40899; MUID:91333012
 A:Accession: C40899
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-204 <DOR>
 A:Cross-references: GB:M73970
 C:Superfamily: AIDS-related virus gag polyprotein
 Query Match 34.2%; Score 50; DB 2; Length 204;
 Best Local Similarity 40.0%; Pred. No. 3.8;
 Matches 10; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

OY 2 WGRSPSLTKAVLVKRFONSPA 26
 DB 90 WPKKMPRTYTSHTSLOGGCGOSSPA 114

RESULT 8

T02693
 S-receptor kinase homolog - rice (fragment)
 C:Species: Oryza sativa (rice)
 C:Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 26-May-2000
 C:Accession: T02693
 R:Yun, C.H.; Lee, J.S.; Park, J.H.; Yoon, U.H.; Eun, M.Y.
 submitted to the EMBL data library, January 1998
 A:Description: Cloning and molecular characterization of receptor-like protein kinase
 A:Reference number: Z14701
 A:Accession: T02693
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-413 <YUN>
 A:Cross-references: EMBL:AF044489; NID:g2832303; PID:g2832304
 A:Experimental source: strain lipoombyeo
 C:Genetics:
 A:Gene: dtp1
 C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase hom

Query Match 34.2%; Score 50; DB 2; Length 413;
 Best Local Similarity 34.8%; Pred. No. 8.4;
 Matches 8; Conservative 5; Mismatches 10; Indels 0; Gaps 0;
 QY 1 EMGPRSTPSLTTRKAVLLVRKFN 23
 DB 374 QMNPKRPSMTKVMNLTGRLO 396

RESULT 9
 T06793
 Receptor kinase homolog LRK10 - wheat
 N:Alternate names: rust resistance kinase LR10
 C:Species: Triticum aestivum (common wheat)
 C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-May-2000
 C:Accession: T06793
 R:Reuillet, C.; Schachermayr, G.; Keller, B.
 Plant J. 11, 45-52, 1997
 A:Title: A novel class of receptor-like kinase mapping to the LR10 locus in wheat.
 A:Reference number: Z15819; MUID:9717795
 A:Accession: T06793
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1636 <FEU>
 A:Cross-references: EMBL:U51330; NID:g1680685; PIDN:AA049629.1; PID:g1680686
 A:Experimental source: leaf
 C:Genetics:
 A:Gene: LRK10
 A:Map position: 1
 A:Intons: 272/1. 280/1
 C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolog

Query Match 33.6%; Score 49; DB 2; Length 636;
 Best Local Similarity 34.8%; Pred. No. 19;
 Matches 8; Conservative 6; Mismatches 9; Indels 0; Gaps 0;
 QY 1 EMGPRSTPSLTTRKAVLLVRKFN 23
 DB 597 QMNPKRPSMTKVMNLTGRLO 619

RESULT 10
 S59861
 band 3 anion transport protein isoform b - rainbow trout
 C:Species: Oncorhynchus mykiss (rainbow trout)
 C:Date: 15-Feb-1996 #sequence_revision 01-Mar-1996 #text_change 20-Aug-1999
 C:Accession: S59861
 R:Eleval, B.; Gabillat, N.; Borgese, F.; Motaïs, R.
 EMBO J. 14, 5158-5169, 1995
 A:Title: Expression of band 3 anion exchanger induces chloride current and taurine trans
 A:Reference number: S59861; MUID:96080151
 A:Accession: S59861
 A:Status: preliminary; nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-912 <FIE>
 A:Cross-references: EMBL:Z50848; NID:g1004316; PIDN:CAA90701.1; PID:g1004317
 C:Superfamily: band 3 anion transport protein

Query Match 33.6%; Score 49; DB 2; Length 912;
 Best Local Similarity 34.6%; Pred. No. 29;
 Matches 9; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

QY 1 EMGPRSTPSLTTRKAVLLVRKFN 26
 DB 104 KMGPSHVSYLTKSLDQKRMSTGA 129

RESULT 11
 S24318
 band 3 anion transport protein - rainbow trout
 C:Species: Oncorhynchus mykiss (rainbow trout)

C:Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 20-Aug-1999
 C:Accession: S24318; S36083; S22173
 R:Ruebner, S.; Michel, F.; Rudloff, V.; Appelhans, H.
 Biochem. J. 285, 17-23, 1992
 A:Title: Amino acid sequence of band-3 protein from rainbow trout erythrocytes derive
 A:Reference number: S24318; MUID:92344566
 A:Accession: S24318

A:Molecule type: mRNA
 A:Residues: 1-918 <HUE1>
 A:Cross-references: EMBL:X61699
 A:Accession: S36083
 A:Molecule type: protein
 A:Residues: 71-89;94-114;570-588 <HUE2>
 R:Appelhans, H.
 submitted to the EMBL Data Library, August 1991
 A:Reference number: S22173
 A:Accession: S22173
 A:Molecule type: mRNA
 A:Residues: 1304,'G',306-918 <APP>
 A:Cross-references: EMBL:X61699; NID:g64308; PIDN:CAA43868.1; PID:g64309
 C:Superfamily: band 3 anion transport protein
 C:Keywords: erythrocyte; transmembrane protein

Query Match 33.6%; Score 49; DB 2; Length 918;
 Best Local Similarity 34.6%; Pred. No. 29;
 Matches 9; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

QY 1 EMGPRSTPSLTTRKAVLLVRKFN 26
 DB 110 KMGPSHVSYLTKSLDQKRMSTGA 135

RESULT 12
 A71056
 probable 5'-methylthiodenosine phosphorylase - Pyrococcus horikoshii
 C:Species: Pyrococcus horikoshii
 C:Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 20-Jun-2000
 C:Accession: A71056
 R:Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Se
 M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudo, Y.; Yamazaki, J.; Kushida, N.; Ogu
 DNA Res. 5, 55-76, 1998
 A:Title: Complete sequence and gene organization of the genome of a hyper-thermophil
 A:Reference number: A71000; MUID:98344137
 A:Accession: A71056
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1265 <KAW>
 A:Cross-references: GB:AP000005; NID:g3236132; PIDN:BAA30243.1; PID:g3257560
 A:Experimental source: strain OT3
 A:Note: this accession replaces an interim accession for a sequence replaced by GenBa
 C:Genetics:
 A:Gene: PH1143
 C:Superfamily: 5'-methylthiodenosine phosphorylase

Query Match 32.9%; Score 48; DB 2; Length 265;
 Best Local Similarity 41.7%; Pred. No. 10;
 Matches 10; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

QY 5 RSTPSLTTRKAVLLVRKFN 28
 DB 235 RETALYTKAIPILPKERNCPCKD 258

RESULT 13
 T24637
 hypothetical protein T07C12.11 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 C:Accession: T24637
 R:McMurray, A.
 submitted to the EMBL Data Library, June 1996

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: December 19, 2001, 16:26:15 ; Search time 48.45 Seconds
(without alignments)
15.892 Million cell updates/sec

Title: US-09-202-104a-5
Perfect score: 102
Sequence: 1 PRSTPSLTAKAVLVRKQNS 21

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues
Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	102	100.0	468	1 IL6A_HUMAN	P08887 homo sapien
2	89	87.3	467	1 IL6A_PIG	P01876 sus scrofa
3	58	56.9	460	1 IL6A_MOUSE	P22272 mus musculu
4	56	54.9	462	1 IL6A_RAT	P22273 rattus norv
5	46	45.1	328	1 MNM2_KIUTA	Q00974 kluyteromyc
6	43	42.2	586	1 PHE1_ARATH	Q43867 arabidopsi
7	43	42.2	686	1 IF2M_SCHPO	Q59683 schizosacch
8	43	42.2	964	1 CAPP_AMANP	Q43299 amarantus
9	42	41.2	1028	1 BGAL_ENTCL	Q47077 enterobacte
10	41	40.2	1234	1 RPA2_NEUCR	Q74633 neurospora
11	40.5	39.7	419	1 VS48_TBRYE	P23070 tomato blac
12	40	39.2	134	1 DC4C_ACIKA	P20370 acinetobact
13	40	39.2	179	1 PTH_CHLTR	O84806 chlamydia t
14	40	39.2	190	1 P5PC_MUSVI	P35245 mustela vis
15	40	39.2	841	1 PHL2_HUMAN	O15127 homo sapien
16	40	39.2	914	1 AFSB_HUMAN	O94823 homo sapien
17	40	39.2	1038	1 CINE_YEAST	P27885 saccharomyc
18	40	39.2	2870	1 NDVB_ARHME	P20471 thizobium m
19	39	38.2	55	1 ATP8_AYTAM	O9xk55 athya amer
20	39	38.2	90	1 YWJC_BACSU	P45883 bacillus su
21	39	38.2	192	1 CUPP_DROPS	P16369 drosophila
22	39	38.2	194	1 P5PC_RAT	P1665 rattus norv
23	39	38.2	330	1 PHOG_EMBNI	Q05534 emericeella
24	39	38.2	342	1 YE4A_YEAST	P40004 saccharomyc
25	39	38.2	457	1 Z185_HUMAN	O15231 homo sapien
26	39	38.2	464	1 DNAA_TREPA	O83047 treponema p
27	39	38.2	960	1 CSE1_YEAST	P33307 saccharomyc
28	39	38.2	966	1 CAP1_SACHY	P29183 saccharum h
29	39	38.2	1176	1 NIR_NEUCR	P38661 neurospora
30	39	38.2	1517	1 YD22_SCHPO	Q10230 schizosacch
31	39	38.2	2774	1 MAPA_RAT	P44926 rattus norv
32	38.5	37.7	225	1 YRNI_CAEEL	O09604 caenorhabdi
33	38.5	37.7	395	1 SDC_DROME	P49415 drosophila

ALIGNMENTS

34	38.5	37.7	419	1 VS48_TBRYC	P22048 tomato blac
35	38	37.3	180	1 PTH_CHLNP	O9z6v6 chlamydia p
36	38	37.3	218	1 Y381_MYCCE	P47621 mycoplasma
37	38	37.3	403	1 YDHC_ECOLI	P37597 escherichia
38	38	37.3	424	1 VS48_TBRYL	P22050 tomato blac
39	38	37.3	424	1 VS48_TBRYL	P22051 tomato blac
40	38	37.3	592	1 HS60_PARRB	O60008 paracoccidi
41	38	37.3	719	1 GROU_DROME	P16371 drosophila
42	38	37.3	926	1 UVRA_AQUAE	O66911 aquilex aeo
43	38	37.3	960	1 CAP1_SORBI	P29195 sorghum bic
44	38	37.3	960	1 CAP2_MESCR	P16097 mesembryant
45	38	37.3	960	1 CAP2_SORBI	P29194 sorghum bic

RESULT 1	IL6A_HUMAN	STANDARD;	PRT;	468 AA.
AC	P08887; 016202;			
DT	01-NOV-1988 (Rel. 09, Created)			
DT	01-NOV-1988 (Rel. 09, Last sequence update)			
DT	20-AUG-2001 (Rel. 40, Last annotation update)			
DE	INTERLEUKIN-6 RECEPTOR ALPHA CHAIN PRECURSOR (IL-6R-ALPHA) (IL-6R 1)			
DE	(CD126 ANTIGEN).			
GN	IL6R.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_TaxID:9606;			
RN	[1]			
RP	SEQUENCE FROM N.A. (LONG ISOFORM).			
RX	MEDLINE-88305347; PubMed-316546;			
RA	Yamasaki K., Taga T., Hirata Y., Yawata H., Kawanishi Y., Seed B.,			
RA	Taniguchi T., Hirano T., Kishimoto T.;			
RT	"Cloning and expression of the human Interleukin-6 (BSF-2/IFN beta 2)			
RT	receptor.";			
RL	Science 241:825-828(1988).			
RN	[2]			
RP	SEQUENCE FROM N.A. (LONG ISOFORM).			
RA	Yamasaki K., Taga T., Hirata Y., Yawata H., Kawanishi Y., Seed B.,			
RA	Taniguchi T., Hirano T., Kishimoto T.;			
RT	"Molecular structure of Interleukin 6 receptor.";			
RL	Proc. Jpn. Acad., B. Phys. Biol. Sci. 64:209-211(1988).			
RN	[3]			
RP	SEQUENCE FROM N.A. (LONG ISOFORM).			
RX	MEDLINE-9136983; PubMed-1872801;			
RA	Schoofli H., Stoyan T., Lenz D., Schmitz H., Hirano T.,			
RA	Kishimoto T., Heinrich P.C., Rose-John S.;			
RT	"Structural and functional studies on the human hepatic interleukin-6			
RT	receptor. Molecular cloning and overexpression in HepG2 cells.";			
RL	Biochem. J. 277:659-664(1991).			
RN	[4]			
RP	SEQUENCE OF 313-365 FROM N.A. (SHORT ISOFORM).			
RX	MEDLINE-94333499; PubMed-8056053;			
RA	Horiuchi S., Koyanagi Y., Zhou Y., Miyamoto H., Tanaka Y., Waki M.,			
RA	Matsuno A., Yamamoto M., Yamamoto N.;			
RT	"Soluble interleukin-6 receptors released from T cell or			
RT	granulocyte/macrophage cell lines and human peripheral blood			
RT	mononuclear cells are generated through an alternative splicing			
RT	mechanism.";			
RL	Eur. J. Immunol. 24:1945-1948(1994).			
RN	[5]			
RP	PARTIAL SEQUENCE, CARBOHYDRATE-LINKAGE SITES, AND DISULFIDE BONDS.			
RX	MEDLINE-99167486; PubMed-10066782;			
RA	Cole A.R., Hall N.F., Treutlein H.R., Eddes J.S., Reid G.E.,			
RA	Moritz R.L., Simpson R.J.;			
RT	"Disulfide bond structure and N-glycosylation sites of the			
RT	extracellular domain of the human Interleukin-6 receptor.";			
RL	J. Biol. Chem. 274:7207-7215(1999).			
RN	[6]			
RP	MUTAGENESIS.			

RX MEDLINE-93223711; PubMed-8467812;
 RA Yawata H., Yasukawa K., Natsuka S., Murakami M., Yamasaki K., Hibi M.,
 RA Taga T., Kishimoto T.;
 RT Structure-function analysis of human IL-6 receptor: dissociation of
 RT amino acid residues required for IL-6-binding and for IL-6 signal
 RT transduction through gp130.;
 RL EMBO J. 12:11705-11712(1993).
 CC -1 FUNCTION: PART OF THE RECEPTOR FOR INTERLEUKIN 6. BINDS TO IL-6
 CC WITH LOW AFFINITY, BUT DOES NOT TRANSDUCE A SIGNAL. SIGNAL
 CC ACTIVATION NECESSITATE AN ASSOCIATION WITH IL6ST. ACTIVATION MAY
 CC LEAD TO THE REGULATION OF THE IMMUNE RESPONSE, ACUTE-PHASE
 CC REACTIONS AND HEATOPOIESIS.
 CC -1 FUNCTION: LOW CONCENTRATION OF A SOLUBLE FORM OF INTERLEUKIN-6
 CC RECEPTOR ACTS AS AN AGONIST OF IL-6 ACTIVITY.
 CC -1 SUBUNIT: HEXAMER OF 2 IL6, 2 IL6R-ALPHA AND 2 IL6ST.
 CC -1 SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (LONG FORM) AND
 CC SECRETED (SHORT FORM).
 CC -1 ALTERNATIVE PRODUCTS: 2 ISOFORMS: A LONG FORM (SHOWN HERE) AND A
 CC SHORT FORM: ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1 TISSUE SPECIFICITY: THE SHORT FORM IS EXPRESSED IN PERIPHERAL
 CC BLOOD MONONUCLEAR CELLS AND WEAKLY FOUND IN URINE AND SERUM.
 CC -1 DOMAIN: THE TWO FIBROBLAST TYPE IIL-LIKE DOMAINS CONTAINED IN THE
 CC N-TERMINAL PART FORM TOGETHER A CYTOXINE-BINDING DOMAIN.
 CC -1 PTM: A SHORT SOLUBLE FORM MAY ALSO BE RELEASED FROM THE MEMBRANE
 CC BY PROTEOLYSIS.
 CC -1 SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
 CC -1 SIMILARITY: CONTAINS 3 FIBRONECTIN TYPE IIL-LIKE DOMAINS.
 CC -1 SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 CC -1 DATABASE: NAME-PROV: NOTE-CD guide CD126 entry;
 CC WWW-<http://www.ncbi.nlm.nih.gov/prov/cd/cd126.htm>
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 CC -----
 DR EMBL: X12830; CAA31312.1; -;
 DR EMBL: X58298; CAA41231.1; -;
 DR EMBL: S72848; AAC60635.1; -;
 DR PIR: A41242; A41242.
 DR PIR: J00080; J00080.
 DR PIR: S14621; S14621.
 DR PIR: S17468; S17468.
 DR MIM: 147880; -;
 DR InterPro: IPR002996; CRA.
 DR InterPro: IPR001777; FN_III.
 DR InterPro: IPR003530; Hematopo_receptor_L_F3.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003598; Ig_C2.
 DR Pfam: PF00041; fn3; 1.
 DR Pfam: PF00047; Ig; 1.
 DR SMART: SM00060; FN3; 1.
 DR SMART: SM00408; IgC2; 1.
 DR PROSITE: PS01354; HEMATOPO_REC_L_F3; 1.
 DR Receptor: Transmembrane; Glycoprotein; Immunoglobulin domain; Repeat;
 DR Alternative splicing; Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 468 INTERLEUKIN-6 RECEPTOR ALPHA CHAIN.
 FT DOMAIN 20 365 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 366 386 POTENTIAL.
 FT DOMAIN 387 468 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 40 103 IG-LIKE C2-TYPE DOMAIN.
 FT DISULFID 25 193
 FT DISULFID 47 96
 FT DISULFID 121 132
 FT DISULFID 165 176
 FT CARBOHYD 55 55 N-LINKED (GLCNAC. . .).
 FT CARBOHYD 93 93 N-LINKED (GLCNAC. . .).
 FT CARBOHYD 221 221 N-LINKED (GLCNAC. . .).
 FT VARSPLIC 356 365 VQSSSVPLP -> GSRHSGCGL (IN SHORT

FT VARSPLIC 366 468
 FT MUTAGEN 121 121 MISSING (IN SHORT ISOFORM).
 FT MUTAGEN 122 122 C->S: COMPLETE LOSS OF LIGAND-BINDING.
 FT MUTAGEN 132 132 F->A: NO CHANGE OF LIGAND-BINDING AND IL6
 FT MUTAGEN 133 132 C->A: COMPLETE LOSS OF LIGAND-BINDING.
 FT MUTAGEN 134 134 W->L: COMPLETE LOSS OF LIGAND-BINDING.
 FT MUTAGEN 140 140 P->G: NO CHANGE OF LIGAND-BINDING AND IL6
 FT MUTAGEN 153 153 F->L: NO CHANGE OF LIGAND-BINDING AND IL6
 FT MUTAGEN 165 165 C->L: COMPLETE LOSS OF LIGAND-BINDING.
 FT MUTAGEN 174 174 F->L: NO CHANGE OF LIGAND-BINDING AND IL6
 FT MUTAGEN 176 176 C->A: COMPLETE LOSS OF LIGAND-BINDING.
 FT MUTAGEN 184 184 D->T: 30% DECREASE OF LIGAND-BINDING AND
 FT MUTAGEN 190 190 IL6 SIGNALING.
 FT MUTAGEN 193 193 V->G: 80% DECREASE OF LIGAND-BINDING AND
 FT MUTAGEN 211 211 NO IL6 SIGNALING.
 FT MUTAGEN 217 217 C->D: COMPLETE LOSS OF LIGAND-BINDING.
 FT MUTAGEN 232 232 C->A: NO CHANGE OF LIGAND-BINDING AND IL6
 FT MUTAGEN 233 233 SIGNALING.
 FT MUTAGEN 254 254 D->V: COMPLETE LOSS OF LIGAND-BINDING.
 FT MUTAGEN 277 277 R->S: 30% DECREASE OF LIGAND-BINDING AND
 FT MUTAGEN 278 278 IL6 SIGNALING.
 FT MUTAGEN 279 279 W->Q: 30% DECREASE OF LIGAND-BINDING AND
 FT MUTAGEN 280 280 INCREASE OF IL6 SIGNALING.
 FT MUTAGEN 281 281 E->A: 50% DECREASE OF LIGAND-BINDING AND
 FT MUTAGEN 285 285 IL6 SIGNALING.
 FT MUTAGEN 291 291 C->D: 30% INCREASE OF LIGAND-BINDING AND
 FT MUTAGEN 293 293 C->D: 30% INCREASE IN IL6 SIGNALING.
 FT SEQUENCE 468 AA; 51547 MW; 62AA239FAL4P1BBB CRC64;
 Query Match 100.0%; Score 102; DB 1; Length 468;
 Best Local Similarity 100.0%; Pred. No. 1; Se-09;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 PRSPSLTTKAVLVKRFONS 21
 Db 136 PRSPSLTTKAVLVKRFONS 156
 RESULT 2
 ID IL6A_PIG STANDARD: PRC: 467 AA.
 AC O18796;
 DT 20-AUG-2001 (Rel. 40, Created)
 DT 20-AUG-2001 (Rel. 40, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE INTERLEUKIN-6 RECEPTOR ALPHA CHAIN PRECURSOR (IL-6R-ALPHA) (IL-6R 1).
 GN IL6R.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OC NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Morris K.R., Strom A.D.G.;
 RT "Cloning and expression of biologically active porcine IL-6 receptor
 RT alpha chain.";
 RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.

```

RN [12]
RP SEQUENCE OF 123-186 FROM N.A.
RC TISSUE=Liver;
RA Kilar U.J., Matheri R.L.;
RL "Partial cDNA sequence of porcine interleukin 6 receptor.";
CC Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
CC -1 FUNCTION: PART OF THE RECEPTOR FOR INTERLEUKIN 6. BINDS TO IL-6
CC WITH LOW AFFINITY. BUT DOES NOT TRANSDUCE A SIGNAL. SIGNAL
CC ACTIVATION NECESSITATE AN ASSOCIATION WITH IL6ST. ACTIVATION MAY
CC LEAD TO THE REGULATION OF THE IMMUNE RESPONSE. ACUTE-PHASE
CC REACTIONS AND HEMATOPOIESIS.
CC -1 SUBUNIT: HEXAMER OF 2 IL6, 2 IL6R-ALPHA AND 2 IL6ST (BY
CC SIMILARITY).
CC -1 SUBCELLULAR LOCATION: TYPE 1 MEMBRANE PROTEIN.
CC -1 TISSUE SPECIFICITY: EXPRESSED IN LIVER.
CC -1 DOMAIN: THE TWO FIBRONECTIN TYPE III-LIKE DOMAINS CONTAINED IN THE
CC C-TERMINAL PART FORM TOGETHER A CYTOKINE-BINDING DOMAIN.
CC -1 SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC -1 SIMILARITY: CONTAINS 3 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -1 SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC
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CC or send an email to license@isb-sib.ch).
CC -----
CC DR EMBL: AF147881; AAF73109.1; -
CC DR EMBL: AF015116; AAB70916.1; -
CC DR HSSP: p16471.1BP3.
CC DR InterPro: IPR002996; CRA.
CC DR InterPro: IPR001777; FN_III.
CC DR InterPro: IPR003530; Hematopo_receptor_L_F3.
CC DR InterPro: IPR003066; Ig_MHC.
CC DR InterPro: IPR003598; Ig_C2.
CC DR Pfam: PF00041; Iu3; 1.
CC DR Pfam: PF00047; Ig; 1.
CC DR SMART: SM00060; FN3; 1.
CC DR SMART: SM00408; IgC2; 1.
CC DR PROSITE: PS00340; RECEPTOR_CYTOKINES_2; 1.
CC KW Receptor; Transmembrane; Glycoprotein; Immunoglobulin domain; Repeat;
CC Signal.
CC
CC FT SIGNAL 1 19 BY SIMILARITY.
CC FT CHAIN 20 467 INTERLEUKIN-6 RECEPTOR ALPHA CHAIN.
CC FT DOMAIN 20 365 EXTRACELLULAR (POTENTIAL).
CC FT TRANSEM 366 386 POTENTIAL.
CC FT DOMAIN 387 467 CYTOPLASMIC (POTENTIAL).
CC FT DOMAIN 40 103 IG-LIKE C2-TYPE DOMAIN.
CC FT DISULFID 25 193 BY SIMILARITY.
CC FT DISULFID 47 96 BY SIMILARITY.
CC FT DISULFID 121 132 BY SIMILARITY.
CC FT DISULFID 165 176 BY SIMILARITY.
CC FT CARBOHYD 55 55 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 93 93 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 221 221 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 350 350 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC SO SEQUENCE 467 AA; 5106 MW; A2B0B884EF21C502 CMC64;

Query Match 87.3%; Score 89; DB 1; Length 467;
Best Local Similarity 90.5%; Pred. No. 2.2e-07;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 1 PRSTPSLTTKAVLVKRFONS 21
111 11 111111111111111
136 PRSPSPPTTKAVLVKRFONS 156

RESULT 3
ID IL6A_MOUSE STANDARD; PRT; 460 AA.

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AC P22272; 1991 (Rel. 19, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE INTERLEUKIN-6 RECEPTOR ALPHA CHAIN PRECURSOR (IL-6R-ALPHA) (IL-6R 1).
GN IL6RA OR IL6R.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId:10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BAIB/C; TISSUE=Spleen;
RX MEDLINE=90278354; PubMed=2112585;
RA Sugita T., Totsuka T., Saito M., Yamasaki K., Taga T., Hirano T.,
RA Kishimoto T.;
RT *Functional murine interleukin 6 receptor with the intracisternal A
RT particle gene product at its cytoplasmic domain. Its possible role in
RT plasmacytomaogenesis.";
RL J. Exp. Med. 171:2001-2009(1990).
RL [2]
RN SEQUENCE FROM N.A.
RP STRAIN=C3H; TISSUE=Liver;
RC Fiorillo M.T., Ciliberto G., Dente L.;
RX Submitted (JUL-1990) to the EMBL/GenBank/DBJ databases.
RA Submitted (JUL-1990) to the EMBL/GenBank/DBJ databases.
RL Submitted (JUL-1990) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: PART OF THE RECEPTOR FOR INTERLEUKIN 6. BINDS TO IL-6
CC WITH LOW AFFINITY, BUT DOES NOT TRANSDUCE A SIGNAL. SIGNAL
CC ACTIVATION NECESSITATE AN ASSOCIATION WITH IL6ST. ACTIVATION MAY
CC LEAD TO THE REGULATION OF AN IMMUNE RESPONSE, ACUTE-PHASE
CC REACTIONS AND HEMATOPOIESIS.
CC -1- SUBUNIT: HEXAMER OF 2 IL6, 2 IL6R-ALPHA AND 2 IL6ST (BY
CC SIMILARITY).
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- DOMAIN: THE TWO FIBROBLAST TYPE III-LIKE DOMAINS CONTAINED IN THE
CC C-TERMINAL PART FORM TOGETHER A CYTOKINE-BINDING DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC -1- SIMILARITY: CONTAINS 3 FIBROBLAST TYPE III-LIKE DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
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CC -----
DR EMBL: X51975; CAA36237.1; -;
DR EMBL: X53802; CAA37610.1; -;
DR PIR: J10144; J10144.
DR PIR: J10145; J10145.
DR PIR: S14543; S14543.
DR HSSP: P16471; 1BP3.
DR MGI: 105304; IL6ra.
DR InterPro: IPR002996; CRLA.
DR InterPro: IPR001777; FN_III.
DR InterPro: IPR003530; Hematopo_rceptor_L_F3.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003598; Ig_C2.
DR Pfam: PF00041; fn3; 1.
DR Pfam: PF00047; Ig; 1.
DR SMART: SMO0060; FN3; 1.
DR SMART: SMO0408; IGC2; 1.
DR PROSITE: PS01354; HEMATOPO_REC_L_F3; 1.
KM Receptor; Transmembrane; Glycoprotein; Immunoglobulin domain; Repeat;
KW Signal.
FT SIGNAL 1 19
FT CHAIN 20 460 INTERLEUKIN-6 RECEPTOR ALPHA CHAIN.
FT DOMAIN 20 364 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 365 385 POTENTIAL.
FT DOMAIN 386 460 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 40 99 IG-LIKE C2-TYPE DOMAIN.
FT DISULFID 25 190 BY SIMILARITY.

KM Transp.; Sugar transport; Transmembrane; Golgi stack.
 FT TRANSMEM 1 21 POTENTIAL.
 FT TRANSMEM 30 50 POTENTIAL.
 FT TRANSMEM 66 86 POTENTIAL.
 FT TRANSMEM 98 118 POTENTIAL.
 FT TRANSMEM 122 142 POTENTIAL.
 FT TRANSMEM 166 186 POTENTIAL.
 FT TRANSMEM 198 218 POTENTIAL.
 FT TRANSMEM 241 261 POTENTIAL.
 FT TRANSMEM 274 294 POTENTIAL.
 FT TRANSMEM 298 318 POTENTIAL.
 SQ SEQUENCE 328 AA; 3666 MW; 93A31FACA804D1EF CRC64;

Query Match 45.1%; Score 46; DB 1; Length 328;
 Best Local Similarity 62.5%; Pred. No. 2.5;
 Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 3 STPSTTTKAVLVKRF 18
 : : : : :
 DB 270 NTDALVLSVLLVRF 285

RESULT 6
 PMEL_ARATH STANDARD; PRT; 586 AA.
 ID PMEL_ARATH 043867;
 AC 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE PECTINESTERASE 1 PRECURSOR (EC 3.1.1.11) (PECTIN METHYLESTERASE 1) (PE
 1).
 GN PMEL OR T18A20.7.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV, COLUMBIA; TISSUE=Shoot;
 RX MEDLINE=95073518; PubMed=7982486;
 RA Richard L., Qin L.X., Gadal P., Goldberg R.;
 RT "Molecular cloning and characterisation of a putative pectin
 methylesterase cDNA in Arabidopsis thaliana (L.).";
 RL FEBS Lett. 355:135-139(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96235136; PubMed=8666246;
 RA Richard L., Qin L., Goldberg R.;
 RT "Clustered genes within the genome of Arabidopsis thaliana encoding
 pectin methylesterase-like enzymes.";
 RL Gene 170:207-211(1996).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV, COLUMBIA;
 RA Federspiel N.A., Palm C.J., Conway A.B., Conn L., Hansen N.F.,
 Altif H., Arujo R., Ruizar L., Kowley D., Buehler E., Dunn P.,
 Gonzalez A., Kremenetskaia I., Kim C., Lenz C., Li J., Liu S.,
 Luirs S., Schwartz J., Shim P., Toriumi M., Vysotskaia V.S.,
 Walker M., Yu G., Ecker J., Theologis A., Davis R.W.;
 RT Submitted (Oct-1999) to the EMBL/GenBank/DBJ databases.
 RL -1- CATALYTIC ACTIVITY: PECTIN + N H(2)O = N METHANOL + PECTATE.
 CC -1- SIMILARITY: BELONGS TO THE PECTINESTERASE FAMILY.
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DR EMBL; X81585; CAA57275.1; -
 DR EMBL; U25649; AAC50024.1; -
 DR EMBL; AC009324; AAF02857.1; -
 DR Mendel; 6818; ARATH.1273.3.
 DR InterPro; IPR000070; Pectinesterase.
 DR Pfam; PF01095; Pectinesterase; 1.
 DR PROSITE; PS00800; PECTINESTERASE_1; 1.
 DR PROSITE; PS00503; PECTINESTERASE_2; 1.
 KW Signal; Hydrolyse; Serine esterase; Cell wall; glycoprotein;
 FT Signal family.
 FT SIGNAL 1 49 POTENTIAL.
 FT CHAIN 1 50 586 PECTINESTERASE 1.
 FT DOMAIN 248 251 POLY-ARG.
 FT CARBOHYD 57 57 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 97 97 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 154 154 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 201 201 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 207 207 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 466 466 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 586 AA; 64149 MW; EF2752BC535BE9 CRC64;

Query Match 42.2%; Score 43; DB 1; Length 586;
 Best Local Similarity 42.9%; Pred. No. 16;
 Matches 9; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 1 PRSTPSITTKAVLVKRFONS 21
 : : : : :
 DB 65 PELTPSTSLKALICSVTRFERS 85

RESULT 7
 IF2M_SCHPO STANDARD; PRT; 686 AA.
 ID IF2M_SCHPO 059683;
 AC 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE TRANSLATION INITIATION FACTOR IF-2, MITOCHONDRIAL PRECURSOR (IF-2MT)
 DE (IF-2(MT)).
 GN SPBC2F6.01 OR SPBC1271.15C.
 OS Schizosaccharomyces pombe (Fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC Schizosaccharomycetes.
 OX NCBI_TaxID=4896;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=972;
 RA Lyne M., Rejzndream M.A., Barrell B.G., Beck A., Borzym K., Klages S.,
 Langer I., Reinhardt R.;
 RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: IF-2, ONE OF THE ESSENTIAL COMPONENTS FOR THE INITIATION
 CC OF PROTEIN SYNTHESIS. PROTECTS FORMYL METHIONYL-TRNA FROM
 CC SPONTANEOUS HYDROLYSIS AND PROMOTES ITS BINDING TO THE 30S
 CC RIBOSOMAL SUBUNIT. IT IS ALSO INVOLVED IN THE HYDROLYSIS OF GTP
 CC DURING THE FORMATION OF THE 70S RIBOSOMAL COMPLEX (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL.
 CC -1- SIMILARITY: BELONGS TO THE IF-2 FAMILY.
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 CC EMBL; AL034353; CAA22205.1; -
 DR InterPro; IPR000795; GTP_EFTU.
 DR InterPro; IPR000178; IF2.
 DR Pfam; PF00009; GTP_EFTU; 1.
 DR Pfam; PF02131; IF2; 1.

DR PRODCM; PD186100; IF2. 1.
 DR PROSITE; PS01176; IF2. 1.
 KW Initiation factor; Protein biosynthesis; GTP-binding; Transit peptide;
 KM Mitochondrion.
 FT TRANSIT 1 2 MITOCHONPRION (POTENTIAL).
 FT CHAIN 2 686 TRANSLATION INITIATION FACTOR IF-2.
 FT DOMAIN 170 322 G-DOMAIN.
 FT NE_BIND 178 185 GTP (BY SIMILARITY).
 FT NE_BIND 226 230 GTP (BY SIMILARITY).
 FT NE_BIND 280 283 GTP (BY SIMILARITY).
 SQ SEQUENCE 686 AA; 75611 MW; 6F5B5CEDC6F3A5CD CRC64;

Query Match 42.2%; Score 43; DB 1; Length 686;
 Best Local Similarity 50.0%; Pred. No. 19;
 Matches 10; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

OY 1 PRPSLTTKAVLLVRKFN 20
 DB 84 PKSTPLTLPVALSVASFAN 103

RESULT 8

CAP_AMAHP STANDARD; PRT; 964 AA.
 AC Q43299;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE PHOSPHOMOLYBDATE CARBOXYLASE (EC 4.1.1.31) (PEPCASE).
 OS Amarantus hypochondriacus (Prince's feather).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophytes; Magnoliophyta; eudicotyledons; core eudicots;
 OC Caryophyllales; Caryophyllales; Amaranthaceae; Amaranthus.
 NCBI_TaxID=28502;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Leaf;
 RA Rydzik E., Berry J.;
 RT "The C4 phosphoenolpyruvate carboxylase (PEPCase) from grain
 Amaranth.";
 RL (in) Plant Gene Register PGR95-135.
 CC -1- FUNCTION: TO FORM OXALOACETATE, A FOUR-CARBON DICARBOXYLIC ACID
 CC SOURCE FOR THE TRICARBOXYLIC ACID CYCLE.
 CC -1- CATALYTIC ACTIVITY: ORTHOPHOSPHATE + OXALOACETATE = H(2)O +
 CC PHOSPHOMOLYBDATE + CO(2).
 CC -1- ENZYME REGULATION: BY LIGHT-REVERSIBLE PHOSPHORYLATION (BY
 CC SIMILARITY).
 CC -1- PATHWAY: TRICARBOXYLIC ACID CYCLE. THIS ISOZYME IS INVOLVED IN
 CC C4 PHOTOSYNTHESIS.
 CC -1- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC -1- SIMILARITY: BELONGS TO THE PEPCASE FAMILY.
 CC -----
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 CC -----
 CC EMBL; Z68125; CAA92209.1; -;
 CC EMBL; L49175; AAB18633.1; -;
 CC InterPro; IPR001449; PEPCase.
 CC Pfam; PF00311; PEPCase; 1.
 CC PRINTS; PR00150; PEPCARXLAASE.
 CC PROSITE; PS00393; PEPCASE_2; 1.
 CC PROSITE; PS00781; PEPCASE_1; 1.
 KW Lyase; Carbon dioxide fixation; Allosteric enzyme; Multigene family;
 KW Tricarboxylic acid cycle; Phosphorylation; Photosynthesis.
 FT MOD_RES 11 11 PHOSPHORYLATION (BY SIMILARITY).
 FT ACT_SITE 172 172 BY SIMILARITY.

FT ACT_SITE 600 600 BY SIMILARITY.
 SQ SEQUENCE 964 AA; 109480 MW; 3E49C2DEBDE11B3 CRC64;

Query Match 42.2%; Score 43; DB 1; Length 964;
 Best Local Similarity 56.2%; Pred. No. 28;
 Matches 9; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

OY 1 PRPSLTTKAVLLVR 16
 DB 292 PRVPEVTRDQVLLAR 307

RESULT 9

BGAL_ENTCL STANDARD; PRT; 1028 AA.
 ID BGAL_ENTCL
 AC Q47077;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update).
 DE BETA-GALACTOSIDASE (EC 3.2.1.23) (LACTASE).
 GN LACZ.
 OS Enterobacter cloacae.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Enterobacter.
 NCBI_TaxID=550;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=GAO;
 RX MEDLINE=95072316; PubMed=7765512;
 RA Nagano H., Kawaguchi T., Omori M., Shoji Z., Arai M.;
 RT "Molecular cloning and nucleotide sequence of the beta-galactosidase
 gene from Enterobacter cloacae GAO.";
 RL Biosci. Biotechnol. Biochem. 58:1866-1869(1994).
 CC -1- CATALYTIC ACTIVITY: HYDROLYSIS OF TERMINAL, NON-REDUCING BETA-D-
 CC GALACTOSE RESIDUES IN BETA-D-GALACTOSIDES.
 CC -1- SIMILARITY: BELONGS TO FAMILY 2 OF GLYCOSYL HYDROLASES.
 CC -----
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 CC -----
 CC EMBL; D42077; BAA07673.1; -;
 CC InterPro; IPR001649; Glyco_hydro_2.
 CC Pfam; PF00703; Glyco_hydro_2; 1.
 CC PRINTS; PR00132; GLYHDLASE2.
 CC PROSITE; PS00719; GLYCOSYL_HYDROL_F2_1; 1.
 CC PROSITE; PS00608; GLYCOSYL_HYDROL_F2_2; 1.
 KW Hydrolyase; Glycosidase.
 FT ACT_SITE 463 463 PROTON DONOR (BY SIMILARITY).
 FT ACT_SITE 539 539 NUCLEOPHILE (BY SIMILARITY).
 SQ SEQUENCE 1028 AA; 116678 MW; F4D61F5F9FEAEC CRC64;

Query Match 41.2%; Score 42; DB 1; Length 1028;
 Best Local Similarity 52.9%; Pred. No. 44;
 Matches 9; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

OY 4 TPSTLTKAVLLVRKFN 20
 DB 4 TPSTLTSALLARRDWEN 20

RESULT 10
 RPA2_NEUCR STANDARD; PRT; 1234 AA.
 ID RPA2_NEUCR
 AC 074633;
 DT 20-AUG-2001 (Rel. 40, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last sequence update)


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DT 20-AUG-2001 (Rel. 40, last annotation update)
DE POLYMERASE I SUBUNIT 2. (EC 2.7.7.6) (RNA
GN ACR-2.
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxId=5441;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=UN-18;
RX MEDLINE=98420098; PubMed=9749669;
RA Onai K., Katagiri S., Akiyama M., Nakashima H.;
RT *Mutation of the gene for the second-largest subunit of RNA polymerase
RT I prolongs the period length of the circadian condensation rhythm in
RT Neurospora crassa.
RL Mol. Gen. Genet. 259:264-271(1998).
CC -1 FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
CC OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
CC SUBSTRATES. RNA POLYMERASE I IS ESSENTIALLY USED TO TRANSCRIBE
CC RIBOSOMAL DNA UNITS.
CC -1 CATALYTIC ACTIVITY: N NUCLEOSIDE TRIPHOSPHATE - N PYROPHOSPHATE +
CC RNA(N).
CC -1 SUBUNIT: RNA POLYMERASE I CONSISTS OF 14 DIFFERENT SUBUNITS. THIS
CC SUBUNIT IS THE SECOND LARGEST COMPONENT OF RNA POLYMERASE I (BY
CC SIMILARITY).
CC -1 SUBCELLULAR LOCATION: NUCLEAR.
CC -1 MISCELLANEOUS: THREE DISTINCT ZINC-CONTAINING RNA POLYMERASES ARE
CC FOUND IN EUKARYOTIC NUCLEI: POLYMERASE I FOR THE RIBOSOMAL RNA
CC PRECURSOR, POLYMERASE II FOR THE MRNA PRECURSOR, AND POLYMERASE
CC II FOR 5S AND 5.8S GENES.
CC -1 SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA CHAIN FAMILY.
CC -----
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CC -----
DR EMBL: AB006052; BAA33445.1; -
DR InterPro: IPR001572; RNA_POL_B.
DR Pfam: PF00562; RNA_POL_B; 1.
DR PROSITE: PS01166; RNA_POL_BETA; 1.
KW Transcripase; DNA-directed RNA polymerase; Transcription; Zinc;
KW Zinc-finger; Nuclear protein.
FT FT 1119 1150
FT ZN-FING
FT VARIANT 976 976
FT C4-TYPE (POTENTIAL).
FT G -> D (IN UN-18; SHOWS A TS PHENOTYPE
FT WITH RESPECT TO BOTH MYCELIAL GROWTH AND
FT THE PERIOD LENGTH OF THE CONDINATION
FT RHYTHM).
SQ SEQUENCE 1234 AA; 138551 MW; B91388C69EDC7C4 CR664;

Query Match 40.2%; Score 41; DB 1; Length 1234;
Best Local Similarity 50.0%; Pred. No. 79;
Matches 8; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 4 TPSTLTKAVLLVKKFQ 19
DB 297 TPSTLDRVALLRTRYK 312

RESULT 11
VS48.TBRVE STANDARD; PRT; 419 AA.
AC P22049;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE SATELLITE RNA 48 KDA PROTEIN.
OS Tomato black ring virus (strain E) (TBRV).

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CC   Viruses ssRNA positive-strand viruses, no DNA stage; Comoviridae;
OC   Nucleovirus.
OX   NCBI_TaxID=12277;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Hemmer O., Meyer M., Greif C., Flitsch C.;
RT   "Comparison of the nucleotide sequences of five tomato black ring
RL   virus satellite RNAs."
RL   J. Gen. Virol. 68:1823-1833(1987).
RN   [2]
RP   REVISIONS.
RA   Flitsch C.;
RL   Submitted (FEB-1988) to the EMBL/GenBank/DDBJ databases.
CC   -----
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CC   -----
DR   EMBL; X05688; CAB59631.1; -.
DR   EMBL; D00143; BAA00091.1; -.
DR   PIR; B27169; SAYVTE.
SQ   SEQUENCE   419 AA;  47792 MW;  78FD7B9C246CC7CB CRC64;

Query Match          39.7%; Score 40.5; DB 1; Length 419;
Best Local Similarity 41.7%; Pred. No. 28;
Matches 10; Conservative 5; Mismatches 4; Indels 5; Gaps 1;

QY   3 STPSL-----TTKAVLYVRKFQNS 21
      |||:      |::||:| |||
Db   121 STPAKIQIKPPESTILNQAQIQNS 144

RESULT  12
DC4C_ACICA          STANDARD;      PRT;   134 AA.
AC   P20370;
DT   01-FEB-1991 (Rel. 17, Created)
DT   01-FEB-1991 (Rel. 17, Last sequence update)
DT   20-AUG-2001 (Rel. 40, Last annotation update)
DE   4-CARBOXYMUCONOLACTONE DECARBOXYLASE (EC 4.1.1.44) (CMD).
GN   PCAC.
OS   Acinetobacter calcoaceticus.
OC   Bacteria; Proteobacteria; gamma subdivision; Moraxellaceae;
OC   Acinetobacter.
OX   NCBI_TaxID=471;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BD413 / ADP1.
RX   MEDLINE=90130333; PubMed=2298704;
RA   Hattnett C., Neidle E.L., Ngai K.-L., Ornstom L.N.;
RT   "DNA sequences of genes encoding Acinetobacter calcoaceticus
RT   proteocatechuate 3,4-dioxygenase: evidence indicating shuffling of
RT   genes and of DNA sequences within genes during their evolutionary
RT   divergence."
RL   J. Bacteriol. 172:956-966(1990).
RL   J. Bacteriol. 172:956-966(1990).
CC   -1- CATALYTIC ACTIVITY: 2-CARBOXY-5-OXO-2,5-DIHYDROFURAN-2-ACETATE =
CC   5-OXO-4,5-DIHYDROFURAN-2-ACETATE + CO(2).
CC   -1- PATHWAY: THIRD STEP IN THE CATABOLISM OF PROTOCATCHUATE TO
CC   SUCCINATE-AND ACETYL-COA IN THE BETA-KETOADIPIATE PATHWAY.
CC   -----
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CC   -----

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DR EMBL: L05770; AAC37152.1; -
 DR PIR: B35119; B35119; CMD.
 DR InterPro: IPR003779; CMD.
 DR Pfam: PF02627; CMD: 1.
 KW Aromatic hydrocarbons catabolism; Lyase; Decarboxylase.
 SQ SEQUENCE 134 AA; 15324 MW; 3AEDDELFEIC2834A CRC64;

Query Match 39.2%; Score 40; DB 1; Length 134;
 Best Local Similarity 71.4%; Pred. No. 9.2;
 Matches 10; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 PRSTPSLTAKAVLL 14
 I I I I I I I I I I
 Db 56 PRHTRSLVITAVLL 69

RESULT 13
 ID PTH_CHLTR STANDARD; PRT; 179 AA.
 AC 084806;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE PEPTIDYL-TRNA HYDROLASE (EC 3.1.1.29) (PTH).
 GN PTH OR CT800.
 OS Chlamydia trachomatis.
 OC Chlamydia trachomatis.
 OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
 NCBI_TaxID=813;
 RX STRAIN-D/UM-3/CX;
 RX MEDLINE=99000809; Pubmed=9784136;
 RA Stephens R.S., Kalan S., Lammel C.J., Fan J., Marathe R., Aravind L.,
 RA Mitchell W.P., Olinger L., Tatunov R.L., Zhao Q., Koonin E.V.,
 RA Davis R.W.;
 RT Genome sequence of an obligate intracellular pathogen of humans:
 RT Chlamydia trachomatis.;
 RT Science 282:754-759(1998).
 CC -1- FUNCTION: THE NATURAL SUBSTRATE FOR THIS ENZYME MAY BE PEPTIDYL-
 CC TRNAS WHICH DROP OFF THE RIBOSOME DURING PROTEIN SYNTHESIS
 CC (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: N-SUBSTITUTED AMINOACYL-TRNA + H(2)O - N-
 CC SUBSTITUTED AMINO ACID + TRNA.
 CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE PTH FAMILY.
 CC -----
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 CC -----
 DR EMBL: AE001352; AAC68395.1; -
 DR HSSP: P23932; PPTH.
 DR InterPro: IPR001328; Pept_trna_hydro.
 DR Pfam: PF001195; Pept_trna_hydro.1.
 DR PRODOM: PD005324; Pept_trna_hydro.1.
 DR PROSITE: PS01195; Pept_trna_hydro.1.
 DR PROSITE: PS01196; Pept_trna_hydro.2.1.
 KW Hydrolase; Complete proteome.
 SQ SEQUENCE 179 AA; 19963 MW; 8E3D6A0D92C533F8 CRC64;

Query Match 39.2%; Score 40; DB 1; Length 179;
 Best Local Similarity 50.0%; Pred. No. 13;
 Matches 9; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

OY 1 PRSTPSLTAKAVLVKRF 18
 I I I I I I I I I I

Db 63 PTTYNLTGKAVLAKKF 80

RESULT 14
 ID PSPC_MUSVI STANDARD; PRT; 190 AA.
 AC P35245;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE PULMONARY SURFACTANT-ASSOCIATED PROTEIN C PRECURSOR (SP-C).
 GN SERP1 OR SERP2.
 OS Mustela vison (American mink).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Mustela.
 NCBI_TaxID=9667;
 RX [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung;
 RA Christensen J., Belousov J., Storgaard T., Aasted B., Alexandersen S.;
 RL Submitted (DEC-1992) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: PULMONARY SURFACTANT ASSOCIATED PROTEINS PROMOTE
 CC ALVEOLAR STABILITY BY LOWERING THE SURFACE TENSION AT THE AIR-
 CC LIQUID INTERFACE IN THE PERIPHERAL AIR SPACES.
 CC -1- SUBCELLULAR LOCATION: EXTRACELLULAR.
 CC -1- MISCELLANEOUS: PULMONARY SURFACTANT CONSISTS OF 90% LIPID AND 10%
 CC PROTEIN. THERE ARE 4 SURFACTANT ASSOCIATED PROTEIN: 2 COLLAGENOUS,
 CC CARBOHYDRATE-BINDING GLYCOPROTEINS (SP-A AND SP-D) AND 2 SMALL
 CC HYDROPHOBIC PROTEINS (SP-B AND SP-C).
 CC -----

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 CC -----

DR EMBL: Z19516; CAI79577.1; -
 DR PIR: S31490; S31490.
 DR HSSP: P15785; ISPF.
 DR InterPro: IPR001729; Pulm_surfact_AP.
 DR Pfam: PF02125; PSAP; 1.
 DR PRODOM: PD009591; Pulm_surfact_AF; 1.
 DR SMART: SM00019; SF_P; 1.
 DR DR PROSITE: PS00341; SURFACT_PALMITOYL_FALSE_NEG.
 DR KW Surface film; Gaseous exchange; Lipoprotein; Palmitate.
 FT PROPEP 1 23
 FT CHAIN 24 58
 FT C.
 FT LIPID 28 28 PALMITATE (BY SIMILARITY).
 FT SQ SEQUENCE 190 AA; 20431 MW; FFA262747A11E27 CRC64;

Query Match 39.2%; Score 40; DB 1; Length 180;
 Best Local Similarity 50.0%; Pred. No. 14;
 Matches 10; Conservative 1; Mismatches 5; Indels 4; Gaps 1;

OY 1 PRSTPSLTAKAVLVKRF 20
 I I I I I I I I I I
 Db 128 PENIPSLTEA---LTRKFN 143

RESULT 15
 ID PHL2_HUMAN STANDARD; PRT; 841 AA.
 AC Q15127;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE PHOSPHATIDYLINOSITOL-GLYCAN-SPECIFIC PHOSPHOLIPASE D 2 PRECURSOR
 DE (EC 3.1.4.50) (PI-G PLD) (GLYCOPROTEIN PHOSPHOLIPASE D) (GLYCOSYL-
 DE PHOSPHATIDYLINOSITOL SPECIFIC PHOSPHOLIPASE D).

GN GPLD2 OR PIGPLD2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Tsang T.C., Fung W.-J.C., Levine J., Metz C.N., Davitz M.A.,
RA Burns D.K., Huang K.-S., Kochan J.P.;
RT Isolation and expression of two human glycosylphosphatidylinositol
phospholipase D (GPI-PLD) cDNAs.*;
RL FASEB J. 6:A1922-A1922(1992).
CC -I- FUNCTION: THIS PROTEIN HYDROLYSES THE INOSITOL PHOSPHATE LINKAGE
IN PROTEINS ANCHORED BY PHOSPHATIDYLINOSITOL GLYCANS (GPI-ANCHOR)
CC THIS RELEASING THESE PROTEINS FROM THE MEMBRANE.
CC -I- CATALYTIC ACTIVITY: GLYCOPROTEIN PHOSPHATIDYLINOSITOL + H(2)O =
CC PHOSPHATIDATE + GLYCOPROTEIN INOSITOL.
CC -I- SUBCELLULAR LOCATION: EXTRACELLULAR.
CC -----
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CC -----
DR EMBL; L11701; AAA36444.1; -.
DR MIM; 602515; -.
DR InterPro; IPR000413; Integrin_alpha.
DR InterPro; IPR001028; Phospholipase_D.
DR Pfam; PF01839; EG-GAP; 6.
DR PRINTS; PR00718; PPHPLIPASD.
DR SMART; SM00191; Int_alpha; 5.
DR HydroLase; Glycoprotein; Signal.
KW SIGNAL
FT 1 24
FT CHAIN 25 841
FT FT
FT CARBOHYD 95 95 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 272 272 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 308 308 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 322 322 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 502 502 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 569 569 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 592 592 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 605 605 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 660 660 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 841 AA; 92666 MW; 656C6FCA6A2D9DC2 CRC64;
BY SIMILARITY.
PHOSPHATIDYLINOSITOL-GLYCAN-SPECIFIC
PHOSPHOLIPASE D 2.
Query Match 39.2%; Score 40; DB 1; Length 841;
Best Local Similarity 53.3%; Pred. No. 75;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
OY 5 PSLTKAVLVKRFQ 19
II::II::II::II
Db 231 PSYSTRKSPFLVEQFQ 245

Search completed: December 19, 2001, 16:26:15
Job time: 570 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: December 19, 2001, 16:25:21 ; Search time 157.32 Seconds
(without alignments)
19.525 Million cell updates/sec

Title: US-09-202-104a-5
Perfect score: 102
Sequence: 1 PRSTPSLTTRKAVLLVRFFONS 21

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: SPTREMBL_17:*
2: sp_archaea:*
3: sp_bacteria:*
4: sp_fungi:*
5: sp_human:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	50	49.0	242	2 09PB03	09pb03 xylella fas
2	46	45.1	627	10 09AT00	09atq0 triticum ae
3	44	43.1	371	11 09D541	09d541 mus musculu
4	44	43.1	534	10 09FMT4	09fnt4 arabidopsi
5	44	43.1	572	4 09HA71	09ha71 homo sapien
6	44	43.1	600	4 09BV36	09bv36 homo sapien
7	44	43.1	1269	5 09VD17	09vd17 drosophila
8	43	42.2	184	5 077159	077159 tetrahymena
9	43	42.2	321	2 P74937	P74937 thermocactin
10	43	42.2	322	2 09KAV3	09kav3 bacillus ha
11	43	42.2	458	5 053624	053624 streptomyce
12	43	42.2	919	5 021750	021750 caenorhabdi
13	43	42.2	1744	3 094192	094192 paracoccidi
14	43	42.2	1967	12 010378	010378 rice transi
15	43	42.2	2831	2 085166	085166 druceella ab
16	42.5	41.7	701	10 09SRL4	09srl4 arabidopsi
17	42.5	41.7	957	5 09V9A3	09v9a3 drosophila
18	42	41.2	296	11 09J142	09j142 rattus norv
19	42	41.2	304	2 09ZA37	09za37 streptomyce

20	42	41.2	535	5 019862	019862 caenorhabdi
21	42	41.2	598	13 P70032	P70032 xenopus lae
22	42	41.2	831	4 09P212	09p212 homo sapien
23	42	41.2	938	4 013111	013111 homo sapien
24	42	41.2	938	4 09UYT8	09uyt8 homo sapien
25	42	41.2	1495	11 P70587	P70587 rattus norv
26	41	40.2	188	5 0917P6	0917p6 drosophila
27	41	40.2	214	2 P73454	P73454 synecocyst
28	41	40.2	304	10 09FTG1	09ftg1 oryza sativ
29	41	40.2	362	5 09GRU8	09gru8 caenorhabdi
30	41	40.2	382	5 001933	001933 caenorhabdi
31	41	40.2	433	5 094478	094478 dictyostell
32	41	40.2	462	10 09ZUF4	09zuf4 pseudomonas
33	41	40.2	515	2 091418	091418 pseudomonas
34	41	40.2	606	11 09Z116	09z116 mus musculu
35	41	40.2	638	10 09AT05	09at05 triticum ae
36	41	40.2	663	10 09FE96	09fe96 oryza sativ
37	41	40.2	672	2 09PLQ0	09plq0 chlamydia m
38	41	40.2	707	5 017047	017047 caenorhabdi
39	41	40.2	1441	4 015074	015074 homo sapien
40	41	40.2	1603	5 09NE14	09ne14 leishmania
41	41	40.2	1750	5 09BK11	09bk11 trypanosoma
42	40	39.2	160	2 09RKV5	09rkv5 streptomyce
43	40	39.2	207	5 022044	022044 caenorhabdi
44	40	39.2	249	5 09VN72	09vn72 drosophila
45	40	39.2	308	10 09FKK5	09fkk5 arabidopsi

ALIGNMENTS

RESULT	1	PRELIMINARY;	PRT;	242 AA.
09PB03	AC	09PB03		
ID	09PB03			
DT	01-OCT-2000 (TREMBLrel. 15, Created)			
DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)			
DT	01-MAR-2001 (TREMBLrel. 16, Last annotation update)			
DE	HYPOTHETICAL PROTEIN XF2042.			
GN	XF2042.			
OS	Xylella fastidiosa.			
OC	Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;			
OC	Xylella.			
OX	NCBI_TaxID=2371;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=9A5C;			
RX	MEDLINE=20365717; PubMed=10910347;			
RA	Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M.,			
RA	Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,			
RA	Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Britones M.R.S.,			
RA	Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carier H.,			
RA	Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,			
RA	Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorry H.,			
RA	Fachinani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferraz J.A.,			
RA	Fraga J.S., Franca S.C., Franco M.C., Frome M., Furlan L.R.,			
RA	Gardner M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,			
RA	Ho P.L., Hohnselt J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,			
RA	Kriegler J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,			
RA	Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,			
RA	Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L.,			
RA	Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,			
RA	Menck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,			
RA	Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,			
RA	Nhani A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,			
RA	de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,			
RA	Pelxoto R.B., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,			
RA	Quaggio R.R., Roberto P.G., Rodrigues V., de Rosa A.J.M.,			
RA	de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,			
RA	da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,			
RA	da Silveira J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,			
RA	de Souza A.P., Terenzi M.F., Truffi D., Teal S.M., Tsunako M.H.,			
RA	Vallela H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,			


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OC 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
DE CDNA FLJ12145 FIS, CLONE MAMMA1000395.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CM Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=MAMMARY GLAND;
RA Issigal T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Mishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
RA Wagasuma M., Hosokiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
RA Matanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
RA Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuko Y.,
RA Niimura K., Iwayanagi T.;
RT "MEDO human cDNA sequencing project.";
RL Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AK022207; BABI3984.1; -.
SQ SEQUENCE 572 AA; 62795 MW; 24CB974A39C8BA54 CRC64;

Query Match 43.1%; Score 44; DB 4; Length 572;
Best Local Similarity 48.0%; Pred. No. 36;
Matches 12; Conservative 2; Mismatches 7; Indels 4; Gaps 1;

OY 1 PRSTPSLTTKAV---LLVRKFSNS 21
Db 502 PNAOPSSSEAKMAMPYLRLRRKFSNS 526

RESULT 6
O9BV36 PRELIMINARY; PRT; 600 AA.
AC O9BV36;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE UNKNOWN (PROTEIN FOR MGC:2771).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CM Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=KIDNEY ADENOCARCINOMA;
RA Strausberg R.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC001653; AAH01653.1; -.
SQ SEQUENCE 600 AA; 65949 MW; 90FA8D0B3250AD98 CRC64;

Query Match 43.1%; Score 44; DB 4; Length 600;
Best Local Similarity 48.0%; Pred. No. 38;
Matches 12; Conservative 2; Mismatches 7; Indels 4; Gaps 1;

OY 1 PRSTPSLTTKAV---LLVRKFSNS 21
Db 530 PNAOPSSSEAKMAMPYLRLRRKFSNS 554

RESULT 7
O9VD17 PRELIMINARY; PRT; 1269 AA.
AC O9VD17;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TReMBLrel. 13, Last annotation update)
DE CG17269 PROTEIN.
OS Drosophila melanogaster (Fruit fly).
```

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Epmydoidea; Drosophilidae; Drosophila.
OX NCBI_taxid=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BKERELEY.
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Vandeell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C.K., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA April J.F., Aghayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu I., Beasley E.M.,
RA Beeson K.Y., Berens P.V., Bernan B.P., Bhargava D., Bolshakov S.,
RA Borokova D., Botchan M.R., Bouck J., Brockstein P., Brotler P.,
RA Butts K.C., Busam D.A., Butler H., Cadieu L.B., Center A., Chandra I.,
RA Cherry J.M., Cavley S., Dahlke C., Davenport L.B., Davies P.,
RA de Paulis B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Fodde C., Gabrieliellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glaser A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Idegawa C.,
RA Jaitai M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lascko P., Lei Y., Levitsky A.A., Li J., Li Z., Jiang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Mosheiff A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacלב J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puiri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Sliden-Klamos I., Simpson M., Skupski M.P., Smal T.,
RA Spraker E., Spreading A.C., Stapleton M., Strong R., Sun E.,
RA Svirsdas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.W., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhao M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster". ;
RL Science 287:2185-2195(2000).
DR EMBL: AF003732; AAF55806.1; -
DR FlyBase: FBgn0038827; CG17269.
SQ SEQUENCE 1269 AA; 143652 MW; 74A2170AFEFD3EAD0 CRC64;

Query Match 43.1%; Score 44; DB 5; Length 1269;
Best Local Similarity 50.0%; Pred. No. 79;
Matches 9; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 2 RSTPSLTTRKAVALVRKFQ 19
 ::| | | | : | : | : |
Db 423 KSPHLTMALELRRELQ 440

RESULT 8
ID 077159 PRELIMINARY; PRY; 184 AA.

AC 077159;
DT 01-NOV-1998 (TREMBLrel_08, Created)
DT 01-NOV-1998 (TREMBLrel_08, Last sequence update)
DT 01-JUN-2001 (TREMBLrel_17, Last annotation update)
DE HETEROCHROMATIN-ASSOCIATED PROTEIN 1-LIKE PROTEIN.
GN HNP1.
OS Tetrahymena thermophila.
OC Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida;
CX Tetrahymenina; Tetrahymena.
NX NCBI_taxid=5911;

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CU428;
 RA Huang H., Wiley E.A., Lending C.R., Allis C.D.;
 RT "An Hp-1-like protein is missing from transcriptionally silent
 RT micronuclei but is enriched in condensed macronuclear chromatin."
 RL Submitted (JUL-1998) to the EMBL/GenBank/DBS databases.
 DR EMBL; AF079405; AAC78328.1; -
 DR InterPro: IPR000953; Chromo.
 DR Pfam: PF00385; chromo. 1.
 DR PROSITE: PS0013; CHROMO_2; 1.
 DR SMART: SM00298; CHROMO. 1.
 SQ SEQUENCE 184 AA; 21140 MW; 8B38D646B09CD38F CRC64;

Query Match 42.2%; Score 43; DB 5; Length 184;
 Best Local Similarity 45.0%; Pred. No. 17;
 Matches 9; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 1 PRSTPSLTTFKAVLVKRFQ 20
 Db 100 PKSTPKLKKALDPVKEIHN 119

RESULT 9
 ID P74937 PRELIMINARY; PRT; 321 AA.
 AC P74937;
 DT 01-FEB-1997 (TREMBLrel. 02, Created)
 DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
 DE INTRACELLULAR ALKALINE PROTEASE.
 GN TIAP.
 OS Thermocactinomycetes sp.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Thermocactinomycetes.
 NC NCBI_TaxID=2025;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-HS682;
 RX MEDLINE=97212029; PubMed=9058969;
 RA Tsuchiya K., Ikeda I., Tsuchiya T., Kilmura T.;
 RT "Cloning and expression of an intracellular alkaline protease gene
 RT from alkaliphilic Thermocactinomycetes sp. HS682."
 RL Biosci. Biotechnol. Biochem. 61:298-303(1997).
 DR EMBL; D87557; BAA13418.1; -
 DR HSSP: P00782; 2SHT.
 DR MEROPS: S08.030; -
 DR InterPro: IPR000209; Peptidase_S8.
 DR Pfam: PF00082; Peptidase_S8; 1.
 DR PRINTS: PR00723; SUBTILISIN.
 DR PROSITE: PS00136; SUBTILASE_ASP; UNKNOWN_1.
 DR PROSITE: PS00137; SUBTILASE_HIS; UNKNOWN_1.
 DR PROSITE: PS00138; SUBTILASE_SER; 1.
 KW Protease.
 SQ SEQUENCE 321 AA; 34664 MW; F15A0E1421368B9 CRC64;

Query Match 42.2%; Score 43; DB 2; Length 321;
 Best Local Similarity 47.1%; Pred. No. 30;
 Matches 8; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 3 STPSLTTFKAVLVKRFQ 19
 Db 251 ATPHTGAALLIEKFE 267

RESULT 10
 ID Q9KAV3 PRELIMINARY; PRT; 322 AA.
 AC Q9KAV3;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)

DE INTRACELLULAR ALKALINE SERINE PROTEINASE (EC 3.4.).
 GN ISP OR BH2183.
 OS Bacillus halodurans.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group;
 OC Bacillus/Staphylococcus group; Bacillus.
 RX NCBI_TaxID=86665;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-C-125 / JCM 9153;
 RX MEDLINE=20512582; PubMed=11058132;
 RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
 RA Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
 RA Horikoshi K.;
 RT "Complete genome sequence of the alkaliphilic bacterium Bacillus
 RT halodurans and genomic sequence comparison with Bacillus subtilis."
 RL Nucleic Acids Res. 28:4317-4331(2000).
 DR EMBL; AP001514; BAB05902.1; -
 DR InterPro: IPR000209; Peptidase_S8.
 DR Pfam: PF00082; Peptidase_S8; 1.
 DR PRINTS: PR00723; SUBTILISIN.
 DR PROSITE: PS00136; SUBTILASE_ASP; UNKNOWN_1.
 DR PROSITE: PS00137; SUBTILASE_HIS; UNKNOWN_1.
 DR PROSITE: PS00138; SUBTILASE_SER; 1.
 KW Hydrolase; Complete proteome.
 SQ SEQUENCE 322 AA; 34763 MW; D90351B41C2235A1 CRC64;

Query Match 42.2%; Score 43; DB 2; Length 322;
 Best Local Similarity 47.1%; Pred. No. 30;
 Matches 8; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 3 STPSLTTFKAVLVKRFQ 19
 Db 252 ATPHTGAALLIEKFE 268

RESULT 11
 ID Q53624 PRELIMINARY; PRT; 458 AA.
 AC Q53624;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DE MYTHRAMYCIN RESISTANCE DETERMINANT, PUTATIVE ABC EXCISION NUCLEASE
 DE REPAIR PROTEIN (FRAGMENT).
 OS Streptomyces argillaceus.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Streptomycinae; Streptomycetaceae; Streptomyces.
 NC NCBI_TaxID=41951;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-ATCC 12956;
 RX MEDLINE=96335144; PubMed=8757400;
 RA Fernandez E., Lombe F., Mendez C., Salas J.A.;
 RT "An ABC transporter is essential for resistance to the antitumor agent
 RT mithramycin in the producer Streptomyces argillaceus."
 RL Mol. Gen. Genet. 251:682-698(1996).
 DR EMBL; U43537; AAC44355.1; -
 DR InterPro: IPR003439; ABC_transport.
 DR Pfam: PF00005; ABC_tran; 1.
 FT NON_TER 1
 SQ SEQUENCE 458 AA; 48267 MW; 0E4D5160D76C252B CRC64;

Query Match 42.2%; Score 43; DB 2; Length 458;
 Best Local Similarity 56.2%; Pred. No. 43;
 Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 PRSTPSLTTFKAVLVK 16
 Db 201 PRSNPATYTKAFNLIR 216


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RESULT 12
ID 021750 PRELIMINARY: PRT: 919 AA.
AC Q21750. Q23517;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, last annotation update)
DE HYPOHECTICAL 103.3 KDA PROTEIN.
GN R05F9.12 OR ZK546.10.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Hallsworth K.;
RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
RN [2]
RC STRAIN-BRISTOL N2;
RP SEQUENCE OF 1-575 FROM N.A.
RA Hallsworth K.;
RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; U41533; AAA83174.1; -.
DR EMBL; U29380; AAA68743.1; -.
DR InterPro: IPR000322; Glyco_hydro. 31.
DR Pfam: PF01055; Glyco_hydro. 31; 1.
DR PROSITE: PS00129; GLYCOSYL_HYDROL_F31_1; 1.
KM Hydrolyse.
SQ SEQUENCE 919 AA: 10314 MW: A487E71BBF3685FC CRC64;

Query Match
Best Local Similarity 42.2%; Score 43; DB 5; Length 919;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 PRSTPSLTTRKA 11
DB 744 PROTPSTTTTA 754

RESULT 13
ID 094192 PRELIMINARY: PRT: 1744 AA.
AC 094192;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-JUN-2001 (TREMBLrel. 17, last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, last annotation update)
DE CHIRIN SYNTHASE.
GN CHS4.
OS Paracoccidioides brasiliensis.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Onygenales; Mitosporic Onygenales; Paracoccidioides.
OX NCBI_TaxID=121759;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE-20210320; PubMed-10746225;
RX Nino-Vega G.A., Munro C.A., San-Bias G., Gooday G.W., Gow N.A.;
RT "Differential expression of chitin synthase genes during temperature-
induced dimorphic transitions in Paracoccidioides brasiliensis.";
RL Med. Mycol. 38:31-39(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Nino-Vega G.A., San-Bias G.;
RT "Sequence analysis of the CHS4 gene of Paracoccidioides
brasiliensis.";
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF107624; AAD1613.2; -.
DR InterPro: IPR001117; Cu-oxidase.
DR InterPro: IPR001173; Glycos_transf_2.
DR InterPro: IPR001609; myosin_head.
DR Pfam: PF00063; myosin_head; 1.
DR SMART; SM00242; MYSC; 1.
DR PROSITE; PS00079; MULTICOPPER_OXIDASE1; UNKNOWN_1.
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SQ SEQUENCE 1744 AA: 193777 MW: DB7622DD0A69F0705 CRC64;

Query Match
Best Local Similarity 42.2%; Score 43; DB 3; Length 1744;
Matches 8; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

OY 1 PRSTPSLTTRKAVLLVRKF 18
DB 118 PLSTPSITRYTALSVIKPF 135

RESULT 14
ID 010378 PRELIMINARY: PRT: 1967 AA.
AC 010378;
DT 01-JUL-1997 (TREMBLrel. 04, Created)
DT 01-JUL-1997 (TREMBLrel. 04, last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, last annotation update)
DE LARGE PROTEIN.
GN L.
OS Rice transitory yellowing virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Rhabdoviridae; unclassified Rhabdoviridae.
OX NCBI_TaxID=59380;
RN [1]
RP SEQUENCE FROM N.A.
RA Fang R., Luo Z., Zhao H.;
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB011257; BAA25160.1; -.
SQ SEQUENCE 1967 AA: 223600 MW: DE70AB80A45FC776 CRC64;
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Query Match
Best Local Similarity 42.1%; Score 43; DB 12; Length 1967;
Matches 8; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

OY 2 RSTPSLTTRKAVLLVRKEON 20
DB 919 RGFPDPVTEALICFLRKEKN 937

RESULT 15
ID 085166 PRELIMINARY: PRT: 2831 AA.
AC 085166;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, last annotation update)
DE CYCLIC BETA 1-2 GLUCAN SYNTHETASE.
GN CGS.
OS Brucella abortus.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Brucellaceae; Brucella.
OX NCBI_TaxID=235;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=519;
RX MEDLINE=98389650; PubMed=9721274;
RT Inon de Iannino N., Briones G., Tolmashy M., Ugalde R.A.;
RT "Molecular cloning and characterization of cgs, the Brucella abortus
cyclic beta(1-2) glucan synthetase gene: genetic complementation of
RT Rhizobium meliloti ncvB and Agrobacterium tumefaciens chvB mutants.";
RL J. Bacteriol. 180:4392-4400(1998).
DR EMBL; AF047823; AAC34747.1; -.
SQ SEQUENCE 2831 AA: 316272 MW: 956A03899A57FC58 CRC64;
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Query Match
Best Local Similarity 42.2%; Score 43; DB 2; Length 2831;
Matches 12; Conservative 1; Mismatches 5; Indels 2; Gaps 1;

OY 1 PRSTPSLTTR--KAVLLVRKF 18
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Db 678 PRVTPSLITGDEASFLOQVP 697

Search completed: December 19, 2001, 16:25:22
Job time: 547 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 19, 2001, 16:20:59 ; Search time 78.52 Seconds
(without alignments)
6.018 Million cell updates/sec

Title: US-09-202-104a-5
Perfect score: 102
Sequence: 1 PRSTPSLTTKAVILVRRKFGNS 21

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/PCITUS.COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/backfilist1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	102	100.0	210	4	US-09-043-785-1
2	102	100.0	323	6	Sequence 1, Appli
3	102	100.0	323	6	Patent No. 5171840
4	102	100.0	344	6	Patent No. 5480796
5	102	100.0	344	6	Patent No. 5171840
6	102	100.0	468	6	Patent No. 5480796
7	102	100.0	468	6	Sequence 5, Appli
8	102	100.0	468	6	Patent No. 5171840
9	92	90.2	201	6	Patent No. 5480796
10	91	89.2	386	6	Patent No. 5171840
11	91	89.2	386	6	Patent No. 5480796
12	40	39.2	1038	4	Sequence 4, Appli
13	38	37.3	211	1	Sequence 4, Appli
14	38	37.3	211	2	Sequence 4, Appli
15	38	37.3	211	3	Sequence 4, Appli
16	38	37.3	211	4	Sequence 4, Appli
17	38	37.3	718	1	Sequence 4, Appli
18	37	36.3	433	4	Sequence 4, Appli
19	37	36.3	433	2	Sequence 18, Appli
20	37	36.3	433	3	Sequence 18, Appli
21	37	36.3	433	5	Sequence 18, Appli
22	37	36.3	433	5	Sequence 18, Appli
23	37	36.3	433	5	Sequence 12, Appli
24	36.5	35.8	282	3	Sequence 18, Appli
25	36.5	35.8	282	3	Sequence 37, Appli
26	36	35.3	60	1	Sequence 10, Appli
27	36	35.3	70	4	Sequence 438, App

28	36	35.3	221	1	US-07-903-710-6	Sequence 6, Appli
29	36	35.3	221	1	US-08-252-966B-8	Sequence 8, Appli
30	36	35.3	221	1	US-08-222-638B-6	Sequence 6, Appli
31	36	35.3	648	1	US-08-321-356-2	Sequence 2, Appli
32	36	35.3	648	1	US-08-321-356-4	Sequence 4, Appli
33	36	35.3	985	2	US-08-680-326-41	Sequence 41, Appli
34	36	35.3	4545	2	US-08-804-227C-14	Sequence 14, Appli
35	36	35.3	4550	2	US-08-804-227C-8	Sequence 8, Appli
36	36	35.3	4550	2	US-08-804-198-2	Sequence 2, Appli
37	35.5	34.8	394	4	US-09-390-721-5	Sequence 5, Appli
38	35.5	34.8	571	2	US-08-796-414B-1	Sequence 1, Appli
39	35	34.3	115	2	US-08-993-228-2	Sequence 2, Appli
40	35	34.3	119	2	US-08-318-157B-5	Sequence 5, Appli
41	35	34.3	136	4	US-09-357-251-16	Sequence 16, Appli
42	35	34.3	166	1	US-08-362-453-8	Sequence 8, Appli
43	35	34.3	166	4	US-09-339-913B-79	Sequence 79, Appli
44	35	34.3	189	1	US-08-026-758-7	Sequence 7, Appli
45	35	34.3	189	1	US-08-026-758-11	Sequence 11, Appli

ALIGNMENTS

invented

RESULT 1
US-09-043-785-1
; Sequence 1, Application US/09043785
; Patent No. 6172042
; GENERAL INFORMATION:
; APPLICANT: CHEBATH, Judith
; APPLICANT: HALIMI, Hubert
; APPLICANT: REVEL, Michel
; TITLE OF INVENTION: SYNTHETIC PEPTIDES THAT INHIBIT IL-6 ACTIVITY
; FILE REFERENCE: Chdbath-1
; CURRENT APPLICATION NUMBER: US/09/043,785
; CURRENT FILING DATE: 1998-09-02
; EARLIER APPLICATION NUMBER: PCT/IL96/00119
; EARLIER FILING DATE: 1996-09-26
; EARLIER APPLICATION NUMBER: 115,453
; EARLIER FILING DATE: 1995-09-26
; EARLIER APPLICATION NUMBER: 118,097
; EARLIER FILING DATE: 1996-05-01
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 210
; TYPE: PPT
; ORGANISM: Human
US-09-043-785-1

Query Match 100.0%; Score 102; DB 4; Length 210;
Best Local Similarity 100.0%; Pred. No. 7.8e-10;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PRSTPSLTTKAVILVRRKFGNS 21
DB 24 PRSTPSLTTKAVILVRRKFGNS 44
RESULT 2
5171840-6
; APPLICANT: KISHIMOTO, TADAMITSU
; TITLE OF INVENTION: RECEPTOR PROTEIN FOR HUMAN B CELL
; STIMULATORY FACTOR-2
; NUMBER OF SEQUENCES: 11
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/298,694
; FILING DATE: 19-JAN-1989
; SEQ ID NO: 6
; LENGTH: 323
5171840-6

Query Match 100.0%; Score 102; DB 6; Length 323;
Best Local Similarity 100.0%; Pred. No. 1.3e-09;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PRSTPSLTKAVLLVRKFQNS 21
|||||
Db 136 PRSTPSLTKAVLLVRKFQNS 156

RESULT 3
5480796-6

; Patent No. 5480796
; APPLICANT: KISHIMOTO, TADAMITSU
; TITLE OF INVENTION: ANTIBODIES AGAINST THE RECEPTOR PROTEIN
; FOR HUMAN B CELL STIMULATORY FACTOR-2
; NUMBER OF SEQUENCES: 8
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/907,650
; FILING DATE: 02-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 298,694
; FILING DATE: 19-JAN-1989
; SEQ ID NO:6:
; LENGTH: 323
5480796-6

Query Match 100.0%; Score 102; DB 6; Length 323;
Best Local Similarity 100.0%; Pred. No. 1.3e-09;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PRSTPSLTKAVLLVRKFQNS 21
|||||
Db 136 PRSTPSLTKAVLLVRKFQNS 156

RESULT 4
5171840-7

; Patent No. 5171840
; APPLICANT: KISHIMOTO, TADAMITSU
; TITLE OF INVENTION: RECEPTOR PROTEIN FOR HUMAN B CELL
; STIMULATORY FACTOR-2
; NUMBER OF SEQUENCES: 11
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/298,694
; FILING DATE: 19-JAN-1989
; SEQ ID NO:7:
; LENGTH: 344
5171840-7

Query Match 100.0%; Score 102; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 1.4e-09;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PRSTPSLTKAVLLVRKFQNS 21
|||||
Db 136 PRSTPSLTKAVLLVRKFQNS 156

RESULT 5
5480796-7

; Patent No. 5480796
; APPLICANT: KISHIMOTO, TADAMITSU
; TITLE OF INVENTION: ANTIBODIES AGAINST THE RECEPTOR PROTEIN
; FOR HUMAN B CELL STIMULATORY FACTOR-2
; NUMBER OF SEQUENCES: 8
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/907,650
; FILING DATE: 02-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 298,694

; FILING DATE: 19-JAN-1989
; SEQ ID NO:7:
; LENGTH: 344
5480796-7

Query Match 100.0%; Score 102; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 1.4e-09;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PRSTPSLTKAVLLVRKFQNS 21
|||||
Db 136 PRSTPSLTKAVLLVRKFQNS 156

RESULT 6
US-08-795-473B-5
; Sequence 5, Application US/08795473B
; Patent No. 6217838
; GENERAL INFORMATION:
; APPLICANT: Galun, Eithan
; APPLICANT: Nahot, Orit
; APPLICANT: Blum, Herbert E.

; TITLE OF INVENTION: A Pharmaceutical Composition for Treating
; TITLE OF INVENTION: Hepatitis B Virus (HBV) Infection
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Davidson, Davidson and Kappel, LLC
; STREET: 1140 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA

; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MS-DOS EDITOR
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/795,473B
; FILING DATE: 11-FEB-1997
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Davidson, Clifford M.
; REGISTRATION NUMBER: 32,728
; REFERENCE/DOCKET NUMBER: 963,1007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)-997-1028
; TELEFAX: (212)-997-1037

; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 468 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
US-08-795-473B-5

Query Match 100.0%; Score 102; DB 4; Length 468;
Best Local Similarity 100.0%; Pred. No. 2e-09;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PRSTPSLTKAVLLVRKFQNS 21
|||||
Db 136 PRSTPSLTKAVLLVRKFQNS 156

RESULT 7
5171840-2

; Patent No. 5171840
; APPLICANT: KISHIMOTO, TADAMITSU
; TITLE OF INVENTION: RECEPTOR PROTEIN FOR HUMAN B CELL
; STIMULATORY FACTOR-2
; NUMBER OF SEQUENCES: 11

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/298,694
; FILING DATE: 19-JAN-1989
; SEQ ID NO:2
; LENGTH: 468
5171840-2
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Query Match          100.0%; Score 102; DB 6; Length 468;
Best Local Similarity 100.0%; Pred. No. 2e-09;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY 1 PRSTPSLTTRKAVLLVRRFQNS 21
    |||||
Db 136 PRSTPSLTTRKAVLLVRRFQNS 156
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RESULT 8
5480796-2
; Patent No. 5480796
; APPLICANT: KISHIMOTO, TADAMITSU
; TITLE OF INVENTION: ANTIBODIES AGAINST THE RECEPTOR PROTEIN
; FOR HUMAN B CELL STIMULATORY FACTOR-2
; NUMBER OF SEQUENCES: 8
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/907,650
; FILING DATE: 02-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 298,694
; FILING DATE: 19-JAN-1989
; SEQ ID NO:2
; LENGTH: 468
5480796-2
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Query Match          100.0%; Score 102; DB 6; Length 468;
Best Local Similarity 100.0%; Pred. No. 2e-09;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY 1 PRSTPSLTTRKAVLLVRRFQNS 21
    |||||
Db 136 PRSTPSLTTRKAVLLVRRFQNS 156
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```
RESULT 9
5171840-11
; Patent No. 5171840
; APPLICANT: KISHIMOTO, TADAMITSU
; TITLE OF INVENTION: RECEPTOR PROTEIN FOR HUMAN B CELL
; STIMULATORY FACTOR-2
; NUMBER OF SEQUENCES: 11
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/298,694
; FILING DATE: 19-JAN-1989
; SEQ ID NO:11
; LENGTH: 201
5171840-11
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Query Match          90.2%; Score 92; DB 6; Length 201;
Best Local Similarity 100.0%; Pred. No. 3.6e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY 1 PRSTPSLTTRKAVLLVRRFQ 19
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Db 14 PRSTPSLTTRKAVLLVRRFQ 32
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RESULT 10
5171840-5
; Patent No. 5171840
; APPLICANT: KISHIMOTO, TADAMITSU
; TITLE OF INVENTION: RECEPTOR PROTEIN FOR HUMAN B CELL
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; STIMULATORY FACTOR-2
; NUMBER OF SEQUENCES: 11
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/298,694
; FILING DATE: 19-JAN-1989
; SEQ ID NO:5
; LENGTH: 386
5171840-5
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Query Match          89.2%; Score 91; DB 6; Length 386;
Best Local Similarity 91.3%; Pred. No. 1.1e-07;
Matches 21; Conservative 0; Mismatches 0; Indels 2; Gaps 1;
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Db 52 PRSTPWSLTTRKAVLLVRRFQNS 74
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RESULT 11
5480796-5
; Patent No. 5480796
; APPLICANT: KISHIMOTO, TADAMITSU
; TITLE OF INVENTION: ANTIBODIES AGAINST THE RECEPTOR PROTEIN
; FOR HUMAN B CELL STIMULATORY FACTOR-2
; NUMBER OF SEQUENCES: 8
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/907,650
; FILING DATE: 02-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 298,694
; FILING DATE: 19-JAN-1989
; SEQ ID NO:5
; LENGTH: 386
5480796-5
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Query Match          89.2%; Score 91; DB 6; Length 386;
Best Local Similarity 91.3%; Pred. No. 1.1e-07;
Matches 21; Conservative 0; Mismatches 0; Indels 2; Gaps 1;
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OY 1 PRSTP--SLTRKAVLLVRRFQNS 21
    |||||
Db 52 PRSTPWSLTTRKAVLLVRRFQNS 74
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RESULT 12
US-09-541-782-4
; Sequence 4; Application US/09541782
; Patent No. 6284480
; GENERAL INFORMATION:
; APPLICANT: NISLOW, COREY
; APPLICANT: SAKOWICZ, ROMAN
; APPLICANT: BERAUD, CHRISTOPHE
; TITLE OF INVENTION: Antifungal Assay
; FILE REFERENCE: 1015
; CURRENT APPLICATION NUMBER: US/09/541,782
; CURRENT FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 1038
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-09-541-782-4
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Query Match          39.2%; Score 40; DB 4; Length 1038;
Best Local Similarity 47.4%; Pred. No. 1.5e+02;
Matches 9; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

OY 1 PRSTPSLTTRKAVLLVRRFQ 19
    ||| ||| ||| :::
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Db 278 PRSLNDLTPKALLRKLR 296

RESULT 13

US-07-915-966C-4
; Sequence 4, Application US/07915966C
; Patent No. 5668006
; GENERAL INFORMATION:
; APPLICANT: Hadcock Dr., John R.
; APPLICANT: Ozenberger Dr., Bradley A.
; APPLICANT: Pausch Dr., Mark H.
; TITLE OF INVENTION: Receptor Identification Method
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: American Home Products Corporation
; STREET: One Campus Drive
; CITY: Parsippany
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07054
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/915,966C
; FILING DATE: 17-JUL-1992
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Matthews, Gale M.
; REGISTRATION NUMBER: 32,269
; REFERENCE/DOCKET NUMBER: 31,829-00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-683-2134
; TELEFAX: 201-683-4117
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 211 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; ORGANISM: Rat
; US-07-915-966C-4

Query Match 37.3%; Score 38; DB 1; Length 211;
Best Local Similarity 47.1%; Pred. No. 51;
Matches 8; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
OY 2 RSTPSLTTKAVLVKRF 18
Db 157 RSEPKVTMVMVVVRLF 173

RESULT 14

US-08-771-182-4
; Sequence 4, Application US/08771182
; Patent No. 5929209
; GENERAL INFORMATION:
; APPLICANT: Hadcock Dr., John R.
; APPLICANT: Ozenberger Dr., Bradley A.
; APPLICANT: Pausch Dr., Mark H.
; TITLE OF INVENTION: Receptor Identification Method
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: American Home Products Corporation
; STREET: One Campus Drive

CITY: Parsippany
STATE: New Jersey
COUNTRY: USA
ZIP: 07054

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/771,182
FILING DATE: 20-DEC-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Matthews, Gale M.
REGISTRATION NUMBER: 32,269
REFERENCE/DOCKET NUMBER: 31,829-D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-683-2134
TELEFAX: 201-683-4117
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 211 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: Rat
US-08-771-182-4

Query Match 37.3%; Score 38; DB 2; Length 211;
Best Local Similarity 47.1%; Pred. No. 51;
Matches 8; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
OY 2 RSTPSLTTKAVLVKRF 18
Db 157 RSEPKVTMVMVVVRLF 173

RESULT 15

US-08-853-194-4
; Sequence 4, Application US/08853194
; Patent No. 6077666
; GENERAL INFORMATION:
; APPLICANT: Hadcock Dr., John R.
; APPLICANT: Ozenberger Dr., Bradley A.
; APPLICANT: Pausch Dr., Mark H.
; TITLE OF INVENTION: Receptor Identification Method
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: American Cyanamid Company
; STREET: One Cyanamid Plaza
; CITY: Wayne
; STATE: NJ
; COUNTRY: United States of America
; ZIP: 06904-0060
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/853,194
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/915,966
; FILING DATE: 17-JUL-1992

ATTORNEY/AGENT INFORMATION:
NAME: Tsevdos Dr., Estelle J.
REGISTRATION NUMBER: 31,145
REFERENCE/DOCKET NUMBER: 31629-00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 203-321-2361
TELEFAX: 203-321-2971
TELEX: 710-474-4059
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 211 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: Internal
ORIGINAL SOURCE:
ORGANISM: Rat
US-08-853-194-4

Query Match .37.3%; Score 38; DB 3; Length 211;
Best Local Similarity 47.1%; Pred. No. 51;
Matches 8; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
QY 2 RSTPSLTAKVLLVRKF 18
DB 157 RSEPKVTRMNVVVRLDF 173

Search completed: December 19, 2001, 16:21:00
Job time: 405 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: December 19, 2001, 16:26:20 ; Search time 48.45 Seconds
(without alignments)
21.189 million cell updates/sec

Title: US-09-202-104A-11

Perfect score: 146
Sequence: 1 EMCPRSTPLTAKVALLVRKFNQNSPAD 28

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	146	100.0	468	1 IL6A_HUMAN	P08887 homo sapien
2	121	82.9	467	1 IL6A_PIG	O18796 sus scrofa
3	72	49.3	460	1 IL6A_MOUSE	P22272 mus musculu
4	70	47.9	462	1 IL6A_RAT	P22273 rattus norv
5	50	34.2	188	1 PSPC_RABIT	P22398 oryctolagus
6	49	33.6	918	1 B3AT_ONCMY	P32847 oncorhynch
7	47	32.2	646	1 YHDA_ECOLI	P13518 escherichia
8	46.5	31.8	455	1 YAGA_ECOLI	P37007 escherichia
9	46.5	31.8	384	1 RADA_TREPA	O83985 treponema p
10	46.5	31.8	832	1 DPOL_HPBVY	P03156 hepatitis b
11	46.5	31.8	1411	1 TCOF_HUMAN	Q13428 homo sapien
12	46	31.5	257	1 SPHR_SYNP7	P39663 synecococc
13	46	31.5	328	1 MNM2_KLUFA	Q00974 kluyveromyc
14	46	31.5	375	1 YKUS_CAEEL	O17778 caenorhabd
15	46	31.5	1049	1 ITA5_HUMAN	P08648 homo sapien
16	45	30.8	179	1 PTH_CHLTR	O84806 chlamydia t
17	45	30.8	272	1 YIS2_SHISO	P16940 shigella so
18	45	30.8	572	1 GAG_IPHA	P04023 hamster int
19	45	30.8	1489	1 YGPO_YEAST	P53115 saccharomyc
20	44.5	30.5	283	1 TR14_HUMAN	O92952 homo sapien
21	44.5	30.5	402	1 PGU1_ERWCA	P18192 erythrina car
22	44.5	30.5	402	1 PGU2_ERWCA	P26509 erythrina car
23	44	30.1	90	1 YWUC_BACSU	P45863 bacillus su
24	44	30.1	613	1 ACES_BOVIN	P23795 bos taurus
25	44	30.1	1038	1 V120_VZVD	P09277 varicella-z
26	43.5	29.8	197	1 YIP7_YEAST	P40452 saccharomyc
27	43.5	29.8	608	1 GIMS_BUCAL	P57138 b glucosami
28	43.5	29.8	750	1 DPOL_HPBVZ	P03153 hepatitis b
29	43.5	29.8	763	1 DPOL_HPBVY	Q03214 hepatitis b
30	43.5	29.8	832	1 DPOL_HPBVL	P12900 hepatitis b
31	43.5	29.8	832	1 DPOL_HPBVY	P04484 hepatitis b
32	43	29.5	134	1 DCAC_ACTIC	P20370 actinobact
33	43	29.5	202	1 DIPAL_HUMAN	Q15634 homo sapien

34	43	29.5	586	1 PMEL_ARATH	Q43867 arabidopsis
35	43	29.5	686	1 IFZM_SCHPO	O59683 schizosacch
36	43	29.5	960	1 CSEL_YEAST	P33307 saccharomyc
37	43	29.5	964	1 CAPR_AMAHP	Q43299 amarantus
38	43	29.5	1227	1 B3A3_MOUSE	P16283 mus musculu
39	43	29.5	1227	1 B3A3_RAT	P23348 rattus norv
40	43	29.5	1233	1 B3A3_RABIT	O18917 oryctolagus
41	43	29.5	1971	1 MC3A_MOUSE	O9wuu9 mus musculu
42	42.5	29.1	481	1 DPOL_HPBVY	P03158 hepatitis b
43	42.5	29.1	556	1 DPOL_HPBV6	P11292 woodchuck h
44	42.5	29.1	845	1 DPOL_HPBV2	P03159 hepatitis b
45	42.5	29.1	879	1 DPOL_MHVI	P03160 woodchuck h

ALIGNMENTS

RESULT ID	IL6A_HUMAN	STANDARD:	PRT:	468 AA.
AC	P08887: Q16202;			
DT	01-NOV-1988 (Rel. 09, Created)			
DT	01-NOV-1988 (Rel. 09, Last sequence update)			
DT	20-AUG-2001 (Rel. 40, Last annotation update)			
DE	INTERLEUKIN-6 RECEPTOR ALPHA CHAIN PRECURSOR (IL-6R-ALPHA) (IL-6R 1)			
DE	(CD126 ANTIGEN).			
CN	IL6R.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A. (LONG ISOFORM).			
RX	MEDLINE=88305347; PubMed=3136546;			
RA	Yamasaki K., Taga T., Hirata Y., Yawata H., Kawanishi Y., Seed B.,			
RA	Taniguchi T., Hirano T., Kishimoto T.;			
RT	*Cloning and expression of the human interleukin-6 (BSF-2/IL6 beta 2)			
RT	receptor.";			
RL	Science 241:825-828(1988).			
RN	[2]			
RP	SEQUENCE FROM N.A. (LONG ISOFORM).			
RA	Yamasaki K., Taga T., Hirata Y., Yawata H., Kawanishi Y., Seed B.,			
RA	Taniguchi T., Hirano T., Kishimoto T.;			
RT	*Molecular structure of interleukin 6 receptor.";			
RL	Proc. Jpn. Acad., B, Phys. Biol. Sci. 64:209-211(1988).			
RN	[3]			
RP	SEQUENCE FROM N.A. (LONG ISOFORM).			
RX	MEDLINE=91336983; PubMed=1872801;			
RA	Schottlink H., Stoyan T., Lenz D., Schmitz H., Hirano T.,			
RA	Kishimoto T., Heinrich P.C., Rose-John S.;			
RT	*Structural and functional studies on the human hepatic interleukin-6			
RT	receptor. Molecular cloning and overexpression in HepG2 cells.";			
RL	Biochem. J. 277:659-664(1991).			
RN	[4]			
RP	SEQUENCE OF 313-365 FROM N.A. (SHORT ISOFORM).			
RX	MEDLINE=94334399; PubMed=8056053;			
RA	Horikuchi S., Koyanagi Y., Zhou Y., Miyamoto H., Tanaka Y., Waki M.,			
RA	Matsumoto A., Yamamoto M., Yamamoto N.;			
RT	*Soluble interleukin-6 receptors released from T cell or			
RT	granulocyte/macrophage cell lines and human peripheral blood			
RT	mononuclear cells are generated through an alternative splicing			
RT	mechanism.";			
RL	Eur. J. Immunol. 24:1945-1948(1994).			
RN	[5]			
RP	PARTIAL SEQUENCE, CARBOHYDRATE-LINKAGE SITES, AND DISULFIDE BONDS.			
RX	MEDLINE=99167486; PubMed=10066782;			
RA	Cole A.R., Hall N.E., Treutlein H.R., Eddes J.S., Reid G.E.,			
RA	Moritz R.L., Simpson R.U.;			
RT	*Disulfide bond structure and N-glycosylation sites of the			
RT	extracellular domain of the human interleukin-6 receptor.";			
RL	J. Biol. Chem. 274:7207-7215(1999).			
RN	[6]			
RP	MUTAGENESIS.			

RX MEDLINE-93223711; PubMed-8467812;
 RA Yawata H., Yasukawa K., Natsuka S., Murakami M., Yamasaki K., Hibl M.,
 RA Taga T., Kishimoto T.;
 CC "Structure-function analysis of human IL-6 receptor: dissociation of
 RT amino acid residues required for IL-6-binding and for IL-6 signal
 RT transduction through gp130.";
 RL EMBL J. 12:1705-1712(1993).
 CC -1- FUNCTION: PART OF THE RECEPTOR FOR INTERLEUKIN 6. BINDS TO IL-6
 CC WITH LOW AFFINITY, BUT DOES NOT TRANSDUCE A SIGNAL. SIGNAL
 CC ACTIVATION NECESSITATE AN ASSOCIATION WITH IL6ST. ACTIVATION MAY
 CC LEAD TO THE REGULATION OF THE IMMUNE RESPONSE, ACUTE-PHASE
 CC REACTIONS AND HEMATOPOIESIS.
 CC -1- FUNCTION: LOW CONCENTRATION OF A SOLUBLE FORM OF INTERLEUKIN-6
 CC RECEPTOR ACTS AS AN AGONIST OF IL-6 ACTIVITY.
 CC -1- SUBUNIT: HEXAMER OF 2 IL6, 2 IL6R-ALPHA AND 2 IL6ST.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (LONG FORM) AND
 CC SECRETED (SHORT FORM).
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: A LONG FORM (SHOWN HERE) AND A
 CC SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: THE SHORT FORM IS EXPRESSED IN PERIPHERAL
 CC BLOOD MONONUCLEAR CELLS AND WEAKLY FOUND IN URINE AND SERUM.
 CC -1- DOMAIN: THE TWO FIBROECTIN TYPE IIT-LIKE DOMAINS CONTAINED IN THE
 CC N-TERMINAL PART FORM TOGETHER A CYTOKINE-BINDING DOMAIN.
 CC -1- PTM: A SHORT SOLUBLE FORM MAY ALSO BE RELEASED FROM THE MEMBRANE
 CC BY PROTEOLYSIS.
 CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
 CC -1- SIMILARITY: CONTAINS 3 FIBROECTIN TYPE IIT-LIKE DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 CC -1- DATABASE: NAME-PROW; NOTE-CD guide CD126 entry;
 CC WWW-http://www.ncbi.nlm.nih.gov/prov/cd/cd126.htm".
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; X12830; CAA1312.1; -;
 DR EMBL; X58298; CAA41231.1; -;
 DR EMBL; S72848; AAC60635.1; -;
 DR PIR; A41242; A41242.
 DR PIR; J00080; J00080.
 DR PIR; S14621; S14621.
 DR PIR; S17468; S17468.
 DR MIM; 147880; -;
 DR InterPro: IPR002996; CRA.
 DR InterPro: IPR001777; FN_III.
 DR InterPro: IPR003530; Hematopo_receptor_L_F3.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003598; Ig_C2.
 DR Pfam; PF00041; fn3; 1.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00060; FN3; 1.
 DR SMART; SM00408; IgC2; 1.
 DR PROSITE; PS01354; HEMATOPO_REC_L_F3; 1.
 DR Receptor; Transmembrane; Glycoprotein; Immunoglobulin domain; Repeat;
 KW Alternative splicing; Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 468 INTERLEUKIN-6 RECEPTOR ALPHA CHAIN.
 FT DOMAIN 20 365 POTENTIAL.
 FT TRANSSEM 366 386 POTENTIAL.
 FT DOMAIN 387 468 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 40 103 IG-LIKE C2-TYPE DOMAIN.
 FT DISULFID 25 193
 FT DISULFID 47 96
 FT DISULFID 121 132
 FT DISULFID 165 176
 FT CARBOHYD 55 55 N-LINKED (GLCNAC. . .).
 FT CARBOHYD 93 93 N-LINKED (GLCNAC. . .).
 FT CARBOHYD 221 221 N-LINKED (GLCNAC. . .).
 FT VARSPLIC 356 365 VOSSSVPLP -> GSKRRSGCL (IN SHORT

FT VARSPLIC 366 468 ISOFORM).
 FT MUTAGEN 121 121 MISSING (IN SHORT ISOFORM).
 FT MUTAGEN 122 122 C->S: COMPLETE LOSS OF LIGAND-BINDING.
 FT MUTAGEN 132 132 F->A: NO CHANGE OF LIGAND-BINDING AND IL6
 FT MUTAGEN 133 132 SIGNALING.
 FT MUTAGEN 134 134 C->A: COMPLETE LOSS OF LIGAND-BINDING.
 FT MUTAGEN 140 140 W->L: COMPLETE LOSS OF LIGAND-BINDING.
 FT MUTAGEN 153 153 P->G: NO CHANGE OF LIGAND-BINDING AND IL6
 FT MUTAGEN 165 165 SIGNALING.
 FT MUTAGEN 174 174 F->L: NO CHANGE OF LIGAND-BINDING AND IL6
 FT MUTAGEN 174 174 SIGNALING.
 FT MUTAGEN 176 176 C->L: COMPLETE LOSS OF LIGAND-BINDING.
 FT MUTAGEN 184 184 F->L: NO CHANGE OF LIGAND-BINDING AND IL6
 FT MUTAGEN 190 190 SIGNALING.
 FT MUTAGEN 193 193 C->D: COMPLETE LOSS OF LIGAND-BINDING.
 FT MUTAGEN 211 211 C->A: NO CHANGE OF LIGAND-BINDING AND IL6
 FT MUTAGEN 217 217 SIGNALING.
 FT MUTAGEN 232 232 D->V: COMPLETE LOSS OF LIGAND-BINDING.
 FT MUTAGEN 233 233 R->S: 30% DECREASE OF LIGAND-BINDING AND
 FT MUTAGEN 254 254 IL6 SIGNALING.
 FT MUTAGEN 277 277 W->Q: 30% DECREASE OF LIGAND-BINDING AND
 FT MUTAGEN 278 278 INCREASE OF IL6 SIGNALING.
 FT MUTAGEN 279 279 E->A: 50% DECREASE OF LIGAND-BINDING AND
 FT MUTAGEN 280 280 IL6 SIGNALING.
 FT MUTAGEN 281 281 C->D: 30% INCREASE OF LIGAND-BINDING AND
 FT MUTAGEN 285 285 100% INCREASE IN IL6 SIGNALING.
 FT MUTAGEN 291 291 V->N: 50% DECREASE OF LIGAND-BINDING AND
 FT MUTAGEN 293 293 50% INCREASE IN IL6 SIGNALING.
 FT SEQUENCE 468 AA; 51547 MW; 62AA239FA14F1BBB CRC64;
 FT MUTAGEN 291 291 G->D: 80% DECREASE OF LIGAND-BINDING AND
 FT MUTAGEN 293 293 NO IL6 SIGNALING.
 FT SEQUENCE 468 AA; 51547 MW; 62AA239FA14F1BBB CRC64;
 FT MUTAGEN 291 291 Q->K: COMPLETE LOSS OF LIGAND-BINDING.
 FT MUTAGEN 293 293 R->G: COMPLETE LOSS OF LIGAND-BINDING.
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 FT MUTAGEN 293 293 NO IL6 SIGNALING.
 FT SEQUENCE 468 AA; 51547 MW; 62AA239FA14F1BBB CRC64;
 FT MUTAGEN 291 291 Q->K: COMPLETE LOSS OF LIGAND-BINDING.
 FT MUTAGEN 293 293 R->G: COMPLETE LOSS OF LIGAND-BINDING.
 FT SEQUENCE 468 AA; 51547 MW; 62AA239FA14F1BBB CRC64;
 FT MUTAGEN 291 291 G->D: 80% DECREASE OF LIGAND-BINDING AND
 FT MUTAGEN 293 293 NO IL6 SIGNALING.
 FT SEQUENCE 468 AA; 51547 MW; 62AA239FA14F1BBB CRC64;
 FT MUTAGEN 291 291 Q->K: COMPLETE LOSS OF LIGAND-BINDING.
 FT MUTAGEN 293 293 R->G: COMPLETE LOSS OF LIGAND-BINDING.
 FT SEQUENCE 468 AA; 51547 MW; 62AA239FA14F1BBB CRC64;
 FT MUTAGEN 291 291 G->D: 80% DECREASE OF LIGAND-BINDING AND
 FT MUTAGEN 293 293 NO IL6 SIGNALING.
 FT SEQUENCE 468 AA; 51547 MW; 62AA239FA14F1BBB CRC64;
 FT MUTAGEN 291 291 Q->K: COMPLETE LOSS OF LIGAND-BINDING.
 FT MUTAGEN 293 293 R->G: COMPLETE LOSS OF LIGAND-BINDING.
 FT SEQUENCE 468 AA; 51547 MW; 62AA239FA14F1BBB CRC64;
 FT MUTAGEN 291 291 G->D: 80% DECREASE OF LIGAND-BINDING AND
 FT MUTAGEN 293 293 NO IL6 SIGNALING.
 FT SEQUENCE 468 AA; 51547 MW; 62AA239FA14F1BBB CRC64;
 FT MUTAGEN 291 291 Q->K: COMPLETE LOSS OF LIGAND-BINDING.
 FT MUTAGEN 293 293 R->G: COMPLETE LOSS OF LIGAND-BINDING.
 FT SEQUENCE 468 AA; 51547 MW; 62AA239FA14F1BBB CRC64;
 FT MUTAGEN 291 291 G->D: 80% DECREASE OF LIGAND-BINDING AND
 FT MUTAGEN 293 293 NO IL6 SIGNALING.
 FT SEQUENCE 468 AA; 51547 MW; 62AA239FA14F1BBB CRC64;
 FT MUTAGEN 291 291 Q->K: COMPLETE LOSS OF LIGAND-BINDING.
 FT MUTAGEN 293 293 R->G: COMPLETE LOSS OF LIGAND-BINDING.
 FT SEQUENCE 468 AA; 51547 MW; 62AA239FA14F1BBB CRC64;
 FT MUTAGEN 291 291 G->D: 80% DECREASE OF LIGAND-BINDING AND
 FT MUTAGEN 293 293 NO IL6 SIGNALING.
 FT SEQUENCE 468 AA; 51547 MW; 62AA239FA14F1BBB CRC64;
 FT MUTAGEN 291 291 Q->K: COMPLETE LOSS OF LIGAND-BINDING.
 FT MUTAGEN 293 293 R->G: COMPLETE LOSS OF LIGAND-BINDING.
 FT SEQUENCE 468 AA; 51547 MW; 62AA239FA14F1BBB CRC64;
 FT MUTAGEN 291 291 G->D: 80% DECREASE OF LIGAND-BINDING AND
 FT MUTAGEN 293 293 NO IL6 SIGNALING.
 FT SEQUENCE 468 AA; 51547 MW; 62AA239FA14F1BBB CRC64;
 FT MUTAGEN 291 291 Q->K: COMPLETE LOSS OF LIGAND-BINDING.
 FT MUTAGEN 293 293 R->G: COMPLETE LOSS OF LIGAND-BINDING.
 FT SEQUENCE 468 AA; 51547 MW; 62AA239FA14F1BBB CRC64;
 FT MUTAGEN 291 291 G->D: 80% DECREASE OF LIGAND-BINDING AND
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 FT SEQUENCE 468 AA; 51547 MW; 62AA239FA14F1BBB CRC64;
 FT MUTAGEN 291 291 Q->K: COMPLETE LOSS OF LIGAND-BINDING.
 FT MUTAGEN 293 293 R->G: COMPLETE LOSS OF LIGAND-BINDING.
 FT SEQUENCE 468 AA; 51547 MW; 62AA239FA14F1BBB CRC64;
 FT MUTAGEN 291 291 G->D: 80% DECREASE OF LIGAND-BINDING AND
 FT MUTAGEN 293 293 NO IL6 SIGNALING.
 FT SEQUENCE 468 AA; 51547 MW; 62AA239FA14F1BBB CRC64;
 FT MUTAGEN 291 291 Q->K: COMPLETE LOSS OF LIGAND-BINDING.
 FT MUTAGEN 293 293 R->G: COMPLETE LOSS OF LIGAND-BINDING.
 FT SEQUENCE 468 AA; 51547 MW; 62AA239FA14F1BBB CRC64;
 FT MUTAGEN 291 291 G->D: 80% DECREASE OF LIGAND-BINDING AND
 FT MUTAGEN 293 293 NO IL6 SIGNALING.
 FT SEQUENCE 468 AA; 51547 MW; 62AA239FA14F1BBB CRC64;
 FT MUTAGEN 291 291 Q->K: COMPLETE LOSS OF LIGAND-BINDING.
 FT MUTAGEN 293 293 R->G: COMPLETE LOSS OF LIGAND-BINDING.
 FT SEQUENCE 468 AA; 51547 MW; 62AA239FA14F1BBB CRC64;
 FT MUTAGEN 291 291 G->D: 80% DECREASE OF LIGAND-BINDING AND
 FT MUTAGEN 293 293 NO IL6 SIGNALING.
 FT SEQUENCE 468 AA; 51547 MW; 62AA239FA14F1BBB CRC64;
 FT MUTAGEN 291 291 Q->K: COMPLETE LOSS OF LIGAND-BINDING.
 FT MUTAGEN 293 293 R->G: COMPLETE LOSS OF LIGAND-BINDING.
 FT SEQUENCE 468 AA; 51547 MW; 62AA239FA14F1BBB CRC64;
 FT MUTAGEN 291 291 G->D: 80% DECREASE OF LIGAND-BINDING AND
 FT MUTAGEN 293 293 NO IL6 SIGNALING.
 FT SEQUENCE 468 AA; 51547 MW; 62AA239FA14F1BBB CRC64;
 FT MUTAGEN 291 291 Q->K: COMPLETE LOSS OF LIGAND-BINDING.
 FT MUTAGEN 293 293 R->G: COMPLETE LOSS OF LIGAND-BINDING.
 FT SEQUENCE 468 AA; 51547 MW; 62AA239FA14F1BBB CRC64;
 FT MUTAGEN 291 291 G->D: 80% DECREASE OF LIGAND-BINDING AND
 FT MUTAGEN 293 293 NO IL6 SIGNALING.
 FT SEQUENCE 468 AA; 51547 MW; 62AA239FA14F1BBB CRC64;
 FT MUTAGEN 291 291 Q->K: COMPLETE LOSS OF LIGAND-BINDING.
 FT MUTAGEN 293 293 R->G: COMPLETE LOSS OF LIGAND-BINDING.
 FT SEQUENCE 468 AA; 51547 MW; 62AA239FA14F1BBB CRC64;
 FT MUTAGEN 291 291 G->D: 80% DECREASE OF LIGAND-BINDING AND
 FT MUTAGEN 293 293 NO IL6 SIGNALING.
 FT SEQUENCE 468 AA; 51547 MW; 62AA239FA14F1BBB CRC64;
 FT MUTAGEN 291 291 Q->K: COMPLETE LOSS OF LIGAND-BINDING.
 FT MUTAGEN 293 293 R->G: COMPLETE LOSS OF LIGAND-BINDING.
 FT SEQUENCE 468 AA; 51547 MW; 62AA239FA14F1BBB CRC64;
 FT MUTAGEN 291 291 G->D: 80% DECREASE OF LIGAND-BINDING AND
 FT MUTAGEN 293 293 NO IL6 SIGNALING.
 FT SEQUENCE 468 AA; 51547 MW; 62AA239FA14F1BBB CRC64;
 FT MUTAGEN 291 291 Q->K: COMPLETE LOSS OF LIGAND-BINDING.
 FT MUTAGEN 293 293 R->G: COMPLETE LOSS OF LIGAND-BINDING.
 FT SEQUENCE 468 AA; 51547 MW; 62AA239FA14F1BBB CRC64;
 FT MUTAGEN 291 291 G->D: 80% DECREASE OF LIGAND-BINDING AND
 FT MUTAGEN 293 293 NO IL6 SIGNALING.
 FT SEQUENCE 468 AA; 51547 MW; 62AA239FA14F1BBB CRC64;
 FT MUTAGEN 291 291 Q->K: COMPLETE LOSS OF LIGAND-BINDING.
 FT MUTAGEN 293 293 R->G: COMPLETE LOSS OF LIGAND-BINDING.
 FT SEQUENCE 468 AA; 51547 MW; 62AA239FA14F1BBB CRC64;
 FT MUTAGEN 291 291 G->D: 80% DECREASE OF LIGAND-BINDING AND
 FT MUTAGEN 293 293 NO IL6 SIGNALING.
 FT SEQUENCE 468 AA; 51547 MW; 62AA239FA14F1BBB CRC64;
 FT MUTAGEN 291 291 Q->K: COMPLETE LOSS OF LIGAND-BINDING.
 FT MUTAGEN 293 293 R->G: COMPLETE LOSS OF LIGAND-BINDING.
 FT SEQUENCE 468 AA; 51547 MW; 62AA239FA14F1BBB CRC64;
 FT MUTAGEN 291 291 G->D: 80% DECREASE OF LIGAND-BINDING AND
 FT MUTAGEN 293 293 NO IL6 SIGNALING.
 FT SEQUENCE 468 AA; 51547 MW; 62AA239FA14F1BBB CRC64;
 FT MUTAGEN 291 291 Q->K: COMPLETE LOSS OF LIGAND-BINDING.
 FT MUTAGEN 293 293 R->G: COMPLETE LOSS OF LIGAND-BINDING.
 FT SEQUENCE 468 AA; 51547 MW; 62AA239FA14F1BBB CRC64;
 FT MUTAGEN 291 291 G->D: 80% DECREASE OF LIGAND-BINDING AND
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 FT SEQUENCE 468 AA; 51547 MW; 62AA239FA14F1BBB CRC64;
 FT MUTAGEN 291 291 Q->K: COMPLETE LOSS OF LIGAND-BINDING.
 FT MUTAGEN 293 293 R->G: COMPLETE LOSS OF LIGAND-BINDING.
 FT SEQUENCE 468 AA; 51547 MW; 62AA239FA14F1BBB CRC64;
 FT MUTAGEN 291 291 G->D: 80% DECREASE OF LIGAND-BINDING AND
 FT MUTAGEN 293 293 NO IL6 SIGNALING.
 FT SEQUENCE 468 AA; 51547 MW; 62AA239FA14F1BBB CRC64;
 FT MUTAGEN 291 291 Q->K: COMPLETE LOSS OF LIGAND-BINDING.
 FT MUTAGEN 293 293 R->G: COMPLETE LOSS OF LIGAND-BINDING.
 FT SEQUENCE 468 AA; 51547 MW; 62AA239FA14F1BBB CRC64;
 FT MUTAGEN 291 291 G->D: 80% DECREASE OF LIGAND-BINDING AND
 FT MUTAGEN 293 293 NO IL6 SIGNALING.
 FT SEQUENCE 468 AA; 51547 MW; 62AA239FA14F1BBB CRC64;
 FT MUTAGEN 291 291 Q->K: COMPLETE LOSS OF LIGAND-BINDING.
 FT MUTAGEN 293 293 R->G: COMPLETE LOSS OF LIGAND-BINDING.
 FT SEQUENCE 468 AA; 51547 MW; 62AA239FA14F1BBB CRC64;
 FT MUTAGEN 291 291 G->D: 80% DECREASE OF LIGAND-BINDING AND
 FT MUTAGEN 293 293 NO IL6 SIGNALING.
 FT SEQUENCE 468 AA; 51547 MW; 62AA239FA14F1BBB CRC64;
 FT MUTAGEN 291 291 Q->K: COMPLETE LOSS OF LIGAND-BINDING.
 FT MUTAGEN 293 293 R->G: COMPLETE LOSS OF LIGAND-BINDING.
 FT SEQUENCE 468 AA; 51547 MW; 62AA239FA14F1BBB CRC64;
 FT MUTAGEN 291 291 G->D: 80% DECREASE OF LIGAND-BINDING AND
 FT MUTAGEN 293 293 NO IL6 SIGNALING.
 FT SEQUENCE 468 AA; 51547 MW; 62AA239FA14F1BBB CRC64;
 FT MUTAGEN 291 291 Q->K: COMPLETE LOSS OF LIGAND-BINDING.
 FT MUTAGEN 293 293 R->G: COMPLETE LOSS OF LIGAND-BINDING.
 FT SEQUENCE 468 AA; 51547 MW; 62AA239FA14F1BBB CRC64;
 FT MUTAGEN 291 291 G->D: 80% DECREASE OF LIGAND-BINDING AND
 FT MUTAGEN 293 293 NO IL6 SIGNALING.
 FT SEQUENCE 468 AA; 51547 MW; 62AA239FA14F1BBB CRC64;
 FT MUTAGEN 291 291 Q->K: COMPLETE LOSS OF LIGAND-BINDING.
 FT MUTAGEN 293 293 R->G: COMPLETE LOSS OF LIGAND-BINDING.
 FT SEQUENCE 468 AA; 51547 MW; 62AA239FA14F1BBB CRC64;
 FT MUTAGEN 291 291 G->D: 80% DECREASE OF LIGAND-BINDING AND
 FT MUTAGEN 293 293 NO IL6 SIGNALING.
 FT SEQUENCE 468 AA; 51547 MW; 62AA239FA14F1BBB CRC64;
 FT MUTAGEN 291 291 Q->K: COMPLETE LOSS OF LIGAND-BINDING.
 FT MUTAGEN 293 293 R->G: COMPLETE LOSS OF LIGAND-BINDING.
 FT SEQUENCE 468 AA; 51547 MW; 62AA239FA14F1BBB CRC64;
 FT MUTAGEN 291 291 G->D: 80% DECREASE OF LIGAND-BINDING AND
 FT MUTAGEN 293 293 NO IL6 SIGNALING.
 FT SEQUENCE 468 AA; 51547 MW; 62AA239FA14F1BBB CRC64;
 FT MUTAGEN 291 291 Q->K: COMPLETE LOSS OF LIGAND-BINDING.
 FT MUTAGEN 293 293 R->G: COMPLETE LOSS OF LIGAND-BINDING.
 FT SEQUENCE 468 AA; 51547 MW; 62AA239FA14F1BBB CRC64;
 FT MUTAGEN 291 291 G->D: 80% DECREASE OF LIGAND-BINDING AND
 FT MUTAGEN 293 293 NO IL6 SIGNALING.
 FT SEQUENCE 468 AA; 51547 MW; 62AA239FA14F1BBB CRC64;
 FT MUTAGEN 291 291 Q->K: COMPLETE LOSS OF LIGAND-BINDING.
 FT MUTAGEN 293 293 R->G: COMPLETE LOSS OF LIGAND-BINDING.
 FT SEQUENCE 468 AA; 51547 MW; 62AA239FA14F1BBB CRC64;
 FT MUTAGEN 291 291 G->D: 80% DECREASE OF LIGAND-BINDING AND
 FT MUTAGEN 293 293 NO IL6 SIGNALING.
 FT SEQUENCE 468 AA; 51547 MW; 62AA239FA14F1BBB CRC64;
 FT MUTAGEN 291 291 Q->K: COMPLETE LOSS OF LIGAND-BINDING.
 FT MUTAGEN 293 293 R->G: COMPLETE LOSS OF LIGAND-B

RN (2)
 RP SEQUENCE OF 123-186 FROM N.A.
 RC TISSUE=Liver;
 RA Klier J.J., Matteri R.L.;
 RT *Partial cDNA sequence of porcine interleukin 6 receptor.*;
 RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
 CC -1 FUNCTION: PART OF THE RECEPTOR FOR INTERLEUKIN 6. BINDS TO IL-6
 CC WITH LOW AFFINITY, BUT DOES NOT TRANSDUCE A SIGNAL. SIGNAL
 CC ACTIVATION NECESSITATE AN ASSOCIATION WITH IL6ST. ACTIVATION MAY
 CC LEAD TO THE REGULATION OF THE IMMUNE RESPONSE, ACUTE-PHASE
 CC REACTIONS AND HEMATOPOIETIS.
 CC -1 SUBUNIT: HEXAMER OF 2 IL6, 2 IL6R-ALPHA AND 2 IL6ST (BY
 CC SIMILARITY).
 CC -1 SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1 TISSUE SPECIFICITY: EXPRESSED IN LIVER.
 CC -1 DOMAIN: THE TWO FIBRONECTIN TYPE III-LIKE DOMAINS CONTAINED IN THE
 CC C-TERMINAL PART FORM TOGETHER A CYTOKINE-BINDING DOMAIN.
 CC -1 SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
 CC -1 SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 CC -----
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 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: AF147881; AAF73109.1; -
 CC DR EMBL: AF015116; AAB70916.1; -
 CC DR HSSP: P16471; 1BP3.
 CC DR InterPro: IPR002996; CRIA.
 CC DR InterPro: IPR001777; FN_III.
 CC DR InterPro: IPR003530; Hematopo_receptor_L_F3.
 CC DR InterPro: IPR003006; Ig_MHC.
 CC DR InterPro: IPR003598; Ig_C2.
 CC DR Pfam: PF00041; fn3; 1.
 CC DR Pfam: PF00047; fn3; 1.
 CC DR SMART: SM00060; FN3; 1.
 CC DR SMART: SM00408; IGC2; 1.
 CC DR PROSITE: PS00340; RECEPTOR_CYTOKINES_2; 1.
 CC KW Receptor; Transmembrane; Glycoprotein; Immunoglobulin domain; Repeat;
 CC Signal.
 CC FT SIGNAL 1 19 BY SIMILARITY.
 CC FT CHAIN 20 467 INTERLEUKIN-6 RECEPTOR ALPHA CHAIN.
 CC FT DOMAIN 20 365 EXTRACELLULAR (POTENTIAL).
 CC FT TRANSMEM 366 386 POTENTIAL.
 CC FT DOMAIN 387 467 CYTOPLASMIC (POTENTIAL).
 CC FT DOMAIN 40 103 IG-LIKE C2-TYPE DOMAIN.
 CC FT DISULFID 25 193 BY SIMILARITY.
 CC FT DISULFID 47 96 BY SIMILARITY.
 CC FT DISULFID 121 132 BY SIMILARITY.
 CC FT DISULFID 165 176 BY SIMILARITY.
 CC FT CARBOHYD 55 55 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 93 93 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 221 221 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 350 350 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC SQ SEQUENCE 467 AA: 51066 MW: 42508868 Da
 CC

Query Match 82.9%; Score 121; DB 1; Length 467;
 Best Local Similarity 85.7%; Pred No. 1,3e-10;
 Matches 24; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 EWGPRSTPSLTTRAVLVKRFNSPAED 28
 Db 133 EWRPRSPPTTRKAVLVKRFNSPVED 160
 RESULT 3
 IL6A_MOUSE STANDARD; PRT; 460 AA.
 ID IL6A_MOUSE

AC P22272;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE INTERLEUKIN-6 RECEPTOR ALPHA CHAIN PRECURSOR (IL-6R-ALPHA) (IL-6R 1).
 GN IL6RA OR IL6R.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/C; TISSUE=Spleen;
 RA MEDLINE=90278354; PubMed=2112585;
 RA Sugita T., Totsuka T., Saito M., Yamasaki K., Taya T., Hirano T.,
 RA Kishimoto T.;
 RT *Functional murine interleukin 6 receptor with the intracisternal A
 RT particle gene product at its cytoplasmic domain. Its possible role in
 RT plasmacytogenesis*;
 RL J. Exp. Med. 171:2001-2009(1990).
 RN (2)
 RP SEQUENCE FROM N.A.
 RC STRAIN=C3H; TISSUE=Liver;
 RA Fiorillo M.T., Ciliberto G., Dente L.;
 RT Submitted (JUL-1990) to the EMBL/GenBank/DBJ databases.
 CC -1 FUNCTION: PART OF THE RECEPTOR FOR INTERLEUKIN 6. BINDS TO IL-6
 CC WITH LOW AFFINITY, BUT DOES NOT TRANSDUCE A SIGNAL. SIGNAL
 CC ACTIVATION NECESSITATE AN ASSOCIATION WITH IL6ST. ACTIVATION MAY
 CC LEAD TO THE REGULATION OF THE IMMUNE RESPONSE, ACUTE-PHASE
 CC REACTIONS AND HEMATOPOIETIS.
 CC -1 SUBUNIT: HEXAMER OF 2 IL6, 2 IL6R-ALPHA AND 2 IL6ST (BY
 CC SIMILARITY).
 CC -1 SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1 DOMAIN: THE TWO FIBRONECTIN TYPE III-LIKE DOMAINS CONTAINED IN THE
 CC C-TERMINAL PART FORM TOGETHER A CYTOKINE-BINDING DOMAIN.
 CC -1 SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
 CC -1 SIMILARITY: CONTAINS 3 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC -1 SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: X51975; CAA36237.1; -
 CC DR EMBL: X53802; CAA37810.1; -
 CC DR PIR: J10144; J10144.
 CC DR PIR: J10145; J10145.
 CC DR PIR: S14543; S14543.
 CC DR HSSP: P16471; 1BP3.
 CC DR MGD: MGI:105304; IL6ra.
 CC DR InterPro: IPR002996; CRIA.
 CC DR InterPro: IPR001777; FN_III.
 CC DR InterPro: IPR003530; Hematopo_receptor_L_F3.
 CC DR InterPro: IPR003006; Ig_MHC.
 CC DR InterPro: IPR003598; Ig_C2.
 CC DR Pfam: PF00041; fn3; 1.
 CC DR Pfam: PF00047; fn3; 1.
 CC DR SMART: SM00060; FN3; 1.
 CC DR SMART: SM00408; IGC2; 1.
 CC DR PROSITE: PS01354; HEMATOPO_REC_L_F3; 1.
 CC KW Receptor; Transmembrane; Glycoprotein; Immunoglobulin domain; Repeat;
 CC Signal.
 CC FT SIGNAL 1 19
 CC FT CHAIN 20 460 INTERLEUKIN-6 RECEPTOR ALPHA CHAIN.
 CC FT DOMAIN 20 364 EXTRACELLULAR (POTENTIAL).
 CC FT TRANSMEM 365 385 POTENTIAL.
 CC FT DOMAIN 386 460 CYTOPLASMIC (POTENTIAL).
 CC FT DOMAIN 40 99 IG-LIKE C2-TYPE DOMAIN.
 CC FT DISULFID 25 190 BY SIMILARITY.

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FT DISULFID 47 92 BY SIMILARITY.
FT DISULFID 117 128 BY SIMILARITY.
FT DISULFID 162 173 BY SIMILARITY.
FT CARBOHYD 32 32 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 35 35 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 150 150 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 374 374 A -> R (IN REF. 2).
SQ SEQUENCE 460 AA; 50454 MW; F85C5906DD08525C4 CRC64;

Query Match 49.3%; Score 72; DB 1; Length 460;
Best Local Similarity 58.3%; Pred. No. 0.003;
Matches 14; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 1 EMCPRSPSLTTKAVLLVRRFONS 24
   ||| ||||| ||||| :
DB 129 EWRPSSPSPPTTKAVLEAKKINTT 152

RESULT 4
ID IL6A_RAT STANDARD; PRT; 462 AA.
AC P22273;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE INTERLEUKIN-6 RECEPTOR ALPHA CHAIN PRECURSOR (IL-6R-ALPHA) (IL-6R 1).
GN IL6R.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_Taxid=10116;
   [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FISCHER 344; TISSUE=Liver;
RX MEDLINE=91060602; PubMed=2174054;
RA Baumann M., Baumann H., Fey G.H.;
RT "Molecular cloning, characterization and functional expression of the
RT rat liver interleukin 6 receptor.";
RN J. Biol. Chem. 265:19853-19862(1990).
RN [2]
RN IDENTIFICATION OF PROBABLE FRAMESHIFT IN 227-261.
RA GIBSON T.;
RL Unpublished observations (FEB-1995).
CC -1- FUNCTIONED: PART OF THE RECEPTOR FOR INTERLEUKIN 6. BINDS TO IL-6
CC WITH LOW AFFINITY, BUT DOES NOT TRANSDUCE A SIGNAL. SIGNAL
CC ACTIVATION NECESSITATE AN ASSOCIATION WITH ILST. ACTIVATION MAY
CC LEAD TO THE REGULATION OF THE IMMUNE RESPONSE, ACUTE-PHASE
CC REACTIONS AND HEMATOPOIESIS.
CC -1- SUBUNIT: HEXAMER OF 2 IL6, 2 IL6R-ALPHA AND 2 ILST (BY
CC SIMILARITY).
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- DOMAIN: THE TWO FIBRONECTIN TYPE III-LIKE DOMAINS CONTAINED IN THE
CC C-TERMINAL PART FORM TOGETHER A CYTOKINE-BINDING DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC -1- SIMILARITY: CONTAINS 3 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL, M58587; AAA41431.1; -.
CC PIR: A37986; A37986.
CC HSSP: P16471; 1B63.
CC InterPro: IPR002296; CR1A.
CC InterPro: IPR001777; FN_III.
CC InterPro: IPR003530; Hematopo_rceptor_L_F3.
CC InterPro: IPR003006; Ig_MHC.

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DR	InterPro: IPR003598; Ig_C2.
DR	Pfam: PF00041; fn3; 1.
DR	Pfam: PF00047; Ig; 1.
DR	SMART: SM00060; FN3; 1.
DR	SMART: SM00408; IGc2; 1.
DR	PROSITE: PS01354; HEMATOPOI_REC_L_F3; 1.
KM	Receptor; Transmembrane; Glycoprotein; Immunoglobulin domain; Repeat; Signal.
FT	SIGNAL
FT	CHAIN
FT	DOMAIN
FT	TRANSMEM
FT	DOMAIN
FT	DISULFID
FT	DISULFID
FT	DISULFID
FT	CARBOHYD
FT	CARBOHYD
FT	CARBOHYD
FT	CONFLICT
SEQUENCE	462 AA; 50398 MW; A4DE064CEDC0537D CRC64;
Query Match	47.9%; Score 70; DR 1; Length 462;
Best Local Similarity	54.2%; Pfdm. NO. 0.006; Mismatches 8; Indels 0; Gaps
Matches 13; Conservative	
Oy	1 EMGPRSPPTTKRAVLVRRKFNQNS 24 : :
Db	129 EWHPSSTPPTTKAVMAFKAKINTT 152
RESULT 5	
PPSPC_RABIT	STANDARD; PRG; 188 AA.
ID	P22398;
AC	P22398;
DT	01-AUG-1991 (Rel. 19, Created)
DT	01-OCT-1996 (Rel. 34, Last sequence update)
DT	15-JUL-1999 (Rel. 38, Last annotation update)
DE	PULMONARY SURFACTANT-ASSOCIATED PROTEIN C PRECURSOR (SP-C) (PULMONARY SURFACTANT-ASSOCIATED PROTEOLIPID SPL(VAL)).
GN	SETPC OR SETP2.
OS	Oryctolagus cuniculus (Rabbit).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelestomi;
OC	Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX	NCBI_Taxid=9986;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN-NEW ZEALAND WHITE; TISSUE=Lung;
RX	MEDLINE=92353123; PubMed=1643107;
RA	Connelly I., Possmaier F.;
RT	"cDNA sequence and alternative mRNA splicing of surfactant-associated protein C (sp-C) in rabbit lung."
RL	Biochim. Biophys. Acta 1127:199-207(1992).
RN	[2]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Lung;
RX	MEDLINE=9118799; PubMed=1335697;
RA	Boggs V., Margana R.K.;
RT	"Rabbit surfactant protein C: cDNA cloning and regulation of alternatively spliced surfactant protein C mRNAs."
RL	Am. J. Physiol. 263:L634-L644(1992).
RN	[3]
RP	SEQUENCE OF 24-188 FROM N.A.
RC	TISSUE=Lung;
RX	MEDLINE=93105936; PubMed=1468410;
RA	Durham P.L., Nanthakumar E.J., Snyder J.M.;
RT	"Developmental regulation of surfactant-associated proteins in rabbit


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YHDA_ECOLI
ID YHDA_ECOLI STANDARD; PRT: 646 AA.
AC P13518;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE HYPOTHETICAL 73.3 KDA PROTEIN IN MREB-ACCB INTERGENIC REGION (F646).
GN YHDA OR B3252.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. II, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12."
RL Science 277:1453-1474(1997).
RN [2]
RP SEQUENCE OF 545-646 FROM N.A.
RC STRAIN-K12;
RX MEDLINE=89008079; PubMed=3049542;
RA Doi M., Wachi M., Ishino F., Tomioka S., Ito M., Sakagami Y.,
RA Suzuki A., Matsubashi M.;
RT "Determinations of the DNA sequence of the mreB gene and of the gene
RT products of the mre region that function in formation of the rod
RT shape of Escherichia coli cells."
RL J. Bacteriol. 170:4619-4624(1988).
RN [3]
RP SMILARITY: BELONGS TO THE YEGE/YHDA/YHUK/YJCC FAMILY.
CC
CC
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CC
CC
CC
CC EMBL: U18997; AAA58055.1; -
CC EMBL: AE000404; AAC76284.1; -
CC EMBL: M22055; AAA83890.1; -
CC PIR: B31843; QOCE5.
CC EcGene: EG10018; Yhda.
CC InterPro: IPR001613; DUF2.
CC InterPro: IPR001601; DUF9.
CC Pfam: PF00565; DUF2.1.
CC Pfam: PF00565; DUF2.1.
CC SMART: SM00267; DUF1.1.
CC SMART: SM00052; DUF2.1.
CC Hypothetical protein: Complete proteome.
CC SEQUENCE 646 AA; 73339 MW; 0387E01BC4D06B8 CRC64;
SQ

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Query Match 32.2%; Score 47; DB 1; Length 646;
Best Local Similarity 41.7%; Pred. No. 25;
Matches 10; Conservative 6; Mismatches 4; Indels 4; Gaps 1;

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RESULT 8
YAGA_ECOLI STANDARD; PRT: 384 AA.
AC P37007; P77312;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)

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DE HYPOTHETICAL 43.8 KDA PROTEIN IN PERR-ARGF INTERGENIC REGION.
GN YAGA OR B0267.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. II, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12."
RL Science 277:1453-1474(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-K12 / W3110;
RX Takemoto K., Mori H., Murayama N., Kataoka K., Yano M., Itoh T.,
RA Yamamoto Y., Inokuchi H., Miki T., Hatada E., Fukuda R., Ichihara S.,
RA Mizuno T., Makino K., Nakata A., Yura T., Saepel K.;
RT "Systematic sequencing of the Escherichia coli genome: analysis of the
RT 4.0 - 6.0 min (189,987 - 281,416bp) region."
RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Schramm S., Duncan M., Allen E., Araujo R., Aparicio A., Chung E.,
RA Davis K., Federspiel N., Hyman R., Kalman S., Komp C., Kurdi O.,
RA Laskari D., Lew H., Lin D., Namath A., Oefner P., Roberts D.,
RA Davis R.W.;
RT Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE OF 245-384 FROM N.A.
RX MEDLINE=94156832; PubMed=8113168;
RA Volker M., Loewen P.C., Switla J., Crowley D., Conley M.;
RT "The delta (argf-lacZ)205(U169) deletion greatly enhances resistance
RT to hydrogen peroxide in stationary-phase Escherichia coli."
RL J. Bacteriol. 176:1297-1302(1994).
RN [5]
RP IDENTIFICATION.
RA Rudd K.E.;
RL Unpublished observations (APR-1994).
CC
CC -1- CAUTION: REF.4 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO A
CC FRAMESHIFT IN POSITION 257.
CC
CC
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CC
CC
CC EMBL: AE000134; AAC73370.1; -
CC EMBL: DB3536; BAA77933.1; -
CC EMBL: U70214; AAB08688.1; -
CC EMBL: L20943; -; NOT_ANNOTATED_CDS.
CC EcGene: EG12338; Yaga.
CC InterPro: IPR001584; Rye.
CC Pfam: PF00665; rve.1.
CC Hypothetical protein: Complete proteome.
CC CONFLICT 261 271 MISSING (IN REF. 1).
CC SEQUENCE 384 AA; 43768 MW; 95619AF7C02FDE5E CRC64;
SQ

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Query Match 31.8%; Score 46.5; DB 1; Length 384;
Best Local Similarity 38.9%; Pred. No. 16;
Matches 14; Conservative 2; Mismatches 9; Indels 11; Gaps 1;

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YQ 2 WGPSTPSLTTRKAVL-----LVKRFNSPA 26
DB 7 WDARDTMSLRTFVFVLFASQDGNIRSLVCRFGISPA 42

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RESULT 9
RADA_TREPA STANDARD: PRT: 455 AA.
AC 083985;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE DNA REPAIR PROTEIN RADA HOMOLOG (DNA REPAIR PROTEIN SMS HOMOLOG).
GN RADA OR SMS OR TP1022.
OS Treponema pallidum.
CC Bacteria: Spirochaetales; Spirochaetaceae; Treponema.
CX NCBI_TaxID=160;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NICHOLS;
RX MEDLINE=98332770; PubMed=9665876;
RA Fraser C.M., Norris S.J., Weinstein G.M., White O., Sutton G.C.,
RA Dodson R., Gwinn M., Hickey E.K., Clayton R., Ketchum K.A.,
RA Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J.,
RA Khaliq H., Richardson D., Howell J.K., Chidambaram M., Ullrich T.,
RA McDonald L., Artlich P., Bowman C., Cotton M.D., Fujii C., Garland S.,
RA Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O.,
RA Venter J.C.;
RT "Complete genome sequence of Treponema pallidum, the syphilis
RT spirochete."
RL Science 281:375-388(1998).
CC -1- FUNCTION: MAY PLAY A ROLE IN THE REPAIR OF ENDOGENOUS ALKYLATION
CC DAMAGE (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE RADA FAMILY.
CC -----
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CC -----
CC EMBL: AE001270; AAC5973.1; -.
DR TIGR: TP1022; -.
DR InterPro: IPR001984; Ion_endopep.
DR PRINTS: PRO00830; ENDOPLAPTASE.
KW DNA repair; ATP-binding; Zinc-finger; DNA-binding; Complete proteome.
FT ZN-FING 11 28 C4-TYPE (POTENTIAL).
FT NP-BIND 97 104 ATP (POTENTIAL).
SQ SEQUENCE 455 AA: 49304 MW: 435C310919A70E77 CRC64;

Query Match 31.8%; Score 46.5; DB 1; Length 455;
Best Local Similarity 39.3%; Pred. No. 20;
Matches 11; Conservative 5; Mismatches 11; Indels 1; Gaps 1;

OY 1 EWGP-RSTPLTKAVLVKRFONSPAE 27
DB 30 EWNSEPTPSLSSGDYAVKAKSSSPVQ 57

RESULT 10
DPOL_HPBVY STANDARD: PRT: 832 AA.
AC P03156;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE P PROTEIN [INCLUDES: DNA-DIRECTED DNA POLYMERASE (EC 2.7.7.7); RNA-
DE DIRECTED DNA POLYMERASE (EC 2.7.7.49); RIBONUCLEASE H (EC 3.1.26.4)]
DE (VERSION 1).
GN P.
OS Hepatitis B virus (subtype ayw).
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10418;

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RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81012091; PubMed=399327;
RA Galibert F., Mandart E., Tlollais P., Charney P.;
RT "Nucleotide sequence of the hepatitis B virus genome (subtype ayw)
RT cloned in E. coli."
RL Nature 281:646-650(1979).
CC -1- CATALYTIC ACTIVITY: N DEOXYNUCLEOSIDE TRIPHOSPHATE -
CC N PYROPHOSPHATE + DNA(N).
CC -1- CATALYTIC ACTIVITY: ENDONUCLEOLYTIC CLEAVAGE TO 5'-PHOSPHO-
CC MONOESTER.
CC -----
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CC -----
CC EMBL: V01460; -. NOT_ANNOTATED_CDS.
DR PIR: A00702; JDLVA.
DR InterPro: IPR001462; DNAPol_viral_C.
DR InterPro: IPR000201; DNAPol_viral_N.
DR InterPro: IPR000477; RYase.
DR Pfam: PF00336; DNA_pol_viral_C; 1.
DR Pfam: PF00242; DNA_pol_viral_N; 1.
DR Pfam: PF0078; rvc; 2.
DR Pfam: PF000814; DNAPol_viral_C; 1.
DR Pfam: PF000814; DNAPol_viral_N; 1.
KW Transferrase; RNA-directed DNA polymerase; DNA-directed DNA polymerase;
KW Hydrolyase; Nuclease; Endonuclease; DNA replication; DNA-binding.
SQ SEQUENCE 832 AA: 93676 MW: 7AB3AAE5BA57D0D6 CRC64;

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Query Match 31.8%; Score 46.5; DB 1; Length 832;
Best Local Similarity 34.2%; Pred. No. 40;
Matches 13; Conservative 4; Mismatches 10; Indels 11; Gaps 1;

OY 1 EWGPRS-----TPSLTKAVLVKRFONSPAE 27
DB 337 DWGPCAHEGHHIRIPRPSRVYGVFLVKNPHNTAE 374

RESULT 11
TCOF_HUMAN STANDARD: PRT: 1411 AA.
AC Q13428; Q99408;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE TREACHER PROTEIN (TREACHER COLLINS SYNDROME PROTEIN).
GN TCOF1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96154183; PubMed=8563749;
RA Dixon J., Edwards S.J., Gladwin A.J., Dixon M.J., Loftus S.K.,
RA Bonner C.A., Koprivnikar K., Wasmuth J.J.;
RT "Positional cloning of a gene involved in the pathogenesis of
RT Treacher Collins syndrome. The Treacher Collins Syndrome
RT Collaborative Group."
RL Nat. Genet. 12:130-136(1996).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=97250498; PubMed=9096354;
RA Wise C.A., Chiang L.C., Paznekas W.A., Sharma M., Musy M.M.,
RA Ashley J.A., Lovett M., Jabs E.W.;
RT "TCOF1 gene encodes a putative nucleolar phosphoprotein that exhibits
RT mutations in Treacher Collins syndrome throughout its coding
RT region."

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RL Proc. Natl. Acad. Sci. U.S.A. 94:3110-3115(1997).
RN [3]
RN VARIANTS L-439; V-810; V-1313 & G-1355, AND VARIANT TCS R-53.
RX MEDLINE-97195537; Pubmed-9042910;
RA Edwards S.J., Gladwin A.J., Dixon M.J.;
RT "The mutational spectrum in Treacher Collins syndrome reveals a
RT predominance of mutations that create a premature-termination
RT codon."
RL Am. J. Hum. Genet. 60:515-524(1997).
CC -1- DISEASE: DEFECTS IN TCOF1 ARE THE CAUSE OF TREACHER COLLINS
CC SYNDROME (TCS). TCS IS A AUTOSOMAL DOMINANT DISORDER OF
CC CRANIOFACIAL DEVELOPMENT THAT OCCURS WITH AN INCIDENCE OF 1/50,000
CC LIVE BIRTHS. THE CLINICAL FEATURES OF TCS ARE BILATERALLY
CC SYMMETRICAL AND INCLUDE: (1) ABNORMALITIES OF THE EXTERNAL EARS,
CC ATRESIA OF THE EXTERNAL EAR CANALS, AND MALFORMATION OF THE MIDDLE
CC EAR OSSICLES, WHICH MAY RESULT IN CONDUCTIVE HEARING LOSS; (2)
CC LATERAL DOWNSLOPING OF PALPEBRAL FISSURES, FREQUENTLY WITH
CC COLONAS OF THE LOWER EYELIDS; (3) HYPOPLASIA OF THE MANDIBLE AND
CC ZYGOMATIC COMPLEX; (4) CLEFT PALATE.
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CC -----
DR EMBL: U40847; AAC50903.1; -;
DR EMBL: U76366; AAC51181.1; -;
DR EMBL: U84664; AAC51185.1; -;
DR EMBL: U84640; AAC51185.1; JOINED.
DR EMBL: U84641; AAC51185.1; JOINED.
DR EMBL: U84642; AAC51185.1; JOINED.
DR EMBL: U84643; AAC51185.1; JOINED.
DR EMBL: U84644; AAC51185.1; JOINED.
DR EMBL: U84645; AAC51185.1; JOINED.
DR EMBL: U84646; AAC51185.1; JOINED.
DR EMBL: U84647; AAC51185.1; JOINED.
DR EMBL: U84648; AAC51185.1; JOINED.
DR EMBL: U84649; AAC51185.1; JOINED.
DR EMBL: U84650; AAC51185.1; JOINED.
DR EMBL: U84651; AAC51185.1; JOINED.
DR EMBL: U84652; AAC51185.1; JOINED.
DR EMBL: U84653; AAC51185.1; JOINED.
DR EMBL: U84654; AAC51185.1; JOINED.
DR EMBL: U84655; AAC51185.1; JOINED.
DR EMBL: U84656; AAC51185.1; JOINED.
DR EMBL: U84657; AAC51185.1; JOINED.
DR EMBL: U84658; AAC51185.1; JOINED.
DR EMBL: U84659; AAC51185.1; JOINED.
DR EMBL: U84660; AAC51185.1; JOINED.
DR EMBL: U84661; AAC51185.1; JOINED.
DR EMBL: U84662; AAC51185.1; JOINED.
DR EMBL: U84663; AAC51185.1; JOINED.
DR MIM: 154500; -;
KW Disease mutation: Polymorphism.
FT DOMAIN 89 97
FT DOMAIN 204 207
FT DOMAIN 616 619
FT DOMAIN 919 924
FT DOMAIN 1285 1289
FT DOMAIN 1375 1386
FT DOMAIN 1398 1405
FT VARIANT 53 53
FT VARIANT 439 439
FT VARIANT 810 810
FT VARIANT 1313 1313
FT VARIANT 1355 1355
D -> G.
/FTId=VAR_005633.
A -> V.
/FTId=VAR_005632.
A -> V.
/FTId=VAR_005633.
D -> G.

FT SEQUENCE 1411 AA; 144312 MW; 3880203D985C2699 CRC64; /FTId=VAR_005634.
SQ
Query Match 31.8%; Score 46.5; DB 1; Length 1411;
Best Local Similarity 46.2%; Pref. No. 75;
Matches 12; Conservative 2; Mismatches 11; Indels 1; Gaps 1;
QY 3 GPRSPSLTKRAVLVRRKFNQSPAE 28
DB 766 GPASVPSV-GKAVATAAQTGPEED 790
RESULT 12
ID SPHR_SYPN7 STANDARD; PRT; 257 AA.
AC P39663;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE ALKALINE PHOSPHATASE SYNTHESIS TRANSCRIPTIONAL REGULATORY PROTEIN
DE SPHR.
GN SPHR.
OS Synecococcus sp. (strain PCC 7942) (Anacystis nidulans R2).
OC Bacteria; Cyanobacteria; Chroococcales; Synecococcus.
OX NCBI_TaxID=1140;
RN [1]
RP MEDLINE-93268103; Pubmed-8497200;
RX Alba H., Nagaya M., Mizuno T.;
RA "Sensor and regulator proteins from the cyanobacterium Synecococcus
RT species PCC7942 that belong to the bacterial signal-transduction
RT protein families: implication in the adaptive response to phosphate
RT limitation.";
RL Mol. Microbiol. 8:81-91(1993).
RN [2]
RP CHARACTERIZATION.
RX MEDLINE-94209219; Pubmed-8157591;
RA Nagaya M., Alba H., Mizuno T.;
RT "The sphr product, a two-component system response regulator protein,
RT regulates phosphate assimilation in Synecococcus sp. strain PCC 7942
RT by binding to two sites upstream from the phoA promoter.";
RL J. Bacteriol. 176:2210-2215(1994).
CC -1- FUNCTION: MEMBER OF THE TWO-COMPONENT REGULATORY SYSTEM SPHR/SPHS.
CC RESPONSE REGULATOR. INVOLVED IN INDUCIBLE PRODUCTION OF ALKALINE
CC PHOSPHATASE IN RESPONSE TO PHOSPHATE LIMITATION AS IT IS DIRECTLY
CC INVOLVED IN THE REGULATION OF PHO A TRANSCRIPTION IN RESPONSE TO
CC PHOSPHATE LIMITATION. BINDS TO TWO DISTINCT SITES UPSTREAM FROM
CC THE PHO A PROMOTER.
CC -1- PM: PHOSPHORYLATED BY SPHS.
CC -1- SIMILARITY: THE N-TERMINAL REGION IS SIMILAR TO THAT OF OTHER
CC REGULATORY COMPONENTS OF SENSORY TRANSDUCTION SYSTEMS.
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DR EMBL: D13172; BAA02453.1; -;
DR PIR: S32931; S32931.
DR HSSP: P03025; 10DD.
DR InterPro: IPR001789; Response_reg.
DR InterPro: IPR001867; Trans_reg_C.
DR Pfam: PF000072; response_reg_1.
DR Pfam: PF00486; trans_reg_C_1.
DR SMART: SM00448; REC; 1.
KW Sensory transduction; Phosphorylation; Transcription regulation;
KW DNA-binding; Activator; Phosphate transport.
FT MOD_RES 83
FT SEQUENCE 257 AA; 29012 MW; A33FDE257044BEB6 CMC64;
PHOSPHORYLATION (BY SIMILARITY).

Query Match 31.5%; Score 46; DB 1; Length 257;
 Best Local Similarity 41.7%; Pred. No. 12;
 Matches 10; Conservative 3; Mismatches 11; Indels 0; Gaps 0;

OY 4 PRSPSLTTKAVLLVRKFPSPAE 27
 DB 134 PRGTRELVARCRALLRSONOPAE 157

RESULT 13
 MN2_KLUUA STANDARD; PRT: 328 AA.

AC Q00974; 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE UDP-N-ACETYLGLUCOSAMINE TRANSPORTER (GOLGI UDP-GLCNAC TRANSPORTER).
 GN MN2.
 OS Kluyveromyces lactis (Yeast).
 CC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 CC Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
 CC NCBI_TaxID=28985;
 CC [1]
 CC SEQUENCE FROM N.A.
 RC STRAIN-MG1/2;
 RX MEDLINE=96234073; PubMed=8650202;
 RA Abelson C., Robbins P.W., Hirschberg C.B.;
 RT "Molecular cloning of the Golgi apparatus uridine diphosphate-N-
 acetylglucosamine transporter from Kluyveromyces lactis";
 RL Proc. Natl. Acad. Sci. U.S.A. 93:5963-5968(1996).
 CC -1- FUNCTION: TRANSPORTS URIDINE DIPHOSPHATE-N-ACETYLGLUCOSAMINE FROM
 THE CYTOSOL INTO GOLGI VESICLES WHERE GLYCOSYLTRANSFERASES
 FUNCTION.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. GOLGI.
 CC -1- SIMILARITY: BELONGS TO THE NUCLEOTIDE-SUGAR TRANSPORTER FAMILY.
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 CC -----
 CC DR EMBL; AF106080; AAC49313.1; -
 CC KM Transpos; Sugar transport; Transmembrane; Golgi stack.
 CC FT TRANSMM 1 21 POTENTIAL.
 CC FT TRANSMM 30 50 POTENTIAL.
 CC FT TRANSMM 66 86 POTENTIAL.
 CC FT TRANSMM 98 118 POTENTIAL.
 CC FT TRANSMM 122 142 POTENTIAL.
 CC FT TRANSMM 166 186 POTENTIAL.
 CC FT TRANSMM 198 218 POTENTIAL.
 CC FT TRANSMM 241 261 POTENTIAL.
 CC FT TRANSMM 274 294 POTENTIAL.
 CC FT TRANSMM 318 338 POTENTIAL.
 CC SQ SEQUENCE 328 AA; 36666 MW; 93A31PACA804D1EF CRC64;

Query Match 31.5%; Score 46; DB 1; Length 328;
 Best Local Similarity 62.5%; Pred. No. 16;
 Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 6 SPPSLTTKAVLLVRKE 21
 DB 270 NTDALFLSVLLVRKE 285

RESULT 14
 YKUS_CAEEL STANDARD; PRT: 375 AA.

AC Q17778; 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE HYPOFETICAL 41.5 KDA PROTEIN C07B5.5 IN CHROMOSOME X PRECURSOR.
 GN C07B5.5.
 OS Caenorhabditis elegans.
 CC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 CC Rhabditidae; Pelodierinae; Caenorhabditis.
 CC NCBI_TaxID=6239;
 CC [1]
 CC SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA Kershaw J.;
 RL Submitted (OCT-1994) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE DNASE II FAMILY.
 CC -----
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 CC -----
 CC DR EMBL; Z46266; CAA66412.1; -
 CC DR WormPeP; C07B5.5; CE00895.
 CC KW Hypothetical protein; Signal; Hydrolase.
 CC FT SIGNAL 1 21 POTENTIAL.
 CC FT CHAIN 22 375 HYPOFETICAL PROTEIN C07B5.5.
 CC FT CAROAND 131 131 N-LINKED (GLCNAC...) (POTENTIAL).
 CC SQ SEQUENCE 375 AA; 41540 MW; E05118983291D3F CRC64;

Query Match 31.5%; Score 46; DB 1; Length 375;
 Best Local Similarity 33.3%; Pred. No. 19;
 Matches 9; Conservative 5; Mismatches 13; Indels 0; Gaps 0;

OY 2 WGRSTPSLTTRAVLLVRKFPNSPAED 28
 DB 110 WGSKSTSGIKLEILSNRYSNVTHD 136

RESULT 15
 ITA5_HUMAN STANDARD; PRT: 1049 AA.

AC P08648; 01-AUG-1988 (Rel. 08, Created)
 DT 01-NOV-1988 (Rel. 09, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE INTEGRIN ALPHA-5 PRECURSOR (FIBRONECTIN RECEPTOR ALPHA SUBUNIT)
 GN ITGA5 OR FNRA.
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 CC NCBI_TaxID=9606;
 CC [1]
 CC SEQUENCE FROM N.A.
 RC MEDLINE=88007843; PubMed=2958481;
 RA Argreaves W.S., Suzuki S., Arai H., Thompson K., Pierschbacher M.D.,
 RA Ruoslahti E.;
 RT "Amino acid sequence of the human fibronectin receptor";
 RL J. Cell Biol. 105:1183-1190(1987).
 CC [2]
 CC SEQUENCE OF 16-1049 FROM N.A.
 CC MEDLINE=88163472; PubMed=2450560;
 CC RA Fitzgerald L.A., Ponce M., Steiner B., Rall S.C., Bennett J.S.,
 CC RA Phillips D.R.;
 CC RT "Comparison of cDNA-derived protein sequences of the human
 CC RT fibronectin and vitronectin receptor alpha-subunits and platelet
 CC RT glycoprotein IIb";
 CC RT Biochemistry 26:8158-8165(1987).

RN [3] SEQUENCE OF 821-1049 FROM N.A.
 RP MEDLINE-87008489; PubMed-2944883;
 RA Argaves W.S., Pyela R., Suzuki S., Millan J.L., Pierschbacher M.D.,
 RT Rosenthal E.,
 RT "CDNA sequences from the alpha subunit of the fibronectin receptor
 RT predict a transmembrane domain and a short cytoplasmic peptide";
 RT J. Biol. Chem. 261:12922-12924(1986).
 RN [4]
 RP SEQUENCE OF 42-55.
 RX MEDLINE-87204112; PubMed-3033641;
 RA Takada Y., Strominger J.L., Hemler M.E.,
 RT "The very late antigen family of heterodimers is part of a
 RT superfamily of molecules involved in adhesion and embryogenesis";
 RT Proc. Natl. Acad. Sci. U.S.A. 84:3239-3243(1987).
 CC -1- FUNCTION: INTEGRIN ALPHA-5/BETA-1 IS A RECEPTOR FOR FIBRONECTIN
 CC AND FIBRINOGEN. IT RECOGNIZES THE SEQUENCE R-G-D IN ITS LIGANDS.
 CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA SUBUNIT. THE ALPHA
 CC SUBUNIT IS COMPOSED OF AN HEAVY AND A LIGHT CHAIN LINKED BY A
 CC DISULFIDE BOND. ALPHA-5 ASSOCIATES WITH BETA-1.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- SIMILARITY: BELONGS TO THE INTEGRIN ALPHA CHAIN FAMILY.
 CC -1- DATABASE: NAME-PROT; NONP-CD guide CDA9e entry;
 CC WWW-<http://www.ncbi.nlm.nih.gov/prot/ed/cda9e.htm>.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: X06256; CAA52601.1; -.
 DR EMBL: M13918; AA52467.1; ALT_SEQ.
 DR PIR: A24697; A24697.
 DR PIR: A27079; A27079.
 DR PIR: E28018; E28018.
 DR HSSP: P11215; 1A8X.
 DR GlycoSiteDB: P08648; -.
 DR MIM: 135620; -.
 DR InterPro: IPR000413; Integrin_alpha.
 DR Pfam: PF01839; FG-GAP 5.
 DR Pfam: PF00357; Integrin_A_1.
 DR PRINTS: PRO1185; INTEGRINA.
 DR SMART: SM00191; Int_alpha; 5.
 DR PROSITE: PS00242; INTEGRIN_ALPHA; 1.
 KW Integrin; Cell adhesion; Receptor; Glycoprotein; Transmembrane;
 KW Signal; Extracellular matrix; Cytoskeleton; Calcium; Repeat.
 FT SIGNAL 1 41
 FT CHAIN 42 1049 INTEGRIN ALPHA-5.
 FT CHAIN 42 894 INTEGRIN ALPHA-5 HEAVY CHAIN.
 FT CHAIN 895 1049 INTEGRIN ALPHA-5 LIGHT CHAIN.
 FT DOMAIN 42 995 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 996 1021 POTENTIAL.
 FT DOMAIN 1022 1049 CYTOPLASMIC (POTENTIAL).
 FT REPEAT 57 119 FG-GAP 1.
 FT REPEAT 131 198 FG-GAP 2.
 FT REPEAT 199 256 FG-GAP 3.
 FT REPEAT 269 322 FG-GAP 4.
 FT REPEAT 323 389 FG-GAP 5.
 FT REPEAT 390 449 FG-GAP 6.
 FT REPEAT 453 505 FG-GAP 7.
 FT CA_BIND 334 342 POTENTIAL.
 FT CA_BIND 401 409 POTENTIAL.
 FT CA_BIND 465 473 POTENTIAL.
 FT SITE 1024 1028 GFEFR MOTIF.
 FT DISULFID 99 108 BY SIMILARITY.
 FT DISULFID 156 176 BY SIMILARITY.
 FT DISULFID 192 205 BY SIMILARITY.
 FT DISULFID 513 522 BY SIMILARITY.
 FT DISULFID 528 584 BY SIMILARITY.

FT	DISULFID	645	651	BY SIMILARITY.
FT	DISULFID	718	731	BY SIMILARITY.
FT	DISULFID	869	911	INTERCHAIN (BY SIMILARITY).
FT	DISULFID	916	921	BY SIMILARITY.
FT	CARBOHYD	84	84	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	182	182	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	297	297	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	307	307	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	316	316	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	524	524	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	530	530	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	593	593	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	609	609	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	675	675	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	712	712	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	724	724	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	773	773	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	868	868	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CONFLICT	26	26	V -> L (IN REF. 2).
FT	CONFLICT	33	33	V -> L (IN REF. 2).
SO	SEQUENCE	1049 AA;	114508 MW;	C3C2CFD0B3739CBB CRC64;

QY	2	WGPRSTPLTKAVLLV	18
DB	17	WGPRRRPVPVLLLLLV	33

Search completed: December 19, 2001, 16:26:20
 Job time: 575 sec

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OM protein - protein search, using sw model

Run on: December 19, 2001, 16:25:28 ; Search time 157.32 Seconds
(without alignments)
26.034 Million cell updates/sec

Title: US-09-202-104A-11
Perfect score: 146
Sequence: 1 EMGPRSTPSLTTRKAVLLVRRKQNSPAED 28

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database :
- 1: SPTRMBL_17:*
 - 2: sp_archaea:*
 - 3: sp_bacteria:*
 - 4: sp_fungi:*
 - 5: sp_human:*
 - 6: sp_invertebrate:*
 - 7: sp_mhc:*
 - 8: sp_organelle:*
 - 9: sp_phage:*
 - 10: sp_plant:*
 - 11: sp_rodent:*
 - 12: sp_virus:*
 - 13: sp_vertebrate:*
 - 14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	59	40.4	627	10 Q9ATQ0	Q9atq0 triticum ae
2	56	38.4	242	2 Q9PBU3	Q9pbu3 xyliella fas
3	54	37.0	304	10 Q9FTG1	Q9ftg1 oryza sativ
4	54	37.0	638	10 Q9ATG5	Q9atg5 triticum ae
5	54	37.0	663	10 Q9FE96	Q9fe96 oryza sativ
6	54	37.0	1269	5 Q9VD17	Q9vd17 drosophila
7	53.5	36.6	534	10 Q9FMT4	Q9fmt4 arabidopsis
8	53	36.3	136	2 Q9A2S3	Q9a2s3 caulobacter
9	52	35.6	630	10 Q9ARW8	Q9arw8 oryza sativ
10	51.5	35.3	317	11 Q9PDU9	Q9pdu9 rattus norv
11	51	34.9	292	2 Q9FAE2	Q9fae2 comamonas t
12	51	34.9	635	10 Q9FUD1	Q9fud1 oryza sativ
13	51	34.9	636	10 Q9FTZ8	Q9ftz8 oryza sativ
14	51	34.9	643	10 Q9FUD4	Q9fud4 oryza sativ
15	51	34.9	648	10 Q9FER4	Q9fer4 oryza sativ
16	51	34.9	650	10 Q9LIS7	Q9lis7 oryza sativ
17	51	34.9	656	10 Q9M576	Q9m576 oryza sativ
18	50	34.2	413	10 Q9ZD06	Q9zd06 oryza sativ
19	50	34.2	652	10 Q9ARM6	Q9arm6 oryza sativ

20	50	34.2	657	10 Q9SWF1	Q9swf1 oryza sativ
21	50	34.2	657	10 Q9LIS5	Q9lis5 oryza sativ
22	49	33.6	301	4 Q9UJA2	Q9uja2 homo sapien
23	49	33.6	344	10 Q9FUD7	Q9fud7 oryza sativ
24	49	33.6	535	1 Q9HLL1	Q9hll1 thermoplas
25	49	33.6	636	10 P93604	P93604 triticum ae
26	49	33.6	641	10 Q9ATG6	Q9atg6 triticum ae
27	49	33.6	912	13 Q9I452	Q9i452 oncorhynch
28	48.5	33.2	442	4 Q9S932	Q9s932 homo sapien
29	48	32.9	265	1 Q9S891	Q9s891 pyrococcus
30	48	32.9	269	5 Q22277	Q22277 caenorhabdi
31	48	32.9	352	10 Q9XGY6	Q9xgy6 simmondsia
32	48	32.9	630	10 Q9XHQ4	Q9xhq4 hordeum vul
33	48	32.9	909	5 Q19857	Q19857 caenorhabdi
34	47	32.2	160	2 Q9RKV5	Q9rkv5 streptomyce
35	47	32.2	312	2 Q9FC67	Q9fc67 streptomyce
36	47	32.2	566	5 Q9W5A9	Q9w5a9 drosophila
37	47	32.2	938	4 Q13111	Q13111 homo sapien
38	47	32.2	938	4 Q9UJY8	Q9ujy8 homo sapien
39	47	32.2	938	4 Q9UJY8	Q9ujy8 homo sapien
40	47	32.2	1001	4 Q9NVH8	Q9nvh8 homo sapien
41	46.5	31.8	355	2 Q9ANE3	Q9ane3 bradyrhizob
42	46.5	31.8	374	2 Q9KMW6	Q9kmw6 vibrio chol
43	46.5	31.8	811	10 Q9LW59	Q9lw59 arabidopsis
44	46.5	31.8	832	12 Q11885	Q11885 hepatitis b
45	46.5	31.8	832	12 Q67874	Q67874 hepatitis b

ALIGNMENTS

RESULT 1	Q9ATQ0	PRELIMINARY:	PRT:	627 AA.
AC	Q9ATQ0:			
DT	01-JUN-2001 (TREMBLrel. 17, Created)			
DT	01-JUN-2001 (TREMBLrel. 17, Last sequence update)			
DT	01-JUN-2001 (TREMBLrel. 17, Last annotation update)			
DE	LRK14.			
GN	LRK14.			
OS	Triticum aestivum (Wheat).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;			
OC	Triticeae; Triticum.			
OX	NCBI_TaxID=4565;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=21140315; PubMed=11244111;			
RA	Feuillet C., Penger A., Gellner K., Mast A., Keller B.;			
RT	"Molecular Evolution of Receptor-Like Kinase Genes in Hexaploid Wheat.			
RT	Independent Evolution of Orthologs after Polyploidization and			
RT	Mechanisms of Local Rearrangements at Paralogous Locl.,"			
RL	Plant Physiol. 125:1304-1313(2001).			
DR	EMBL; AF325198; AAK20743.1; "			
SO	SEQUENCE 627 AA; 70483 MW; 9D38A872D19F64FA CRC64;			
Query Match	40.4%;	Score 59;	DB 10;	Length 627;
Best Local Similarity	43.5%;	Pred. No. 1;		
Matches 10;	Conservative	5;	Mismatches 8;	Indels 0;
			Gaps 0;	
QY	1 EMGPRSTPSLTTRKAVLLVRRKQNSPAED 23			
DB	596 QMPPRRPSMTKVVNMLKGFQF 618			
RESULT 2	Q9PBU3	PRELIMINARY:	PRT:	242 AA.
AC	Q9PBU3:			
DT	01-OCT-2000 (TREMBLrel. 15, Created)			
DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)			
DT	01-MAR-2001 (TREMBLrel. 16, Last annotation update)			

DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE PUTATIVE RECEPTOR KINASE.
GN P0698G03.12 OR P0463F06.31.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Euphorbiaceae; Oryzaeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. NIPPONBARE;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nippobare(GA3) genomic DNA, chromosome 1, PAC
clone:p0698G03.12";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. NIPPONBARE;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nippobare(GA3) genomic DNA, chromosome 1, PAC
clone:p0463F06.31";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP002747; BAB1733.1; -;
DR EMBL; AP002867; BAB17139.1; -;
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR002290; Ser_thr_kin_actsite.
DR InterPro: IPR001245; Tyr_kin.
DR Pfam: PF00069; pkinase; 1.
DR SMART; SM00221; STYK; 1.
DR SMART; SM00220; STYK; 1.
DR SMART; SM00219; TYRK; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR ATP-binding; Kinase; Receptor; Transferase.
SQ SEQUENCE 663 AA; 74660 MW; 65D0EC3C260ACD57 CRC64;

Query Match 37.0%; Score 54; DB 10; Length 663;
Best Local Similarity 39.1%; Pred. No. 6.4;
Matches 9; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

OY 1 EWGPRSTPLTKAVILVKKFQ 23
DB 624 QWNPRLPMTKVVNLTGLQN 646

RESULT 6
ID Q9VDI7 PRELIMINARY; PRT; 1269 AA.
AC Q9VDI7;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE CG17269 PROTEIN.
GN CG17269.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Eukaryota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RA MEDLINE-20196006; PubMed-10731132;
RA Adams M.D., Ceiniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazek R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Aydayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,
RA Balles R.M., Basu A., Baxendale J., Bayraktaroglu I., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burris J.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Daveport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Garfield A.E., Gary N.S., Gelbart W.M., Glasser K.,
RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Idegawa C.,
RA Jaitani M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svitskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou S., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
DR EMBL; AE003732; AAF55806.1; -;
DR Flybase; FBgn0038827; CG17269.
SQ SEQUENCE 1269 AA; 143662 MW; 74A2170AFD03EAO CRC64;

Query Match 37.0%; Score 54; DB 5; Length 1269;
Best Local Similarity 45.8%; Pred. No. 12;
Matches 11; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

OY 5 RSPSLTKAVILVKKFQNSPA 28
DB 423 KSPSLTKAVILVKKFQNSPA 446

RESULT 7
ID Q9FMT4 PRELIMINARY; PRT; 534 AA.
AC Q9FMT4;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE SIMILARITY TO UNKNOWN PROTEIN.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosida II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=COLIMBIA;
RA MEDLINE-98162728; PubMed-9501997;
RA Nakamura Y., Sato S., Kaneko T., Kotani H., Asamizu E., Miyajima N.,
RA Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. III.
RT Sequence features of the regions of 1,191,918 bp covered by seventeen
RT physically assigned P1 clones.";
RL DNA Res. 4:401-414(1997).
DR EMBL; AB007650; BAB08296.1; -;
DR InterPro: IPR003121; SWIB.
DR Pfam; PF02201; SWIB; 1.
DR SMART; SM00151; SWIB; 1.
SQ SEQUENCE 534 AA; 59270 MW; 4231FP2324C18D9D CRC64;

Query Match 36.6%; Score 53.5; DB 10; Length 534;
 Best Local Similarity 52.2%; Pred. No. 6.2;
 Matches 12; Conservative 4; Mismatches 6; Indels 1; Gaps 1;

QY 3 GPRSTPSLTTRKAVLVKRFQNSP 25
 DB 93 GP-SSPSLTTPGSLMKRFOOKP 114

RESULT 8

Q9A2S3 PRELIMINARY; PRT; 136 AA.
 AC Q9A2S3;
 DT 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE HYPOTHETICAL PROTEIN CC3483.
 GN CC3483.
 OS Caulobacter crescentus.
 OC Bacteria; Proteobacteria; alpha subdivision; Caulobacter group;
 OC Caulobacter.
 OX NCBI_TaxID=69394;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21173696; PubMed=11259647;
 RA Nielsen W.C., Feldblum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
 RA Elesen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
 RA Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,
 RA Deboy R.T., Dodson R.J., Durkin A.S., Gwin M.L., Haft D.H.,
 RA Kolony J.F., Sait J., Craven M.B., Khouri H., Shetty J., Berry K.,
 RA Uetebach T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O.,
 RA Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;
 RT "Complete genome sequence of Caulobacter crescentus."
 RT Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
 DR EMBL: AEO06007; AAK25445.1; -.
 KW Hypothetical protein; Complete proteome.
 DR TIGR: CC3483; -.
 SQ SEQUENCE 136 AA; 15352 MW; ED4D2DF525776D23 CRC64;

Query Match 36.3%; Score 53; DB 2; Length 136;
 Best Local Similarity 46.2%; Pred. No. 1.9;
 Matches 12; Conservative 2; Mismatches 12; Indels 0; Gaps 0;

QY 2 WGRSTPSLTTRKAVLVKRFQNSPAE 27
 DB 6 WSDRLAPSLDPAVLAKQAFDLPAP 31

RESULT 9

Q9ARM8 PRELIMINARY; PRT; 630 AA.
 AC Q9ARM8;
 DT 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE PUTATIVE RECEPTOR KINASE.
 GN CJ1212_B09.2.
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Eriatoidae; Oryzaceae; Oryza.
 OX NCBI_TaxID=4530;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. NIPPONBARE;
 RA Sasaki T., Matsumoto T., Yamamoto K.;
 RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, BAC
 clone:CU1212_B09."
 RT Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AP003338; BAB39435.1; -.
 KW Receptor; Kinase.
 SQ SEQUENCE 630 AA; 71067 MW; 74E038CD370FAB54 CRC64;

Query Match 35.6%; Score 52; DB 10; Length 630;
 Best Local Similarity 34.8%; Pred. No. 12;
 Matches 8; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

QY 1 EWGRSTPSLTTRKAVLVKRFQNS 23
 DB 591 QWNRNRPMSMTKVVMITGRLO 613

RESULT 10

Q99PJ9 PRELIMINARY; PRT; 317 AA.
 AC Q99PJ9;
 DT 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE ZINC FINGER PROTEIN HIT-4.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SPRAGUE-DAWLEY; TISSUE=BRAIN;
 RA Hirano A., Araki K., Nawa H.;
 RT "Cloning and characterization of a novel transcription factor HIT-4 in
 the brain."
 RT Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF277900; AAG53886.1; -.
 SQ SEQUENCE 317 AA; 36203 MW; C560BE63E040769 CRC64;

Query Match 35.3%; Score 51.5; DB 11; Length 317;
 Best Local Similarity 42.3%; Pred. No. 7.4;
 Matches 11; Conservative 5; Mismatches 9; Indels 1; Gaps 1;

QY 2 WGRSTP-SLTTRKAVLVKRFQNSPA 26
 DB 194 WGRSSPQSLSPTKTRRLMTAA 219

RESULT 11

Q9FAE2 PRELIMINARY; PRT; 292 AA.
 AC Q9FAE2;
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
 DE TESB, ORF1, ORF2, ORF3 GENES, COMPLETE CDS.
 OS Comamonas testosteroni (Pseudomonas testosteroni).
 OC Bacteria; Proteobacteria; beta subdivision; Comamonadaceae; Comamonas.
 OX NCBI_TaxID=285;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=TA441;
 RA Horinouchi M., Yamamoto T., Taguchi K., Arai H., Kudo T.;
 RT "Cloning of genes involved in testosterone degradation in Comamonas
 testosteroni TA441: a meta-cleavage enzyme and four putative
 proteins."
 RT Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AB040808; BAB15810.1; -.
 SQ SEQUENCE 292 AA; 32067 MW; 698F65FFD197656A CRC64;

Query Match 34.9%; Score 51; DB 2; Length 292;
 Best Local Similarity 40.7%; Pred. No. 8.2;
 Matches 11; Conservative 3; Mismatches 7; Indels 6; Gaps 1;

QY 2 WGRSTPSLTTRKAVLVKRFQNSPAED 28
 DB 26 WGRPKP-----MALVRELLRSPVKD 46


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RESULT 12
ID Q9FU01 PRELIMINARY: PRT: 635 AA.
AC Q9FU01;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE PUTATIVE RECEPTOR KINASE.
GN P0698G03.29.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV, NIPPONBARE;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
clone:P0698G03."
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP002747; BAB17345.1;
DR InterPro: IPR000719; Euk_kinase.
DR InterPro: IPR002290; Ser_thr_kin_actsite.
DR Pfam: PF00069; pkinase; 1.
DR SMART; SM00221; STYKC; 1.
DR SMART; SM00219; TYRKC; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR ATP-binding; Kinase; Receptor; Transferase.
SQ SEQUENCE 635 AA; 71171 MW; 6A692134F6F1B83 CRC64;

Query Match 34.9%; Score 51; DB 10; Length 635;
Best Local Similarity 34.8%; Pred. No. 18;
Matches 8; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

QY 1 EMGPRSTPLTTKAVLVKRFON 23
:|::||:|:|:|
Db 596 QMNPKNRPSMTKVVMILGRLO 618

RESULT 13
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AC Q9FTZ8;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE PUTATIVE RECEPTOR KINASE.
GN P0698G03.32.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV, NIPPONBARE;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
clone:P0698G03."
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP002747; BAB17348.1;
DR InterPro: IPR000719; Euk_kinase.
DR InterPro: IPR002290; Ser_thr_kin_actsite.
DR Pfam: PF00069; pkinase; 1.
DR SMART; SM00221; STYKC; 1.
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DR SMART; SM00220; S_TKC; 1.
DR SMART; SM00219; TYRKC; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR ATP-binding; Kinase; Receptor; Transferase.
SQ SEQUENCE 636 AA; 70968 MW; E6B05D9E1DF43462 CRC64;

Query Match 34.9%; Score 51; DB 10; Length 636;
Best Local Similarity 34.8%; Pred. No. 18;
Matches 8; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

QY 1 EMGPRSTPLTTKAVLVKRFON 23
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Db 588 QMNPKNRPSMTKVVMILGRLO 610

RESULT 14
ID Q9FU04 PRELIMINARY: PRT: 643 AA.
AC Q9FU04;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE PUTATIVE RECEPTOR KINASE.
GN P0698G03.26.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV, NIPPONBARE;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
clone:P0698G03."
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP002747; BAB17342.1;
DR InterPro: IPR000719; Euk_kinase.
DR InterPro: IPR002290; Ser_thr_kin_actsite.
DR Pfam: PF00069; pkinase; 1.
DR SMART; SM00221; STYKC; 1.
DR SMART; SM00220; S_TKC; 1.
DR SMART; SM00219; TYRKC; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR ATP-binding; Kinase; Receptor; Transferase.
SQ SEQUENCE 643 AA; 71525 MW; BFB45CB172A6F15A CRC64;

Query Match 34.9%; Score 51; DB 10; Length 643;
Best Local Similarity 34.8%; Pred. No. 18;
Matches 8; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

QY 1 EMGPRSTPLTTKAVLVKRFON 23
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Db 604 QMNPKNRPSMTKVVMILGRLO 626

RESULT 15
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AC Q9FE84;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE PUTATIVE RECEPTOR KINASE.
GN P0698G03.1 OR P0463F06.20.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
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OK protein - protein search, using sw model

Run on: December 19, 2001, 16:21:03 ; Search time 78.52 seconds
(without alignments)
8.025 Million cell updates/sec

Title: US-09-202-104A-11

Perfile score: 146
Sequence: 1 EMGPRSTPSTLTAKAVLVKRFKNSPAED 28

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Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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3: /cgn2_6/ptodata/2/1aa/6A.COMB.pep:*
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6: /cgn2_6/ptodata/2/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	146	100.0	210	4 US-09-043-785-1	Sequence 1, Appl 1
2	146	100.0	323	6 5171840-6	Patent No. 5171840
3	146	100.0	323	6 5480796-6	Patent No. 5480796
4	146	100.0	344	6 5171840-7	Patent No. 5171840
5	146	100.0	344	6 5480796-7	Patent No. 5480796
6	146	100.0	468	4 US-08-795-473B-5	Sequence 5, Appl 1
7	146	100.0	468	6 5171840-2	Patent No. 5171840
8	146	100.0	468	6 5480796-2	Patent No. 5480796
9	119	81.5	386	6 5171840-5	Patent No. 5171840
10	119	81.5	386	6 5480796-5	Patent No. 5480796
11	114	78.1	201	6 5171840-11	Patent No. 5171840
12	45	30.8	272	2 US-08-160-524A-7	Sequence 7, Appl 1
13	43.5	29.8	38	4 US-09-146-950-5	Sequence 5, Appl 1
14	43.5	29.8	38	4 US-09-146-950-21	Sequence 21, Appl 1
15	43.5	29.8	193	4 US-09-146-950-2	Sequence 2, Appl 1
16	43.5	29.8	197	4 US-09-146-950-18	Sequence 18, Appl 1
17	43.5	29.8	283	4 US-08-509-024-2	Sequence 2, Appl 1
18	43.5	29.8	283	4 US-09-333-279-2	Sequence 2, Appl 1
19	43.5	29.8	283	5 PCT-US96-12374-2	Sequence 2, Appl 1
20	43.5	29.8	419	4 US-08-509-024-7	Sequence 7, Appl 1
21	43.5	29.8	419	4 US-09-333-279-7	Sequence 7, Appl 1
22	42.5	29.1	845	6 5196194-17	Patent No. 5196194
23	42	28.8	682	1 US-07-998-003A-107	Sequence 107, App
24	42	28.8	682	1 US-08-453-274B-107	Sequence 107, App
25	42	28.8	682	1 US-08-453-695A-107	Sequence 107, App
26	42	28.8	682	1 US-08-268-161A-107	Sequence 107, App
27	42	28.8	682	2 US-08-453-702A-107	Sequence 107, App

28	42	28.8	682	4 US-09-099-639-107	Sequence 107, App
29	42	28.8	682	5 PCT-US93-12588-107	Sequence 107, App
30	42	28.8	682	5 PCT-US95-08071-107	Sequence 107, App
31	42	28.8	836	1 US-07-998-003A-105	Sequence 105, App
32	42	28.8	836	1 US-08-453-274B-105	Sequence 105, App
33	42	28.8	836	1 US-08-453-695A-105	Sequence 105, App
34	42	28.8	836	2 US-08-268-161A-105	Sequence 105, App
35	42	28.8	836	2 US-08-453-702A-105	Sequence 105, App
36	42	28.8	836	4 US-09-099-639-105	Sequence 105, App
37	42	28.8	836	5 PCT-US93-12588-105	Sequence 105, App
38	42	28.8	836	5 PCT-US95-08071-105	Sequence 105, App
39	42	28.8	904	1 US-07-998-003A-97	Sequence 97, Appl
40	42	28.8	904	1 US-08-453-274B-97	Sequence 97, Appl
41	42	28.8	904	1 US-08-453-695A-97	Sequence 97, Appl
42	42	28.8	904	1 US-08-268-161A-97	Sequence 97, Appl
43	42	28.8	904	2 US-08-453-702A-97	Sequence 97, Appl
44	42	28.8	904	4 US-09-099-639-97	Sequence 97, Appl
45	42	28.8	904	5 PCT-US93-12588-97	Sequence 97, Appl

ALIGNMENTS

RESULT 1
US-09-043-785-1
; Sequence 1, Application US/09043785
; Patent No. 6172042
; GENERAL INFORMATION:
; APPLICANT: CHEBATH, Judith
; APPLICANT: HALIMI, Hubert
; APPLICANT: REVEL, Michel
; TITLE OF INVENTION: SYNTHETIC PEPTIDES THAT INHIBIT IL-6 ACTIVITY
; FILE REFERENCE: Chebath-1
; CURRENT APPLICATION NUMBER: US/09/043,785
; EARLIER FILING DATE: 1998-09-02
; EARLIER APPLICATION NUMBER: PCT/TL96/00119
; EARLIER FILING DATE: 1996-09-26
; EARLIER APPLICATION NUMBER: 115,453
; EARLIER FILING DATE: 1995-09-26
; EARLIER APPLICATION NUMBER: 118,097
; EARLIER FILING DATE: 1996-05-01
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1
; LENGTH: 210
; TYPE: PRT
; ORGANISM: Human
; US-09-043-785-1

Query Match 100.0%; Score 146; DB 4; Length 210;
Best Local Similarity 100.0%; Pred. No. 1.7e-15;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EMGPRSTPSTLTAKAVLVKRFKNSPAED 28
DB 21 EMGPRSTPSTLTAKAVLVKRFKNSPAED 48
RESULT 2
5171840-6
; APPLICANT: KISHIMOTO, TADAMITSU
; TITLE OF INVENTION: RECEPTOR PROTEIN FOR HUMAN B CELL
; STIMULATORY FACTOR-2
; NUMBER OF SEQUENCES: 11
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/298,694
; FILING DATE: 19-JAN-1989
; SEQ ID NO: 6
; LENGTH: 323
5171840-6

Query Match 100.0%; Score 146; DB 6; Length 323;
Best Local Similarity 100.0%; Pred. No. 2.8e-15;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EMGPRSTPLTKAVLVKRFQNSPAED 28
|||||
Db 133 EMGPRSTPLTKAVLVKRFQNSPAED 160

RESULT 3

5480796-6
; Patent No. 5480796
; APPLICANT: KISHIMOTO, TADAMITSU
; TITLE OF INVENTION: ANTIBODIES AGAINST THE RECEPTOR PROTEIN
; FOR HUMAN B CELL STIMULATORY FACTOR-2
; NUMBER OF SEQUENCES: 8
; CURRENT APPLICATION DATA:
; FILING DATE: 02-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 298,694
; FILING DATE: 19-JAN-1989
; SEQ ID NO: 6:
; LENGTH: 323
5480796-6

Query Match 100.0%; Score 146; DB 6; Length 323;
Best Local Similarity 100.0%; Pred. No. 2.8e-15;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EMGPRSTPLTKAVLVKRFQNSPAED 28
|||||
Db 133 EMGPRSTPLTKAVLVKRFQNSPAED 160

RESULT 4

5171840-7
; Patent No. 5171840
; APPLICANT: KISHIMOTO, TADAMITSU
; TITLE OF INVENTION: RECEPTOR PROTEIN FOR HUMAN B CELL
; STIMULATORY FACTOR-2
; NUMBER OF SEQUENCES: 11
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/298,694
; FILING DATE: 19-JAN-1989
; SEQ ID NO: 7:
; LENGTH: 344
5171840-7

Query Match 100.0%; Score 146; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 3.1e-15;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EMGPRSTPLTKAVLVKRFQNSPAED 28
|||||
Db 133 EMGPRSTPLTKAVLVKRFQNSPAED 160

RESULT 5

5480796-7
; Patent No. 5480796
; APPLICANT: KISHIMOTO, TADAMITSU
; TITLE OF INVENTION: ANTIBODIES AGAINST THE RECEPTOR PROTEIN
; FOR HUMAN B CELL STIMULATORY FACTOR-2
; NUMBER OF SEQUENCES: 8
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/907,650
; FILING DATE: 02-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 298,694

; FILING DATE: 19-JAN-1989
; SEQ ID NO: 7:
; LENGTH: 344
5480796-7

Query Match 100.0%; Score 146; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 3.1e-15;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EMGPRSTPLTKAVLVKRFQNSPAED 28
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Db 133 EMGPRSTPLTKAVLVKRFQNSPAED 160

RESULT 6

US-08-795-473B-5
; Sequence 5, Application US/08795473B
; Patent No. 6217858
; GENERAL INFORMATION:
; APPLICANT: Galun, Elhan
; APPLICANT: Nahot, Orit
; APPLICANT: Blum, Herbert E.
; TITLE OF INVENTION: A Pharmaceutical Composition for Treating
; TITLE OF INVENTION: Hepatitis B Virus (HBV) Infection
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Davidson, Davidson and Kappel, LLC
; STREET: 1140 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA

ZIP: 10036
COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MS-DOS EDITOR
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/795,473B
; FILING DATE: 11-FEB-1997
; CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:
; NAME: Davidson, Clifford M.
; REGISTRATION NUMBER: 32,728
; REFERENCE/DOCKET NUMBER: 963.1007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)-997-1028
; TELEFAX: (212)-997-1037
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 468 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
US-08-795-473B-5

Query Match 100.0%; Score 146; DB 4; Length 468;
Best Local Similarity 100.0%; Pred. No. 4.4e-15;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EMGPRSTPLTKAVLVKRFQNSPAED 28
|||||
Db 133 EMGPRSTPLTKAVLVKRFQNSPAED 160

RESULT 7

5171840-2
; Patent No. 5171840
; APPLICANT: KISHIMOTO, TADAMITSU
; TITLE OF INVENTION: RECEPTOR PROTEIN FOR HUMAN B CELL
; STIMULATORY FACTOR-2
; NUMBER OF SEQUENCES: 11

;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/07/298,694
;; FILING DATE: 19-JAN-1989
;; SEQ ID NO:2:
;; LENGTH: 468
5171840-2

Query Match 100.0%; Score 146; DB 6; Length 468;
Best Local Similarity 100.0%; Pred. No. 4.4e-15;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EWGPRSTPSLTTKAVLVKRFQNSPAED 28
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DB 133 EWGPRSTPSLTTKAVLVKRFQNSPAED 160

RESULT 8
5480796-2
; Patent No. 5480796
; APPLICANT: KISHIMOTO, TADAMITSU
; TITLE OF INVENTION: ANTIBODIES AGAINST THE RECEPTOR PROTEIN
; FOR HUMAN B CELL STIMULATORY FACTOR-2
; NUMBER OF SEQUENCES: 8
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/907,650
; FILING DATE: 02-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 298,694
; FILING DATE: 19-JAN-1989
; SEQ ID NO:2:
; LENGTH: 468
5480796-2

Query Match 100.0%; Score 146; DB 6; Length 468;
Best Local Similarity 100.0%; Pred. No. 4.4e-15;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EWGPRSTPSLTTKAVLVKRFQNSPAED 28
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DB 133 EWGPRSTPSLTTKAVLVKRFQNSPAED 160

RESULT 9
5171840-5
; Patent No. 5171840
; APPLICANT: KISHIMOTO, TADAMITSU
; TITLE OF INVENTION: RECEPTOR PROTEIN FOR HUMAN B CELL
; STIMULATORY FACTOR-2
; NUMBER OF SEQUENCES: 11
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/298,694
; FILING DATE: 19-JAN-1989
; SEQ ID NO:5:
; LENGTH: 386
5171840-5

Query Match 81.5%; Score 119; DB 6; Length 386;
Best Local Similarity 92.9%; Pred. No. 6.3e-11;
Matches 26; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 3 GPRSTP--SLTTKAVLVKRFQNSPAED 28
|||||
DB 51 GPRSTPWSLTTKAVLVKRFQNSPAED 78

RESULT 10
5480796-5
; Patent No. 5480796
; APPLICANT: KISHIMOTO, TADAMITSU
; TITLE OF INVENTION: ANTIBODIES AGAINST THE RECEPTOR PROTEIN

;; FOR HUMAN B CELL STIMULATORY FACTOR-2
;; NUMBER OF SEQUENCES: 8
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/07/907,650
;; FILING DATE: 02-JUL-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 298,694
;; FILING DATE: 19-JAN-1989
;; SEQ ID NO:5:
;; LENGTH: 386
5480796-5

Query Match 81.5%; Score 119; DB 6; Length 386;
Best Local Similarity 92.9%; Pred. No. 6.3e-11;
Matches 26; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 3 GPRSTP--SLTTKAVLVKRFQNSPAED 28
|||||
DB 51 GPRSTPWSLTTKAVLVKRFQNSPAED 78

RESULT 11
5171840-11
; Patent No. 5171840
; APPLICANT: KISHIMOTO, TADAMITSU
; TITLE OF INVENTION: RECEPTOR PROTEIN FOR HUMAN B CELL
; STIMULATORY FACTOR-2
; NUMBER OF SEQUENCES: 11
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/298,694
; FILING DATE: 19-JAN-1989
; SEQ ID NO:11:
; LENGTH: 201
5171840-11

Query Match 78.1%; Score 114; DB 6; Length 201;
Best Local Similarity 100.0%; Pred. No. 1.8e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EWGPRSTPSLTTKAVLVKRFQ 22
|||||
DB 11 EWGPRSTPSLTTKAVLVKRFQ 32

RESULT 12
US-08-160-524A-7
; Sequence 7, Application US/08160524A
; Patent No. 5851761
; GENERAL INFORMATION:
; APPLICANT: MCADAM, Ruth Anne
; APPLICANT: Dale, Jeremy W.
; APPLICANT: Zainuddin, Zainul Fadzliruddin B.
; APPLICANT: Catly, David
; TITLE OF INVENTION: PROBES, KITS AND METHODS FOR THE
; TITLE OF INVENTION: DETECTION AND DIFFERENTIATION OF MYCOBACTERIA
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert,
; ADDRESSEE: Attn: Walter H. Dreger
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/160,524A

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:      FILING DATE: 01-DEC-1993
:      CLASSIFICATION: 435
:      PRIOR APPLICATION DATA:
:      APPLICATION NUMBER: US 07/752,661
:      FILING DATE: 18-OCT-1991
:      PRIOR APPLICATION DATA:
:      APPLICATION NUMBER: GB 8903968.9
:      FILING DATE: 22-FEB-1989
:      PRIOR APPLICATION DATA:
:      APPLICATION NUMBER: GB 9000411.0
:      FILING DATE: 09-JAN-1990
:      PRIOR APPLICATION DATA:
:      APPLICATION NUMBER: PCT/GB90/00276
:      FILING DATE: 22-FEB-1990
:      ATTORNEY/AGENT INFORMATION:
:      NAME: Dreger, Walter H.
:      REGISTRATION NUMBER: 24,190
:      REFERENCE/DOCKET NUMBER: A-55387-1/WHD
:      TELECOMMUNICATION INFORMATION:
:      TELEPHONE: (415) 781-1989
:      TELEFAX: (415) 398-3249
:      TELEX: 910 277299
:      INFORMATION FOR SEQ ID NO: 7:
:      SEQUENCE CHARACTERISTICS:
:      LENGTH: 272 amino acids
:      TYPE: amino acid
:      TOPOLOGY: unknown
:      US-08-106-524A-7

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[illegible]

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RESULT 13
US-09-146-950-5
: Sequence 5, Application US/09146950A
: Patent No. 6287808
: GENERAL INFORMATION:
: APPLICANT: Busfield, Samantha J.
: TITLE OF INVENTION: NOVEL MOLECULES OF THE HERPESVIRUS-ENTRY-MEDIATOR-RELATED
: FILE REFERENCE: 09404/057001
: CURRENT APPLICATION NUMBER: US/09/146,950A
: CURRENT FILING DATE: 1998-09-03
: NUMBER OF SEQ ID NOS: 25
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 5
: LENGTH: 38
: TYPE: PR1
: ORGANISM: Homo sapiens
US-09-146-950-5

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      29.8%; Score 43.5; DB 4; length 38;
Query Match          35.7%; Pred. No.3,2;
Best Local Similarity
Matches 10; Conservative 4; Mismatches 11; Indels 3; Gaps 1
Oy 1 EWGP---RSTPSLTTKAVLVYKFFONSP 25
      :||| |||| :||| | :||
Ob 6 DWGPPWRRSTPRDVLRLVLYLTFLGAP 33

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RESULT 14
US-09-146-950-21
; Sequence 21, Application US/09146950A
; Patent No. 6287808
; GENERAL INFORMATION:

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? APPLICANT: Busfield, Samantha J.
? TITLE OF INVENTION: NOVEL MOLECULES OF THE HERPESVIRUS-ENTRY-MEDIATOR-RELATED
? TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
? FILE REFERENCE: 09404/057001
? CURRENT APPLICATION NUMBER: US/09/146,950A
? CURRENT FILING DATE: 1998-09-03
? NUMBER OF SEQ ID NOS: 25
? SOFTWARE: FastSeq for Windows Version 3.0
? SEQ ID NO 21
? LENGTH: 38
? TYPE: PRT
? ORGANISM: Homo sapiens
US-09-146-950-21

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	29.8%;	Score 43.5;	DB 4;	Length 38;
Best Local Similarity	35.7%;	Pred. No. 3.2;		
Matches 10; Conservative	4;	Mismatches	11;	Indels 3; Gaps 1.
OY	1 EMGP---	RSTPSITTKAVLLVKKRQNSP	25	
	:		:	:
	6 DMGPPNPSTPTDVLRLVLTLYLTFGAP	33		

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RESULT 15
US-09-146-950-2
; Sequence 2, Application US/09146950A
; Patent No. 6287808
; GENERAL INFORMATION:
; APPLICANT: Busfield, Samantha J.
; TITLE OF INVENTION: NOVEL MOLECULES OF THE HERPESVIRUS-ENTRY-MEDIATOR-RELATED
; FILE REFERENCE: 09404/057001
; CURRENT APPLICATION NUMBER: US/09/146,950A
; CURRENT FILING DATE: 1998-09-03
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 193
; TYPE: PRN
; ORGANISM: Homo sapiens
US-09-146-950-2

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Query Match          29.8%   Score 43.5; DB 4; Length 193;
Best Local Similarity 35.7%; Pred. No. 22;
Matches    10; Conservative    4; Mismatches    11; Indels    3; Gaps    1
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OY 1 ENGP---RSPSLITKAVLVKKRQNSP 25
 :||| |||| :||| | :|
Db 6 DMGPPWRSPRTDVLRLVLYLTFGAP 33

Search completed: December 19, 2001, 16:21:03
Job time: 408 sec

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